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From: Whiteman, Brian
Sent: Tuesday, August 12, 2003 9:43 AM
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Subject: seq search

09/380,546 11/29/99 Wallach et al.

search seq id nos: 1-4 against us patent and us patent application databases

Thanks,
Brian Whiteman, 11e12
Patent Examiner - Art Unit 1635
United States Patent and Trademark Office
Crystal Mall 1, 11A16
(703) 305-0775

Searcher: _____
Phone: _____
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Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
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Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
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OM nucleic - nucleic search, using sw model

Run on: August 22, 2003, 05:36:22 ; Search time 618.438 Seconds
(without alignments)
9790.540 Million cell updates/sec

Title: US-09-380-546A-1
Perfect score: 2243
Sequence: 1 ggcgcgcggcattacaat.....ctcttaaaaaaaaaa 2243

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_19Jun03:*

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- 3: /SIDSL1/gcgdata/geneseq/geneseq-emb1/NA1982.DAT:*
- 4: /SIDSL1/gcgdata/geneseq/geneseq-emb1/NA1983.DAT:*
- 5: /SIDSL1/gcgdata/geneseq/geneseq-emb1/NA1984.DAT:*
- 6: /SIDSL1/gcgdata/geneseq/geneseq-emb1/NA1985.DAT:*
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- 14: /SIDSL1/gcgdata/geneseq/geneseq-emb1/NA1993.DAT:*
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- 20: /SIDSL1/gcgdata/geneseq/geneseq-emb1/NA1999.DAT:*
- 21: /SIDSL1/gcgdata/geneseq/geneseq-emb1/NA2000.DAT:*
- 22: /SIDSL1/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT:*
- 23: /SIDSL1/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:*
- 24: /SIDSL1/gcgdata/geneseq/geneseq-emb1/NA2002.DAT:*
- 25: /SIDSL1/gcgdata/geneseq/geneseq-emb1/NA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2243	100.0	2243	19 AAV52968	Human G1 protein i
2	2169.4	96.7	2352	21 AAV47926	Human apoptosis as
3	2165.6	96.5	2188	19 AAV31375	Human FIN-1 encodi
4	2124	94.7	2143	20 AAV39040	Human FLICE-like i
5	2124	94.7	2143	24 ABL52333	Human FLIP-c encod
6	2123	94.7	2143	19 AAV61937	Human CFLIP-L DNA.
7	2006.8	89.5	2034	19 AAV44806	I-FLICE-1 coding s
8	1991	88.8	2040	21 AAV48769	Human CLARP coding

9	1979.2	88.2	1996	20 AAX25508	Human MACH related
10	1952.2	87.0	2045	19 AAV50436	Human Casper gene.
11	1708.6	76.2	2084	21 AAV56987	Usurin-alpha poly
12	1619.2	72.2	1750	20 AAV74136	Human FLAME-1 CDNA
13	1619.2	72.2	1750	24 AAV43202	Human FLAME-1 CDNA
14	1439.2	64.2	1517	21 AAV43301	FLIP with detectab
15	1300.8	58.0	1389	21 AAV56988	Usurin-beta polyp
16	1209.6	53.9	1319	22 AAD16535	Human novel protei
17	1209.6	53.9	1319	22 AAS34790	cDNA encoding nove
18	1209.6	53.9	1319	24 ABS64125	Human apoptosis re
19	1087.4	48.5	1373	19 AAV52969	Human G1 protein i
20	1025.2	45.7	1308	20 AAX25510	Human MACH related
21	1019.2	45.4	2420	20 AAX25509	Human MACH related
22	899.6	40.1	2597	19 AAV44807	I-FLICE-2 coding s
23	849.6	37.9	2413	24 ABL52342	Mouse FLIP-c encod
24	849.6	37.9	2452	19 AAV61938	Mouse CFLIP-L DNA.
25	813.6	36.3	2770	24 ABL52325	Mouse FLIP-c encod
26	813.6	36.3	2770	25 AAV72474	Nucleotide sequenc
27	791.4	35.3	879	21 AAV56989	Usurin-gamma poly
28	731.8	32.6	1062	20 AAX39041	Human FLICE-like i
29	731.8	32.6	1062	24 ABL52332	Human FLIP-c encod
30	731.8	32.6	1190	19 AAV61936	Human CFLIP-S DNA.
31	598.4	26.7	834	24 ABL83474	Human cDNA differe
32	543.6	24.2	8003	22 AAK85877	Human immune/haema
33	408	18.2	38358	22 AAK73535	Human immune/haema
34	337.8	15.1	1611	24 ABL52343	Mouse FLIP-c encod
35	311.4	13.9	3114	19 AAV46493	Human FLIP DNA. H
36	276	12.3	437	22 ABA44441	Human breast cell
37	276	12.3	437	22 ABA54888	Human foetal liver
38	276	12.3	437	22 ABA24654	Probe #3120 for ge
39	276	12.3	437	22 AAK03164	Human brain expres
40	276	12.3	437	22 AAK28614	Human bone marrow
41	276	12.3	437	22 AAI13188	Probe #3121 for ge
42	276	12.3	437	22 AAI34540	Probe #3226 used t
43	276	12.3	437	22 AAT03093	Probe #3084 used t
44	276	12.3	437	23 ABS28210	Human liver single
45	276	12.3	437	24 ABS03125	Human genome-deriv

ALIGNMENTS

RESULT 1
AAV52968
ID AAV52968 standard; cDNA; 2243 BP.
XX
XX AAV52968;
AC
XX
DT 11-JAN-1999 (first entry)
XX
XX Human G1 protein isoform alpha (CASH-alpha) cDNA.
DE
DE G1 protein; CASH-alpha; human; caspase homologue; Fas receptor;
KW modulator; apoptosis; cell death; inflammation; tumour; HIV;
KW therapy; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FT CDS 482..1294
FT /*tag= a
XX
XX WO9839435-A1.
XX
XX 11-SEP-1998.
XX
XX 26-FEB-1998; 98WO-IL00098.
XX
XX 01-MAY-1997; 97IL-0120759.
XX
XX 03-MAR-1997; 97IL-0120367.
XX
XX (YEDA) YEDA RES & DEV CO LTD.
PA
XX

PI Brodianski V, Goltsev Y, Kovalenko A, Varfolomeev E;
PI Wallach D;

XX WPI; 1998-495842/42.

DR P-PSDB; AAW78903.

XX New DNA encoding isoforms of G1 protein which bind MORT-1 - and
PT regulate the effects of FAS and tumour necrosis factor receptors,
PT useful for killing of cells e.g. HIV and cancer cells

XX Claim 3; Fig 1A; 132pp; English.

XX This cDNA sequence codes for the alpha isoform (see AAW78903) of novel
CC human G1 protein. It was isolated from a skin fibroblast cDNA
CC library using a cDNA probe corresponding to the G1 sequence.
CC G1-alpha (also called CASH alpha, CASH being caspase homologue)
CC and a shorter isoform, G1-beta (see AAW78904), represent 2 splice
CC variants of the G1 protein. These G1 proteins are capable of
CC binding to, or interacting directly or indirectly, with MORT-1
CC or with MORT-binding proteins such as Mch4 (CASP-10) and MACH
CC (CASP-8), and thereby of binding to the intracellular domain of
CC the FAS-R receptor, to which MORT-1 binds, or of binding to the
CC intracellular domain of the p55 tumour necrosis factor (TNF)
CC receptor, to which TRADD binds and to which TRADD protein MORT-
CC 1 binds. Hence, they are considered as mediators or modulators of
CC FAS-R having a role in e.g. the signalling process that is initiated
CC by the binding of FAS ligand to FAS-R, and also having a role in
CC the signalling process initiated by the binding of TNF to p55-R.
CC G1 (I) and polypeptide (II), vectors and fragments are used to
CC regulate cell death or inflammatory processes. (II) is used to
CC inhibit cell death, and its inhibitors augment/enhance the
CC processes. (I) and (II) regulate the FAS-R ligand or TNF effect on
CC cells carrying an FAS-R or p55-R. Tumour, HIV-infected or other
CC diseased cells can be treated using a viral vector encoding a viral
CC surface protein, which binds a specific cell surface receptor and a
CC sequence encoding (II), which kills the cell. Antisense
CC oligonucleotides, introduced using the above vector, block the
CC expression of (II) and can also regulate the above effects. These
CC effects can also be regulated using a vector encoding a ribozyme
CC that interacts with a cellular mRNA encoding (II), and allows (II)
CC expression.

XX Sequence 2243 BP; 620 A; 511 C; 603 G; 509 T; 0 other;

Query Match	100.0%	Score 2243;	DB 19;	Length 2243;
Best Local Similarity	100.0%	Pred. No. 0;	Mismatches 0;	Indels 0;
Matches 2243;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY 1	GGACGTCGAGGCAATACAAATCGGAAACCAAGCCATAGCATGAAACAGCGAGCTTGCAGC	60		
DB 1	GGACGTCGAGGCAATACAAATCGGAAACCAAGCCATAGCATGAAACAGCGAGCTTGCAGC	60		
QY 61	CTACCGGACGAGTCTCAACTAAAGGACTCCGGAGCTCCGGAGCTAGGGGTGGGGCTCA	120		
DB 61	CTACCGGACGAGTCTCAACTAAAGGACTCCGGAGCTCCGGAGCTAGGGGTGGGGCTCA	120		
QY 121	CACAGTGAAGTGGCGCTATTGAGCTTTCTCCAGTGCAGCTCAGACACACAGGACCG	180		
DB 121	CACAGTGAAGTGGCGCTATTGAGCTTTCTCCAGTGCAGCTCAGACACACAGGACCG	180		
QY 181	GGAGGAGGTGTAGGAGAGAGCGCGCAACAGCGATCCCGCAGCACCAAGTCCCGTTCC	240		
DB 181	GGAGGAGGTGTAGGAGAGAGCGCGCGCAACAGCGATCCCGCAGCACCAAGTCCCGTTCC	240		
QY 241	AGGCTTTCGGTTTCTTTGCTCCATCTTGGGTGCGCTTTCCCGGCTCTAGGGAGCGAA	300		
DB 241	AGGCTTTCGGTTTCTTTGCTCCATCTTGGGTGCGCTTTCCCGGCTCTAGGGAGCGAA	300		
QY 301	GGCTGAGGTGGCAGCGGACGAGAGTCCGGCCGCGACAGGACGAACCTCCCGACCTGGAAA	360		
DB 301	GGCTGAGGTGGCAGCGGACGAGAGTCCGGCCGCGACAGGACGAACCTCCCGACCTGGAAA	360		
QY 361	GGATTCTGAAGAAATGAAGTCAGCCCTCAGAAATGAAGTTGACTGCCTGGCTTTCC	420		

Db	361	GGATTCTGAAGAAATGAAGTCAGCCCTCAGAAATGAAGTTGACTGCCTGCTGGCTTCC	420
QY	421	TGTTGACTGCCCGGAGCTGTACTGCAAGACCCCTTGTGAGCTTCCCTAGTCTAAGAGTAG	480
Db	421	TGTTGACTGCCCGGAGCTGTACTGCAAGACCCCTTGTGAGCTTCCCTAGTCTAAGAGTAG	480
QY	481	GATGCTGCTGAAGTCAATCCATCAGCTTGAAGAAGCACTTGATACAGATGAGAAGAGAT	540
Db	481	GATGCTGCTGAAGTCAATCCATCAGCTTGAAGAAGCACTTGATACAGATGAGAAGAGAT	540
QY	541	GCTGCTCTTTTGTGCGCGGATGCTTCTATAGATGCTGTTCCACCTAATGTCCAGGACCT	600
Db	541	GCTGCTCTTTTGTGCGCGGATGCTTCTATAGATGCTGTTCCACCTAATGTCCAGGACCT	600
QY	601	TCGGAATATTTACGGGAAGAGGTAAGCTGTCTGCGGGGACTTGGCTGAACCTGCTCTA	660
Db	601	TCGGAATATTTACGGGAAGAGGTAAGCTGTCTGCGGGGACTTGGCTGAACCTGCTCTA	660
QY	661	CAGAGTGAGCGGATTTGACCTGCTCAAGCTATCTTGAAGATGGACAGAAAGCTGTGA	720
Db	661	CAGAGTGAGCGGATTTGACCTGCTCAAGCTATCTTGAAGATGGACAGAAAGCTGTGA	720
QY	721	GACCCACCTGCTCAGGAACCCCTCACCTTGTTCGGACTATAGAGTGTCTGATGCGAGAT	780
Db	721	GACCCACCTGCTCAGGAACCCCTCACCTTGTTCGGACTATAGAGTGTCTGATGCGAGAT	780
QY	781	TGCTGAGGATTTGGATAAATCTGATGTCTCTCATTAATTTTCTCATGAAGATTTACAT	840
Db	781	TGCTGAGGATTTGGATAAATCTGATGTCTCTCATTAATTTTCTCATGAAGATTTACAT	840
QY	841	GGGCCGAGGCAATGAAGCAAGGAAGAGTGTCTTGGACCTTGTGGTGTGAGTTGAGAA	900
Db	841	GGGCCGAGGCAATGAAGCAAGGAAGAGTGTCTTGGACCTTGTGGTGTGAGTTGAGAA	900
QY	901	ACTAAATTTGTTGCCCGCAGATCACTGGAATTTATTAGAAAATGCTTAAGAACATCCA	960
Db	901	ACTAAATTTGTTGCCCGCAGATCACTGGAATTTATTAGAAAATGCTTAAGAACATCCA	960
QY	961	CAGAATAGACCTGAAGACAAAAATCCAGAAGTACAAGCAGTCTGTTCAGAGGACGGAC	1020
Db	961	CAGAATAGACCTGAAGACAAAAATCCAGAAGTACAAGCAGTCTGTTCAGAGGACGGAC	1020
QY	1021	AGTTACAGGAATGTTCTCCAGCAGCAATCCAAAAGAGTCTCAAGGATCCTTCAATAA	1080
Db	1021	AGTTACAGGAATGTTCTCCAGCAGCAATCCAAAAGAGTCTCAAGGATCCTTCAATAA	1080
QY	1081	CTTCAGGCTCCATATATGGGAGAGTAAAGAACAAAGACTTAAGAACAGCTTGGCGCTCA	1140
Db	1081	CTTCAGGCTCCATATATGGGAGAGTAAAGAACAAAGACTTAAGAACAGCTTGGCGCTCA	1140
QY	1141	ACAAGAACAGTGAAGAAATCCATTCAGGAATCAGAAAGCTTTTTCGCTCAGAGCATACC	1200
Db	1141	ACAAGAACAGTGAAGAAATCCATTCAGGAATCAGAAAGCTTTTTCGCTCAGAGCATACC	1200
QY	1201	TGAAGAGATACAAGATGAAGCAAGCCCTTAGGAATCTGCCTGATATCGATTGCAT	1260
Db	1201	TGAAGAGATACAAGATGAAGCAAGCCCTTAGGAATCTGCCTGATATCGATTGCAT	1260
QY	1261	TGCGAATGAGCAGAGCTTCTTCGAGACACCTTCACTTCCCTGGGCTATGAAAGTCAGAA	1320
Db	1261	TGCGAATGAGCAGAGCTTCTTCGAGACACCTTCACTTCCCTGGGCTATGAAAGTCAGAA	1320
QY	1321	ATTCTTGATCTCAGTATGATATCCAGATTTCTTGGCAATTTTCCCTGTATGCC	1380
Db	1321	ATTCTTGATCTCAGTATGATATCCAGATTTCTTGGCAATTTTCCCTGTATGCC	1380
QY	1381	CGAGCACCGAGACTAGCAGAGCTTGTGTGCTCTGGTGGAGGAGGCTCCAGAG	1440
Db	1381	CGAGCACCGAGACTAGCAGAGCTTGTGTGCTCTGGTGGAGGAGGCTCCAGAG	1440
QY	1441	TGTTGATGTTGGGATCAGACTCAGCTCAGGCTCCCGCTGCATCAGATCAGAGGATGTT	1500
Db	1441	TGTTGATGTTGGGATCAGACTCAGCTCAGGCTCCCGCTGCATCAGATCAGAGGATGTT	1500

1441	TGTTGATGGTGTGGATCAGACTCACTCAGGGCTCCCCCTGCATCAATCAGGAGGATGTT	1500
1501	CATGGGAGATTTCATGCCCTTTATCTAGCAGGGAAGCCAAAGATGCTTTTATTTATTCAGAACTA	1560
1501	CATGGGAGATTTCATGCCCTTTATCTAGCAGGGAAGCCAAAGATGCTTTTATTTATTCAGAACTA	1560
1561	TGTTGGTGTTCAGAGGGCCAGCTGGAGAACAGCAGCCTCTTTGGAGGTGGATGGGCCACGGCAT	1620
1561	TGTTGGTGTTCAGAGGGCCAGCTGGAGAACAGCAGCCTCTTTGGAGGTGGATGGGCCACGGCAT	1620
1621	GAAGAAATGTGGAATTCAAAGCTCAGAAAGCAGAGGGCTGTGCACAGTTCACCCGAGAACTGA	1680
1621	GAAGAAATGTGGAATTCAAAGCTCAGAAAGCAGAGGGCTGTGCACAGTTCACCCGAGAACTGA	1680
1681	CTTCTCTCGAGGCTGTGTACTCGGACATGTGCCCTGTGGACAGTCTCACAGCTCACC	1740
1681	CTTCTCTCGAGGCTGTGTACTCGGACATGTGCCCTGTGGACAGTCTCACAGCTCACC	1740
1741	GTCCCTGTACTCGAGTGCCTCTCCAGAAACTTGAGACAAGAAAGAAACGCCCATCTCCT	1800
1741	GTCCCTGTACTCGAGTGCCTCTCCAGAAACTTGAGACAAGAAAGAAACGCCCATCTCCT	1800
1801	GGATCTTCACATTTCAACTCAATGGCTACATGTATGATGGAACAGCAGAGACTTTTCGCCAA	1860
1801	GGATCTTCACATTTCAACTCAATGGCTACATGTATGATGGAACAGCAGAGACTTTTCGCCAA	1860
1861	GGAGAAATATTATGCTCTGGCTGGCAGCACACTCTGAGAAAGAAACTTATCCTCTCCTACAC	1920
1861	GGAGAAATATTATGCTCTGGCTGGCAGCACACTCTGAGAAAGAAACTTATCCTCTCCTACAC	1920
1921	ATAGAAACCAAAAGGCTGGGCGTAGTGGCTCACACTGTAACTCCAGCACTTTGGGAGG	1980
1921	ATAGAAACCAAAAGGCTGGGCGTAGTGGCTCACACTGTAACTCCAGCACTTTGGGAGG	1980
1981	CCAAGGAGGCAGATCATCTTCAGTCAAGGAGTTTCAGACCAAGCCTGGCCCAACATGGTAAA	2040
1981	CCAAGGAGGCAGATCATCTTCAGTCAAGGAGTTTCAGACCAAGCCTGGCCCAACATGGTAAA	2040
2041	CGCTGTCCCTAGTAAAAATGCAAAAATTAGCTGGGTGTGGGTGGGTACTCTGTGTTCCC	2100
2041	CGCTGTCCCTAGTAAAAATGCAAAAATTAGCTGGGTGTGGGTGGGTACTCTGTGTTCCC	2100
2101	AGTTACTTGGGAGGCTGAGTGGGAGGATCTTTTGAACCCAGAGGTTTCAGGGTTCATAGCA	2160
2101	AGTTACTTGGGAGGCTGAGTGGGAGGATCTTTTGAACCCAGAGGTTTCAGGGTTCATAGCA	2160
2161	TGCTGTGATTGTGCCTACGAATAGCCACTGCATACCAACTGGGCAATATAGCAAGATCC	2220
2161	TGCTGTGATTGTGCCTACGAATAGCCACTGCATACCAACTGGGCAATATAGCAAGATCC	2220
2221	CATCTCTTTTAAAAAATAAAAAA 2243	
2221	CATCTCTTTTAAAAAATAAAAAA 2243	

DEPT 7

RESULT 2

AAZ47926
ID AAZ47926 standard; cDNA; 2352 BP.

XX

2000

AC
AAZXX
DT 10-MAR-2000 (first entry)

XX

DE Human apoptosis associated protein HAPOP-1 encoding cDNA.

XX

Human; apoptosis associated protein; HAPOP; diagnosis; cytostatic; antiarteriosclerotic; antiarthritic; hepatotropic; apoptosis regulator; cell proliferative disorder; atherosclerosis; arteriosclerosis; cancer; immune disorder; rheumatoid arthritis; systemic lupus erythematosus; reproductive disorder; tumour; gastrointestinal disorder; cirrhosis; colitis; hepatitis; pancreatitis; ss.

XX

OS Homo sapiens.

XX
PN W09958692-A2.

XX
PD 18-NOV-1999.

XX
PF 11-MAY-1999; 99WO-US10386.

XX
PR 13-MAY-1998; 98US-0078402.

XX
PA (INCY-) INCYTE PHARM INC.

XX PI Hillman JL, Corley NC, Guegler KJ, Patterson C, Baughn M;

XX
DR WPI; 2000-062303/05.
DR P-PSDB; AAY57606.

XX New protein for diagnosing, treating or preventing disorders associated with increased or decreased apoptosis -

XX
PS Claim 7; Page 71-72; 81pp; English.

The present sequence encodes a human apoptosis associated protein designated HAPOP-1. HAPOP proteins are apoptosis regulators which have antiarteriosclerotic, cytostatic, antiarthritic and hepatotropic activity. A pharmaceutical composition comprising HAPOP in conjunction with a carrier, a purified antagonist of HAPOP, vectors and agonists of HAPOP, are administered for diagnosing, treating or preventing disorders associated with increased or decreased apoptosis, e.g. cell proliferative disorders such as atherosclerosis, arteriosclerosis and cancers; immune disorders such as rheumatoid arthritis, systemic lupus erythematosus; reproductive disorders such as prostate cancer, endometrial and ovarian tumours; and gastrointestinal disorders such as cirrhosis, colitis, hepatitis and pancreatitis. The polynucleotides encoding HAPOP proteins may be useful to detect and quantitate expression of HAPOP genes which are correlated with diseases and are also useful to detect differences in the chromosomal location due to translocation, inversion etc., among normal, carrier, or affected individuals. The combination of the therapeutic agents may act synergistically to effect the treatment or prevention of various disorders providing improved efficacy with lower dosages of each agent and thus reducing the potential for adverse side effects.

Sequence 2352 BP; 652 A; 546 C; 628 G; 526 T; 0 other;
SQ
XX

Query Match	96.7%	Score 2169.4;	DB 21;	Length 2352;
Best Local Similarity	99.2%	Pred. NO. 0;		
Matches 2190:	Conservative	0;	Mismatches	16;
			Indels	1;
			Gaps	1

QY 16 ACAATCGGAACCAAGCCATAGCATGAACAGCGAGCTTGCAGCCTCACCAGCAGTCT 75

Db 147 ATAC^TTAGTCACACAAGGCATAGCAGGAACAGCGAGCTTGCAGCCTCACCAGCAGCT^T 206

Qy 76 CAACATAAAGGGAACCTCCGGAGCTAGGGGTGGGGACTCGGCTCACACAGTGAGTGCCGG 135

Db 207 CAACATAAAGGAGACTCCGGGAGCTAGGGTGGGGACTCGGCCCTCACACAGTGAAGTGCCGG 266

QY 136 CTATTGGACUUTTTGTCAGTGACAGCTGAGACAACAAAGACCACGGGAGGAGGTGTAGGA 195

Db 267 CTATTGGACTTTTGTCCAGTGACAGCTGAGACAACAAGGACCACGGGAGGAGGTGTAGGA 326

QY 196 GAGAGCGCGCGGAACACGGATCGCCCAAGCCCAACTCCGGTTCCAGGCTTTCGGTTCT 255

[illegible]

Db	1586	TCAGACTCACTCCGGGGTCCCCCTGCGATCACATCAGAGGATGTTTCATGGGAGATTCAATG	1644
Qy	1516	CCCTTATCTAGCAGGGAAGCAAAAGATGTTTTTTTATTCAGAACTATGTGTTGTCAGAGGG	1575
Db	1646	CCCTTATCTAGCAGGGAAGCAAAAGATGTTTTTTTATTCAGAACTATGTGTTGTCAGAGGG	1705
Qy	1576	CCAGCTGGGAAACAGCAGCCCTCTTTGGAGTGGATGGGCCACGCGATGAAGAATGTGGAATT	1635
Db	1706	CCAGCTGGAGGACAGCAGCCCTCTTTGGAGTGGATGGGCCACGCGATGAAGAATGTGGAATT	1765
Qy	1636	CAAGGCTCAGAAGCAGAGGGCTGTGCACAGTTCCGGAAGAGCTTGACTTCTTCCTGGAGCCT	1695
Db	1766	CAAGGCTCAGAAGCAGAGGGCTGTGCACAGTTCCGGAAGAGCTTGACTTCTTCCTGGAGCCT	1825
Qy	1696	GTGTACTGGGACATGTCCTGCTGGAGCAGTCTCACAGCTCACCGTCCCTGTACCTGCA	1755
Db	1826	GTGTACTGGGACATGTCCTGCTGGAGCAGTCTCACAGCTCACCGTCCCTGTACCTGCA	1885
Qy	1756	GTGCTCTCCAGAACTGAGACAGAAAGAAACGCCCACTCCTGATCTTTCACATTGA	1815
Db	1886	GTGCTCTCCAGAACTGAGACAGAAAGAAACGCCCACTCCTGATCTTTCACATTGA	1945
Qy	1816	ACTCAATGGCTACATGTATGATTGGACACAGAGTTTTCTGCCAAGGAGAAATATTATGT	1875
Db	1946	ACTCAATGGCTACATGTATGATTGGACACAGAGTTTTCTGCCAAGGAGAAATATTATGT	2005
Qy	1876	CTGGCTGCACACACTCTGAGAAAGAACTTNTCTCTCTACACATAGAAACCAAAAG	1935
Db	2006	CTGGCTGCACACACTCTGAGAAAGAACTTNTCTCTCTACACATAGAAACCAAAAG	2065
Qy	1936	CGTGGCGTAGTGGCTCACACCTGTATCCACAGCACCTTGGGAGGCCAAGGAGGGCAGAT	1995
Db	2066	CGTGGCGTAGTGGCTCACACCTGTATCCACAGCACCTTGGGAGGCCAAGGAGGGCAGAT	2125
Qy	1996	CACCTCAGGTCAGGAGTTCAGACACGCTCGGCCACATGGTAAACGCTGTCCCTAGTAA	2055
Db	2126	CACCTCAGGTCAGGAGTTCAGACACGCTCGGCCACATGGTAAACGCTGTCCCTAGTAA	2185
Qy	2056	AAATGCAAAAATTAGCTGGGTGTGGGTACCTGTCTGCCAGTTTACTTTGGGAGGC	2115
Db	2186	AAATACAAAATTAGCTGGGTGTGGGTACCTGTATCCAGTTTACTTTGGGAGGC	2245
Qy	2116	TGAGGTGGGAGGATCTTTTGAACCCAGAGGTTCAGGTCATAGCATGCTGTGATGTGCC	2175
Db	2246	TGAGGTGGGAGGATCTTTTGAACCCAGAGGTTCAGGTCATAGCATGCTGTGATGTGCC	2305
Qy	2176	TAGCAATAGCCACTGTCATACCACCTGGGCAATATAGCAAGTCCCA	2222
Db	2306	TAGCAATAGCCACTGTCATACCACCTGGGCAATATAGCAAGTCCCA	2352
RESULT	3		
AAV31375			
ID	AAV31375	standard; cdna; 2188 BP.	
XX	XX		
AC	AAV31375;		
XX	XX		
DT	07-SEP-1998	(first entry)	
XX	XX		
DE	Human	FIN-1 encoding cdna.	
XX	XX		
KW	Human; FIN-1; FLICE inhibitor-1; ICE-LAP7; death effector domain; DEP;		
KW	apoptosis-related protein; caspase; viral infection; cancer; tumour;		
KW	diagnosis; ischaemic injury; neuro-degenerative disorder; ds.		
XX	XX		
OS	Homo sapiens.		
XX	XX		
Key	Location/Qualifiers		
FT	CDS	422..1864	
FT	FT	/*tag= a	
XX	XX	/product= "FIN-1"	
XX	XX		
PN	EP841399-A2.		

1620 TGAAGATGTCGATTCAGGCTCAGAGCGAGGCTGTGCACAGTTCACCGAGAGCTG 1679
1560 TGAAGATGTCGATTCAGGCTCAGAGCGAGGCTGTGCACAGTTCACCGAGAGCTG 1619
1680 ACTTCTCTGGAGCTGTACTGTGGGACATGCTCCCTGTGGAGCAGTCTCACAGCTCAC 1739
1620 ACTTCTCTGGAGCTGTACTGTGGGACATGCTCCCTGTGGAGCAGTCTCACAGCTCAC 1679
1740 CGTCCCTGTACTGTAGTCCCTCTCCAGAACTGAGACAAGAAAGAAAGCCCACTCC 1799
1680 CGTCCCTGTACTGTAGTCCCTCTCCAGAACTGAGACAAGAAAGAAAGCCCACTCC 1739
1800 TGGATCTTACATTTGAATCAATGCTACATGATGATGGAACAGCAGAGTTCTTGCCA 1859
1740 TGGATCTTACATTTGAATCAATGCTACATGATGATGGAACAGCAGAGTTCTTGCCA 1799
1860 AGGAGAAATATTATGCTGGCTGCAGCACACTCTGAGAAGAACTTATCTCTCTACA 1919
1800 AGGAGAAATATTATGCTGGCTGCAGCACACTCTGAGAAGAACTTATCTCTCTACA 1859
1920 CATAGAAACCAAGGCTGGGCTAGTGGCTCACACCTGTAATCCAGCACTTTGGGAG 1979
1860 CATAGAAACCAAGGCTGGGCTAGTGGCTCACACCTGTAATCCAGCACTTTGGGAG 1919
1980 GCCAAGGAGGCGAGTCACTTCAAGTCCAGAGTTCGAGACACCGCTGGCCAACTGGTAA 2039
1920 GCCAAGGAGGCGAGTCACTTCAAGTCCAGAGTTCGAGACACCGCTGGCCAACTGGTAA 1979
2040 ACGTGCTCCCTAGTAAATGCAAAATAGCTGGGTGGGTGGGTGGGTGGGTGGGTGGGT 2099
1980 ACGTGCTCCCTAGTAAATGCAAAATAGCTGGGTGGGTGGGTGGGTGGGTGGGTGGGT 2039
2100 CAGTTACTTGGAGGCTGAGTGGGAGGATCTTTTGAACCCAGAGTTCAGGCTCATAGC 2159
2040 CAGTTACTTGGAGGCTGAGTGGGAGGATCTTTTGAACCCAGAGTTCAGGCTCATAGC 2099
2160 ATGCTGTGATGTGCTTACGAATAGCCACTGCATACCACTGGGCAATATAGCAAGATC 2219
2100 ATGCTGTGATGTGCTTACGAATAGCCACTGCATACCACTGGGCAATATAGCAAGATC 2159
2220 CCATCTCTTTAAAAAATAAAAAA 2243
2160 CCATCTCTTTAAAAAATAAAAAA 2183

RESULT 4
AAZ39040
ID AAZ39040 standard; cDNA: 2143 BP.
XX
AC AAZ39040;
XX
DT 25-FEB-2000 (first entry)
DE Human FLICE-like inhibitory protein long form nucleotide sequence.
XX
KW Human; FLICE-like inhibitory protein long form; FLIP-L; FLIP-S;
KW FLICE-like inhibitory protein short form; apoptosis inhibitor;
KW arteriosclerosis; vascular wall inflammation; vascular injury;
KW Fas ligand-mediated apoptosis; arteriosclerosis; transplant;
XX
OS Homo sapiens.
XX
FH Key
FT CDS
FT 383..1825
FT /*tag= a
FT /product= "FLICE-like inhibitory protein long form"
FT /note= "FLIP-L; apoptosis inhibitor"
XX
PN W09942570-AL.
XX
PD 26-AUG-1999.
XX

PF 19-FEB-1999; 99WO-US03558.
XX
PR 20-FEB-1998; 98US-0075471.
XX
PA (SELI-) ST ELIZABETH'S MEDICAL CENT BOSTON INC.
XX
PI Walsh K;
XX
DR WPI; 1999-527469/44.
XX
DR P-PSDB; AAY57454.
XX
PT Treating conditions characterized by vascular wall inflammation
XX
PS Claim 14; Page 68-69; 105pp; English.
XX
CC The present sequence encodes human FLICE-like inhibitory protein long
CC form, designated FLIP-L. The present invention describes a new treatment
CC of a condition characterized by vascular wall inflammation in a subject
CC comprising administering a FLIP molecule to inhibit Fas ligand-mediated
CC apoptosis of vascular endothelial cells in the subject. The method can
CC be used to treat arteriosclerosis, transplant arteriosclerosis and
CC vascular injury.
XX
SQ Sequence 2143 BP; 590 A; 482 C; 576 G; 495 T; 0 other;
Query Match 94.7%; Score 2124; DB 20; Length 2143;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2138; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
QY 99 TAGGGGTGGGACTCGGCTCACAGTGAAGTGGCGGCTATTGGACTTTTGTCCAGTGC 158
DB 1 TAGGGGTGGGACTCGGCTCACAGTGAAGTGGCGGCTATTGGACTTTTGTCCAGTGC 60
QY 159 AGCTGAGACAACAAGACACCGGAGGAGTGTAGGAGAGAAGCCGCGACAGCATC 218
DB 61 AGCTGAGACAACAAGACACCGGAGGAGTGTAGGAGAGAAGCCGCGACAGCATC 120
QY 219 GCCCAGCACCAGTCCGCTTCCAGGCTTCCAGGCTTTCGCTTCTTTCCTCCATCTTGGGTGGCCT 278
DB 121 GCCCAGCACCAGTCCGCTTCCAGGCTTTCGCTTCTTTCGCTTCTTTCGCTTCTTGGGTGGCCT 180
QY 279 TCCCGGCTCTAGGGAGCGAAGGCTGAGGTGGCAGCGCAGGAGATCCCGCCGCGACA 338
DB 181 TCCCGGCTCTAGGGAGCGAAGGCTGAGGTGGCAGCGCAGGAGATCCCGCCGCGACA 240
QY 339 GGACGAACCTCCCGCTGAGGAGGATCTGAAGAAATGAAGTCAAGCTCAGAAATGAA 398
DB 241 GGACGAACCTCCCGCTGAGGAGGATCTGAAGAAATGAAGTCAAGCTCAGAAATGAA 300
QY 399 GTTGACTGCTGCTGGCTTTCCTGTTGACTGGCCGCGAGCTGTACTGCAAGACCTTGTG 458
DB 301 GTTGACTGCTGCTGGCTTTCCTGTTGACTGGCCGCGAGCTGTACTGCAAGACCTTGTG 359
QY 459 AGTTCCCTAGTCTAAGAGTGAAGTGTCTGTAAGTCAATCATAGTTGAAGAGCAC 518
DB 360 AGTTCCCTAGTCTAAGAGTGAAGTGTCTGTAAGTCAATCATAGTTGAAGAGCAC 419
QY 519 TTGATACAGATGAGAGGAGATGCTGCTCTTTTGTGCGGGATGTTGCTATAGATGTGG 578
DB 420 TTGATACAGATGAGAGGAGATGCTGCTCTTTTGTGCGGGATGTTGCTATAGATGTGG 479
QY 579 TTCCACCTAATGTCAGGAGCTTCTGATATTTTACGGAAAGAGGTAAGCTGTCTGTGCG 638
DB 480 TTCCACCTAATGTCAGGAGCTTCTGATATTTTACGGAAAGAGGTAAGCTGTCTGTGCG 539
QY 639 GGGACTTGGTGAACCTGCTTACAGAGTGAAGGATTTGACCTGCTCAACGCTATCTGA 698
DB 540 GGGACTTGGTGAACCTGCTTACAGAGTGAAGGATTTGACCTGCTCAACGCTATCTGA 599
QY 699 AGATGGACAAAAGCTGTGGAGACCCACCTGCTGAGGAACCTCACCCTGTTTTCGACT 758
DB 600 AGATGGACAAAAGCTGTGGAGACCCACCTGCTGAGGAACCTCACCCTGTTTTCGACT 659

759 ATAGAGTGTGATGGCAGAGATTGGTGAGGATTTGGATAAATCTGATGTGTCTCATTA 818
1199
660 ATAGAGTGTGATGGCAGAGATTGGTGAGGATTTGGATAAATCTGATGTGTCTCATTA 719
1199
819 TTTTCTCTCATGAAGGATTTACATGGCGGAGGCAAGATAAGCAAGAGGAAGTTCTTGG 878
1199
720 TTTTCTCTCATGAAGGATTTACATGGCGGAGGCAAGATAAGCAAGAGGAAGTTCTTGG 779
1199
879 ACCTTGTGGTTGAGTTGGAGAACTAAATTTGGTTGCCCCAGATCAACTGGATTTATTAG 938
1199
780 ACCTTGTGGTTGAGTTGGAGAACTAAATTTGGTTGCCCCAGATCAACTGGATTTATTAG 839
1199
939 AAAAATGCCCTAAAGAACATCCACAGATAGACCTGAGACAAAATCCAGAACTACAGC 998
1199
840 AAAAATGCCCTAAAGAACATCCACAGATAGACCTGAGACAAAATCCAGAACTACAGC 899
1199
999 AGTCTGTCTCAAGGAGGAGGACAAAGTTACAGGAATTTCTCCAGCAGCAATCCAAAAGA 1058
1199
900 AGTCTGTCTCAAGGAGGAGGACAAAGTTACAGGAATTTCTCCAGCAGCAATCCAAAAGA 959
1199
1059 GTCTCAAGGATCTTCAATAAATCTCAGGCTCCATATGGGAGAAAGTAAAGAACAAAGAC 1118
1199
960 GTCTCAAGGATCTTCAATAAATCTCAGGCTCCATATGGGAGAAAGTAAAGAACAAAGAC 1019
1199
1119 TTAAGGAACAGCTTGGCGCTCAACAGAACCCAGTGAAGAAATCCATTTCAGGAATCAGAG 1178
1199
1020 TTAAGGAACAGCTTGGCGCTCAACAGAACCCAGTGAAGAAATCCATTTCAGGAATCAGAG 1079
1199
1179 CTTTTTTGGCTCAGAGCATACCTGAAGAGAGATACAAAGATGAAGAGCAAGCCCTTAGGAA 1238
1199
1080 CTTTTTTGGCTCAGAGCATACCTGAAGAGAGATACAAAGATGAAGAGCAAGCCCTTAGGAA 1139
1199
1239 TCTGCTGTGATTCGATTTGGCAATGAGACAGAGCTTTTCGAGACACCTTCACATT 1298
1199
1140 TCTGCTGTGATTCGATTTGGCAATGAGACAGAGCTTTTCGAGACACCTTCACATT 1199
1199
1299 CCCTGGGCTATGAAGTCCAGAAATCTTGATCTCAGTATGATGATGATATCCAGATTC 1358
1199
1200 CCCTGGGCTATGAAGTCCAGAAATCTTGATCTCAGTATGATGATGATATCCAGATTC 1259
1199
1359 TTGGCCAAATTTGGCTGTATGCCGAGCAGCAGAGACTACGAGAGCTTTGTGTGCTCTGG 1418
1199
1260 TTGGCCAAATTTGGCTGTATGCCGAGCAGCAGAGACTACGAGAGCTTTGTGTGCTCTGG 1319
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1419 TGAGCCGAGAGGCTCCAGAGTGTGTATGGTGTGATGATGATGATGATGATGATGATGAT 1478
1199
1320 TGAGCCGAGAGGCTCCAGAGTGTGTATGGTGTGATGATGATGATGATGATGATGATGAT 1379
1199
1479 TGATCATCATCAGAGGATTTTCATGGAGATTCATGCCCTTTATCTAGCAGGAGGACCAA 1538
1199
1380 TGATCATCATCAGAGGATTTTCATGGAGATTCATGCCCTTTATCTAGCAGGAGGACCAA 1439
1199
1539 AGATGTTTTTTTATTCAGAACTATGTGTGTGAGAGGCGGAGCTGGAGAACAGCAGCTCT 1598
1199
1440 AGATGTTTTTTTATTCAGAACTATGTGTGTGAGAGGCGGAGCTGGAGAACAGCAGCTCT 1499
1199
1599 TGGAGTGGATGGGCGAGGATGAAGAAATGGAAATTCAGAGCTCAAGAGGAGGCTGT 1658
1199
1500 TGGAGTGGATGGGCGAGGATGAAGAAATGGAAATTCAGAGCTCAAGAGGAGGCTGT 1559
1199
1659 GCACAGTTCACCGAGAGCTGATCTTCTCGAGAGCTGTGATGAGGAGATGCTCCCTGC 1718
1199
1560 GCACAGTTCACCGAGAGCTGATCTTCTCGAGAGCTGTGATGAGGAGATGCTCCCTGC 1619
1199
1719 TGGAGGAGTCTCAGAGCTCAAGCTGCTGTGATGAGGAGCTGCTCCAGAACTAGAG 1778
1199
1620 TGGAGGAGTCTCAGAGCTCAAGCTGCTGTGATGAGGAGCTGCTCCAGAACTAGAG 1679
1199
1779 AAGAAAGAAACGCCCTCTGATCTTCCATATTCAGAACTCAATGGCTACATGATGAT 1838
1199
1680 AAGAAAGAAACGCCCTCTGATCTTCCATATTCAGAACTCAATGGCTACATGATGAT 1739
1199
1839 GGAACAGCAGAGTTCTGCCAAGAGAGAAATATTATGTCTGGCTGACACACTCTGAGAA 1898
1199

1740 GGAACAGCAGAGTTTCTGCCAAGAGAGAAATATTATGTCTGGCTGACACACTCTGAGAA 1799
1199
1899 AGAAACTTATCTCTCTACACATAAGAAACCAAGAGCTGGCGGTAGTGGCTCACACCT 1958
1199
1800 AGAAACTTATCTCTCTACACATAAGAAACCAAGAGCTGGCGGTAGTGGCTCACACCT 1859
1199
1959 GTAATCCAGCAGCTTTGGGAGGCAAGAGGAGGAGATCACTTTCAGGTCAGGAGTTCGAGA 2018
1199
1860 GTAATCCAGCAGCTTTGGGAGGCAAGAGGAGGAGATCACTTTCAGGTCAGGAGTTCGAGA 1919
1199
2019 CCAGCCTGGGCAACATGTTAAAGCTGTCCCTAGTAAATATGAAAAATAGCTGGGTGT 2078
1199
1920 CCAGCCTGGGCAACATGTTAAAGCTGTCCCTAGTAAATATGAAAAATAGCTGGGTGT 1979
1199
2079 GGTGTGGGTACCTTGTCTCCAGATTTGGGAGGCTGAGGTGGGAGGATCTTTTGAAC 2138
1199
1980 GGTGTGGGTACCTTGTCTCCAGATTTGGGAGGCTGAGGTGGGAGGATCTTTTGAAC 2039
1199
2139 CCAGGAGTTCAGGCTCATAGCATGCTGTGATTTGGCTAGCAATAGCCACTGCATACCAA 2198
1199
2040 CCAGGAGTTCAGGCTCATAGCATGCTGTGATTTGGCTAGCAATAGCCACTGCATACCAA 2099
1199
2199 CCTGGGCAATATAGCAAGATCCCATCTCTTTAAAAA 2242
1199
2100 CCTGGGCAATATAGCAAGATCCCATCTCTTTAAAAA 2143
1199

RESULT 5
ABL52333
ID= ABL52333 standard; cDNA; 2143 BP.
XX ABL52333;
XX AC
XX XX
DT 15-JUL-2002 (first entry)
XX
DE Human FLIP-c encoding cDNA SEQ ID NO:11.
XX
KW Human; FLIP-c; caspase 8 dominant negative regulator; antiinflammatory;
KW anti-tumour; FLIP-c inhibitor; apoptosis; antisense gene therapy;
KW phosphorothioate; antisense modulation; infection; inflammation;
KW tumour; gene; as.
XX
OS Homo sapiens.
XX
FH Key
FT CDS
FT Location/Qualifiers
FT 383..1825
FT /*tag= a
FT /product= "FLIP-c"
XX
PN WO200224717-A1.
XX
PD 28-MAR-2002.
XX
PF 14-SEP-2001; 2001WO-US28732.
XX
PR 20-SEP-2000; 2000US-0666269.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Ackermann EJ, Bennett CF, Zhang H, Watt AT, Ricketts W, Dean NM;
XX
XX WPI; 2002-401983/43.
XX P-PSDB; ABB09294.
XX
XX Novel antisense compound that hybridizes and inhibits nucleic acid
XX encoding a natural dominant negative regulator of caspase 8, FLIP-c,
XX useful for preventing or delaying infection, inflammation or tumor
XX formation
XX
XX Example 13; Page 118-120; 154pp; English.
XX
CC The present invention describes a compound (I) 8-50 nucleobases in length

CC targeted to a nucleic acid molecule (II) encoding a natural dominant
 CC negative regulator of caspase 8, FLIP-c, where (I) specifically
 CC hybridises with and inhibits expression of the protein, or specifically
 CC hybridises with at least an 8-nucleobase portion of an active site on
 CC (II). (I) has antinflammatory and anti-tumour activities. (I) is an
 CC inhibitor of FLIP-c expression, a modulator of apoptosis and can be used
 CC in antisense gene therapy. (I) is useful for inhibiting the expression of
 CC FLIP-c in cells or tissues, and for treating an animal having a disease
 CC or condition associated with FLIP-c. (I) is also useful for modulating
 CC apoptosis in a cell, where a caspase such as caspase 8, caspase 3 or
 CC caspase 7 is activated, and the FLIP-c is the long form of FLIP-c. (I) is
 CC also useful for diagnostics, therapeutics, prophylaxis, as research
 CC reagents and kits, for distinguishing functions of various members of a
 CC biological pathway, and in antisense gene therapy. (I) is also useful
 CC prophylactically, e.g., to prevent or delay infection, inflammation or
 CC tumour formation. The present sequence encodes human FLIP-c as given in
 CC an example from the present invention.

XX Sequence 2143 BP; 590 A; 482 C; 576 G; 495 T; 0 other;

Query Match 94.7%; Score 2124; DB 24; Length 2143;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 2138; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY	99	TAGGGTGGGACTCGGCTCACACAGTCAGTCCGGCTATTGGACTTTGTCAGTGAC	158
DB	1	TAGGGTGGGACTCGGCTCACACAGTCAGTCCGGCTATTGGACTTTGTCAGTGAC	60
QY	159	AGCTGAGACAACAAGACACACGGGAGAGGTGTAGGAGAGAAGCCGCGAACACGCGATC	218
DB	61	AGCTGAGACAACAAGACACACGGGAGAGGTGTAGGAGAGAAGCCGCGAACACGCGATC	120
QY	219	GCCAGCACCAAGTCGGCTTCAGGCTTTCAGGCTTTCGGTTCCTTCATCTTGGGTGGCCT	278
DB	121	GCCAGCACCAAGTCGGCTTTCAGGCTTTCGGTTCCTTCATCTTGGGTGGCCT	180
QY	279	TCCCGCGTCTAGGGAGGAGGAGGTGAGTGGCAGCGCAGAGAGTCCGCGCCGACA	338
DB	181	TCCCGCGTCTAGGGAGGAGGAGGTGAGTGGCAGCGCAGAGAGTCCGCGCCGACA	240
QY	339	GGACGAACCTCCCACTGAAAGGATTTCTGAAGAAATGAAGTCAGCCCTCAGAATGAA	398
DB	241	GGACGAACCTCCCACTGAAAGGATTTCTGAAGAAATGAAGTCAGCCCTCAGAATGAA	300
QY	399	GTTGACTGCTGCTGGCTTTCCTGTTGACTGGCCGGAGCTGTACTGAGACCCCTGTG	458
DB	301	GTTGACTGCTGCTGGCTTTCCTGTTGACTGGCCGGAGCTGTACTGAGACCCCTGTG	359
QY	459	AGCTTCCCTAGTCTAAGACTAGGATGCTGCTGAAGTCAATCCATCAGGTTGAAGAGCAC	518
DB	360	AGCTTCCCTAGTCTAAGACTAGGATGCTGCTGAAGTCAATCCATCAGGTTGAAGAGCAC	419
QY	519	TTGATACAGATGAGAAGGAGATGCTGCTCTTTTGTGCGGGATGTTGCTATAGATGGG	578
DB	420	TTGATACAGATGAGAAGGAGATGCTGCTCTTTTGTGCGGGATGTTGCTATAGATGGG	479
QY	579	TTCCACCTAATGTCAGGGACCTCTGGATATTTCAGGGAAGAGGTAGCTGTCTGTCG	638
DB	480	TTCCACCTAATGTCAGGGACCTCTGGATATTTCAGGGAAGAGGTAGCTGTCTGTCG	539
QY	639	GGGACTTGGCTGAACCTGCTACAGAGTCAGGCGATTTGACCTGCTCAACACGTATCTGA	698
DB	540	GGGACTTGGCTGAACCTGCTACAGAGTCAGGCGATTTGACCTGCTCAACACGTATCTGA	599
QY	699	AGATGACAGAAAGCTGTGGAGACCCACTGCTCAGGAACCCCTCACCTTTTTCGGACT	758
DB	600	AGATGACAGAAAGCTGTGGAGACCCACTGCTCAGGAACCCCTCACCTTTTTCGGACT	659
QY	759	ATAGAGTGTGTGGCAGAGATGTTGAGGATTTGGATAAATCTGATGTCTCATTAA	818
DB	660	ATAGAGTGTGTGGCAGAGATGTTGAGGATTTGGATAAATCTGATGTCTCATTAA	719
QY	819	TTTTCTCATGAAGGATTACATGGGCGGAGCAAGATAAGCAAGGAGAGAGTTCCTTGG	878

DB	720	TTTTCTCATGAAGGATTACATGGCCCGAGGAGATAGCAAGGAGAGTTCCTTGG	779
QY	879	ACCTTGTGTTGAGTTGGAGAACTAAATTTGGTTGCCCCAGATCAACTGGATTTATTAG	938
DB	780	ACCTTGTGTTGAGTTGGAGAACTAAATTTGGTTGCCCCAGATCAACTGGATTTATTAG	839
QY	939	AAAAATGCTTAAAGAACATCCACAGATAGACCTCAAGACAAAAATCAGAAAGTAAAGC	998
DB	840	AAAAATGCTTAAAGAACATCCACAGATAGACCTCAAGACAAAAATCAGAAAGTAAAGC	899
QY	999	AGTCTGTTCAAGGACAGGACAACTTACAGGAATGTTCTCCAGCAGCAATCCAAAGA	1058
DB	900	AGTCTGTTCAAGGACAGGACAACTTACAGGAATGTTCTCCAGCAGCAATCCAAAGA	959
QY	1059	GTCTCAAGGATCCTTCAAAATAACTTCAGGCTCCATAATGGGAGAAAGTAAAGAACAAAGAC	1118
DB	960	GTCTCAAGGATCCTTCAAAATAACTTCAGGCTCCATAATGGGAGAAAGTAAAGAACAAAGAC	1019
QY	1119	TTAAGGAACAGCTTGGCGCTCAACGAACACAGTGAAGAAATCCATTCCAGGAATCAGAG	1178
DB	1020	TTAAGGAACAGCTTGGCGCTCAACGAACACAGTGAAGAAATCCATTCCAGGAATCAGAG	1079
QY	1179	CTTTTTCCTCAGAGCATACCTGAAGAGATACAAGATGAAGAGAGCCCTTAGGAA	1238
DB	1080	CTTTTTCCTCAGAGCATACCTGAAGAGATACAAGATGAAGAGAGCCCTTAGGAA	1139
QY	1239	TCTGCTGATATCGATTGCAATGGCAATGAGACAGAGCTTCTCGAGACACCTTCACCT	1298
DB	1140	TCTGCTGATATCGATTGCAATGGCAATGAGACAGAGCTTCTCGAGACACCTTCACCT	1199
QY	1299	CCCTGGGCTATGAAGTCCAGAAATTTTGCATCTCAGTATGATGATATCCAGATTC	1358
DB	1200	CCCTGGGCTATGAAGTCCAGAAATTTTGCATCTCAGTATGATGATATCCAGATTC	1259
QY	1359	TTGGCCAAATTTGCCCTGTATGCCGAGCACCGAGACTAGACAGCTTTGTGTGCTCTGG	1418
DB	1260	TTGGCCAAATTTGCCCTGTATGCCGAGCACCGAGACTAGACAGCTTTGTGTGCTCTGG	1319
QY	1419	TGAGCCGAGGAGGCTCCAGAGTGTATGGTGTGGATCAGACTCAGTCAGGGCTCCCTC	1478
DB	1320	TGAGCCGAGGAGGCTCCAGAGTGTATGGTGTGGATCAGACTCAGTCAGGGCTCCCTC	1379
QY	1479	TGCATCAGATCAGGAGGATTTCTATGGGAGATTCATGCCCTTATCTAGCAGGAAGCCAA	1538
DB	1380	TGCATCAGATCAGGAGGATTTCTATGGGAGATTCATGCCCTTATCTAGCAGGAAGCCAA	1439
QY	1539	AGATGTTTTTTTATTCAGAACTATGTTGTCAGAGGGCCAGCTGGAGAACAGCAGCTCT	1598
DB	1440	AGATGTTTTTTTATTCAGAACTATGTTGTCAGAGGGCCAGCTGGAGAACAGCAGCTCT	1499
QY	1599	TGGAGTGGATGGGCGAGGATGAGATGTTGGATTCAGGCTCAGAAAGCAGGGCTGT	1658
DB	1500	TGGAGTGGATGGGCGAGGATGAGATGTTGGATTCAGGCTCAGAAAGCAGGGCTGT	1559
QY	1659	GCACAGTTTCCAGGAGAGCTGACTTCTCTGGAGCTGTGTACTGCGGACATGTCCTGTC	1718
DB	1560	GCACAGTTTCCAGGAGAGCTGACTTCTCTGGAGCTGTGTACTGCGGACATGTCCTGTC	1619
QY	1719	TGGAGCTGCTCAGAGCTCACCTCCCTGCTACCTGAGTGCCTCTCCCAAGAACTGAGAC	1778
DB	1620	TGGAGCTGCTCAGAGCTCACCTCCCTGCTACCTGAGTGCCTCTCCCAAGAACTGAGAC	1679
QY	1779	AGAAGAAAGAACGCCACTCTCTGGATCTTCACATTGAACTCAATGGCTACATGTATGAT	1838
DB	1680	AGAAGAAAGAACGCCACTCTCTGGATCTTCACATTGAACTCAATGGCTACATGTATGAT	1739
QY	1839	GGAAACAGCAGAGTTTCTGCCAAGGAGAAATATTATGCTGTGGCTGAGCAGCAGCTCTGAGAA	1898
DB	1740	GGAAACAGCAGAGTTTCTGCCAAGGAGAAATATTATGCTGTGGCTGAGCAGCAGCTCTGAGAA	1799
QY	1899	AGAAACTTATCTCTCTCCTACATAGAAACCAAGGCTGGGCTGAGGCTCAGACCT	1958

Db	1800	AGAACTTATCCCTCTACACATAAGAAACCAAAAGGCTGGGCGTAGTGGCTCACACCT	1855
Qy	1959	GTAATCCAGCACTTTGGGAGGCCAAGGAGGGCAGATCACTTCAGGTCAGGAGTTCGAGA	2018
Db	1860	GTAATCCAGCACTTTGGGAGGCCAAGGAGGGCAGATCACTTCAGGTCAGGAGTTCGAGA	1919
Qy	2019	CCAGCCTGGCCACATGGTAAACGCTGTCCCTAGTAAATGCAAAATTAGCTGGGTGT	2078
Db	1920	CCAGCCTGGCCACATGGTAAACGCTGTCCCTAGTAAATGCAAAATTAGCTGGGTGT	1979
Qy	2079	GGGTGTGGGTACCTGTCTCCAGTACTTTGGGAGGCTGAGGTGGGAGGATCTTTTGAAC	2138
Db	1980	GGGTGTGGGTACCTGTATCCAGTACTTTGGGAGGCTGAGGTGGGAGGATCTTTTGAAC	2039
Qy	2139	CCAGGAGTTCAGGGTCATAGCATGCTGTGATTGTGCTACGAATAGCCACTGCATACCAA	2198
Db	2040	CCAGGAGTTCAGGGTCATAGCATGCTGTGATTGTGCTACGAATAGCCACTGCATACCAA	2099
Qy	2199	CTGTGGCAATATAGCAGATCCCATCTCTTTAAAAA	2242
Db	2100	CTGTGGCAATATAGCAGATCCCATCTCTTTAAAAA	2143
RESULT 6			
AAV61937			
ID	AAV61937 standard; DNA; 2143 BP.		
XX	AAV61937;		
XX	12-JUL-1999 (first entry)		
DT	Human CFLIP-L DNA.		
XX	Death effector domain; human; murine; anti-apoptotic; treatment;		
KW	HIV infection; autoimmune disease; FLIP protein; ss.		
KW	Homo sapiens.		
OS	Key		
XX	Location/Qualifiers		
PH	383..1825		
FT	/*tag= a		
FT	/product= "CFLIP-L"		
XX	DE19713393-Al.		
PN	08-OCT-1998.		
XX	01-APR-1997; 97DE-1013393.		
XX	01-APR-1997; 97DE-1013393.		
PR	(TSCCH/) TSCHOPP J. .		
XX	(APOT-) APOTECH SA.		
PI	Bodmer J, Burns K, French EL, Hahne M, Hoffmann K;		
PI	Irmeler M, Rimoldi D, Schneider P, Schroeter M, Steiner V;		
PI	Thome M, Tschopp J, Hofmann K;		
XX	WPI; 1998-532710/46.		
DR	P-PSDB; AAW76631.		
XX	New DNA encoding for anti-apoptotic gene product - used to treat HIV		
XX	infections and autoimmune diseases		
XX	Claim 20; Fig 4B; 45pp; German.		
XX	This invention describes novel human and mouse anti-apoptotic gene		
CC	products which contain at least one death effector domain. The products		
CC	of the invention are used in the treatment of HIV infections and		
CC	autoimmune diseases.		
XX	Sequence 2143 BP; 589 A; 482 C; 576 G; 495 T; 1 other;		
SQ			

DT	21-MAR-2000	(first entry)	QY	167	CAACAAGGACACCGGAGGAGGTCTAGAGAGAAAGCGCGGAAACACAGCATCGCCCAAGCA	226
XX	Human CLARP coding sequence.		Db	121	CAACAAGGACACCGGAGGAGGTCTAGAGAGAAAGCGCGGAAACACAGCATCGCCCAAGCA	180
XX	RICK; human; RIP-like interacting CLARP kinase; apoptosis regulator; ARC;		QY	227	CCAGTCCGCTTCCAGGCTTTCGGTCTTCTTCCCTCCATCTTGGTGGCGCTTCCCGCG	286
KW	caspase-8; caspase-10; CD95 signalling; apoptosis signalling pathway;		Db	181	CCAGTCCGCTTCCAGGCTTTCGGTCTTCTTCCCTCCATCTTGGTGGCGCTTCCCGCG	240
KW	CIDE-A; CIDE-B; DREP-1; diagnosis; cell growth; apoptosis dysregulation;		QY	287	TCTAGGAGAGCAAGGCTGAGTGGCAGCGGAGAGTCCGCGCGGAGAGCAAGCAAC	346
KW	gene therapy; cardiac disorder; cancer; neurodegenerative disorder; AIDS;		Db	241	TCTAGGAGAGCAAGGCTGAGTGGCAGCGGAGAGTCCGCGCGGAGAGCAAGCAAC	300
KW	aplastic anaemia; ischaemic injury; toxin-induced liver disease;		QY	347	TCGCCACTGGAAAGGATCTGAAAGAAATGAAGTACAGCCCTCAGAAATGAAGTTGACTG	406
XX	CLARP; ss.		Db	301	TCGCCACTGGAAAGGATCTGAAAGAAATGAAGTACAGCCCTCAGAAATGAAGTTGACTG	360
OS	Homo sapiens.		QY	407	CCTGCTGGCTTTCCTGTTGACTGGCCCGGAGCTGTACTGCAAGACCCCTTGTGAGCTTCCC	466
XX	WO955134-A2.		Db	361	CCTGCTGGCTTTCCTGTTGACTGGCCCGGAGCTGTACTGCAAGACCCCTTGTGAGCTTCCC	420
XX	04-NOV-1999.		QY	467	TAGTCTAAGAGTAGGATGCTGCTGAAAGTATCCATCAGTTGAAGAGCACTTGATACA	526
XX	27-APR-1999; 99WO-US09183.		Db	421	TAGTCTAAGAGTAGGATGCTGCTGAAAGTATCCATCAGTTGAAGAGCACTTGATACA	480
XX	27-APR-1998; 98US-0069023.		QY	527	GATGAGAGGAGATGCTGCTCTTTTGTGCGGGAGTGTGCTATAGATGTGTTCCACCT	586
XX	(UNMI) UNIV MICHIGAN.		Db	481	GATGAGAGGAGATGCTGCTCTTTTGTGCGGGAGTGTGCTATAGATGTGTTCCACCT	540
PI	Nunez G, Inohara N, Koseki T;		QY	587	AATGTCAGGAGCTTCTCTGGATATTTACGGGAAGAGGTAAAGCTGCTGTCGGGAGCTTG	646
XX	WPI; 2000-072163/06.		Db	541	AATGTCAGGAGCTTCTGGATATTTACGGGAAGAGGTAAAGCTGCTGTCGGGAGCTTG	600
DR	P-PSDB; AAY59414.		QY	647	GCTGAACCTGCTACAGAGTAGGCGATTTGACCTGCTCAACAGTATCTTGAAGATGAC	706
XX	Compositions for identifying apoptosis signalling pathway inhibitors		Db	601	GCTGAACCTGCTACAGAGTAGGCGATTTGACCTGCTCAACAGTATCTTGAAGATGAC	660
XX	useful for treating diseases -		QY	707	AGAAAGCTGTGAGACACCCCTGCTCAGGAACCCCTCACTTGTTCGGAGCTATAGAGTG	766
XX	Example 10; Fig 21a; 93pp; English.		Db	661	AGAAAGCTGTGAGACACCCCTGCTCAGGAACCCCTCACTTGTTCGGAGCTATAGAGTG	720
XX	This sequence encodes the human CLARP protein. The invention relates to		QY	767	CTGATGGCAGAGATTGGTGGAGATTGGATAAATCTGATGTCTCATTAATTTTCTC	826
XX	the human RICK (RIP-like interacting CLARP kinase) protein. The RICK		Db	721	CTGATGGCAGAGATTGGTGGAGATTGGATAAATCTGATGTCTCATTAATTTTCTC	780
XX	protein acts as a positive regulator of apoptosis, potentiating apoptosis		QY	827	ATGAGGATTACATGGCGGAGGAGAGATAAGCAGAGAGAGTTCCTTGGACCTTGTG	886
XX	induced by caspase-8 and caspase-10 during CD95 signalling. The invention		Db	781	ATGAGGATTACATGGCGGAGGAGAGATAAGCAGAGAGAGTTCCTTGGACCTTGTG	840
XX	provides methods for identifying apoptosis signalling pathway inhibitors		QY	887	GTTGAGTTGAGAAACTAAATTTGTTGCCCGAGATCAACTGGATTTATTAGAAAATGC	946
XX	and activators, and methods and compositions for screening compounds		Db	841	GTTGAGTTGAGAAACTAAATTTGTTGCCCGAGATCAACTGGATTTATTAGAAAATGC	900
XX	which will modulate the interactions of the various compositions		QY	947	CTAAGAAGCATCCACAGATAGACCTGTAAGACAAAATCCAGAGTACAGCAGTCTGT	1006
XX	Identified: ARC, RICK, and the CIDE family of activators (CIDE-A, CIDE-B		Db	901	CTAAGAAGCATCCACAGATAGACCTGTAAGACAAAATCCAGAGTACAGCAGTCTGT	960
XX	and DREP-1). RICK is useful in screening assays for agents, useful in the		QY	1007	CAAGGAGGAGGAGGAGTACAGGATGTTCTCCAGCAGCAATCCAAAGAGTCTCAAG	1066
XX	diagnosis, prognosis or treatment of disease associated with excess cell		Db	961	CAAGGAGGAGGAGGAGTACAGGATGTTCTCCAGCAGCAATCCAAAGAGTCTCAAG	1020
XX	growth and dysregulation of apoptosis. Complexes containing RICK and		QY	1067	GATCCTTTCAAAATCACTTCAGGCTCCATAATGGGAGAGTAAAGAACAAAGACTTAAGAA	1126
XX	CLARP can be used in drug screening assays to identify inhibitor		Db	1021	GATCCTTTCAAAATCACTTCAGGCTCCATAATGGGAGAGTAAAGAACAAAGACTTAAGAA	1080
XX	molecules blocking CD95-mediated apoptosis. Overexpression of ARC in an		QY	1127	CAGCTTGGCGCTCAACAAGAACCCAGTGAAGAAATCCATTCAGGAATCAGAACTTTT	1186
XX	in vitro cell system can be used to identify inhibitors of the enzymatic		Db	1081	CAGCTTGGCGCTCAACAAGAACCCAGTGAAGAAATCCATTCAGGAATCAGAACTTTT	1140
XX	activity of caspase-8. Identification of ARC-like inhibitory compounds		QY	1187	CCTCAGAGCATACCTGAAGAGAGATACAAGATGAAGCAAGCCCTTAGGAATCTGCCTG	1246
XX	may be useful for gene therapy treatment of disease with increased cell		Db	1141	CCTCAGAGCATACCTGAAGAGAGATACAAGATGAAGCAAGCCCTTAGGAATCTGCCTG	1200
XX	death in muscle tissue and cardiac disorders. Therapeutic compositions of		QY	1247	ATAATCGATTGCTATGGCAATGAGACAGAGCTTCTTCGAGACACCTTCACTTCCCTGGGC	1306
XX	CIDEs can be used to treat e.g. cancer, AIDS, neurodegenerative					
XX	disorders, aplastic anaemia, ischaemic injury, and toxin-induced liver					
XX	disease. AntiRICK antibodies can be used as reagents for the preparation					
XX	or affinity chromatography media, and for diagnostically measuring RICK					
XX	levels. A specific inhibitor of an essential step in the biochemistry of					
XX	apoptosis is needed. RICK interaction with intracellular factors such as					
XX	CLARP and FADD appears to be essential for apoptosis, inhibitors of RICK					
XX	binding to intracellular apoptosis factors are potential drug candidates.					
XX	Sequence 2040 BP; 574 A; 467 C; 543 G; 456 T; 0 other;					
XX	Query Match 88.88; Score 1991; DB 21; Length 2040;					
XX	Best Local Similarity 99.08; Pred. No. 0;					
XX	Matches 2003; Conservative 0; Mismatches 20; Indels 0; Gaps 0;					
QY	47 AGCGAGTTGAGGCTCACCGACGAGTCTCAACTAAAAGGAGCTCCCGGAGCTAGGGTG	106				
Db	1 AGCGAGTTGAGGCTCACCGACGAGTCTCAACTAAAAGGAGCTCCCGGAGCTAGGGTG	60				
QY	107 GGGACTCGGCTCACACAGTGAAGTGGCGGCTATTGGACTTTTGTCCAGTGACAGCTGAGA	166				
Db	61 GGGACTCGGCTCACACAGTGAAGTGGCGGCTATTGGACTTTTGTCCAGTGACAGCTGAGA	120				


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287 TCTAGGGAGGAGGCTGAGGTGGCAGCGGACGAGAGTCCGGCCGACAGACGAGAAC 346
1320 TTTTGGCTGTATGCCGAGCACCAGAGACTACGACAGCTTGTGTGTCTCTGTGTGAGCCGA 1379
241 TCTAGGGAGGAGGCTGAGGTGGCAGCGGACGAGAGAGTCCGGCCGACAGACGAGAAC 300
1427 GGAGGCTCCACAGAGTGTGTATGGTGGATCAGACTCACTCAGGCTCCCTCGATCAC 1486
1380 GGAGGCTCCACAGAGTGTGTATGGTGGATCAGACTCACTCAGGCTCCCTCGATCAC 1439
301 TCCCCCACTGAAAGAGTCTGAAAGAAATGAAGTCAAGCCCTCAGAAATGAAGTGTGACTG 360
1487 ATCAGGAGGATGTTTCATGGGAGATTCATGCCCTTATCTAGCAGGGAAGCAAGATGTTT 1546
407 CCTGCTGGCTTTCCTGTGTGACTGGCCGGAGCTGTACTGCAAGACCTCTGTGAGCTTCCC 466
1440 ATCAGAGGATGTTTCATGGGAGATTCATGCCCTTATCTAGCAGGGAAGCAAGATGTTT 1499
361 CCTGCTGGCTTT-CTGTGTGACTGGCCGGAGCTGTACTGCAAGACCTCTGTGAGCTTCCC 419
1547 TTTTATTCAGAACTATGTGTGTGAGGCGGACAGTGGAGAAACAGACGCTCTTGGAGGTG 1606
467 TAGTCTAAGAGTGTGAGTGTGCTGAAAGTATCCATCAGGTTGAAGACACTTGTATACA 526
420 TAGTCTAAGAGTGTGAGTGTGCTGAAAGTATCCATCAGGTTGAAGACACTTGTATACA 479
527 GATGAGAAGGAGTGTCTCTTTTGTGCGGGATGTGCTATAGATGTGGTTTCCACCT 586
480 GATGAGAAGGAGTGTCTCTTTTGTGCGGGATGTGCTATAGATGTGGTTTCCACCT 539
587 AATGTCAGGAGCTTCTGGATATTTTACGGGAAGAGTGTGCTGTGCGGGACTTG 646
540 AATGTCAGGAGCTTCTGGATATTTTACGGGAAGAGTGTGCTGTGCGGGACTTG 599
647 GCTGAACCTGCTACAGAGTGTGAGGCTGTTGACCTGCTCAAACTATCTTGAAGATGGAC 706
600 GCTGAACCTGCTACAGAGTGTGAGGCTGTTGACCTGCTCAAACTATCTTGAAGATGGAC 659
707 AGAAAGCTGTGGAGACCCCTGCTCAGGAACCTCACCCTGTTTGGGACTATAGAGTG 766
660 AGAAAGCTGTGGAGACCCCTGCTCAGGAACCTCACCCTGTTTGGGACTATAGAGTG 719
767 CTGATGGCAGAGATGTTGAGGATTTGGATAAATCTGATGTCTCTCATTAATTTTCTC 826
720 CTGATGGCAGAGATGTTGAGGATTTGGATAAATCTGATGTCTCTCATTAATTTTCTC 779
827 ATGAAGGATTTACATGGCCGAGGCAAGATAAGCAAGAGAGAGTGTCTTGGACCTTGTG 886
780 ATGAAGGATTTACATGGCCGAGGCAAGATAAGCAAGAGAGAGTGTCTTGGACCTTGTG 839
887 GTTGAGTGTGGAGAACTAAATTTGTTGCCAGATCAACTGATTTATAGAAAATGC 946
840 GTTGAGTGTGGAGAACTAAATTTGTTGCCAGATCAACTGATTTATAGAAAATGC 899
947 CTAAGAAGATCCACAGATAGACCTGAGACAAAATCCAGAGTACAAGCAGTCTTT 1006
900 CTAAGAAGATCCACAGATAGACCTGAGACAAAATCCAGAGTACAAGCAGTCTTT 959
1007 CAAGGAGCAGGACAGTTTACAGGATGTTCTCCAGCAGCAATCCAAAGAGTCTCAAG 1066
960 CAAGGAGCAGGACAGTTTACAGGATGTTCTCCAGCAGCAATCCAAAGAGTCTCAAG 1019
1067 GATCCTTCAAAATCACTTCAAGGCTCCATATGGGAGAGTAAAGACAAAGACTTAAAGAA 1126
1020 GATCCTTCAAAATCACTTCAAGGCTCCATATGGGAGAGTAAAGACAAAGACTTAAAGAA 1079
1127 CAGCTTGGGCTCAACAGAACAGTGAAGAATCCATTCAGGAATCAGAACTTTTGTG 1186
1080 CAGCTTGGGCTCAACAGAACAGTGAAGAATCCATTCAGGAATCAGAACTTTTGTG 1139
1187 CCTCAGAGCATACCTCAGAGAGATACAAAGATGAAGCAAGCCCTAGGAATCTGCCTG 1246
1140 CCTCAGAGCATACCTCAGAGAGATACAAAGATGAAGCAAGCCCTAGGAATCTGCCTG 1199
1247 ATATCGATTGCAATGGCAATGAGACAGAGCTTCTTCGAGACACCTTCACTTCCCTGGGC 1306
1200 ATATCGATTGCAATGGCAATGAGACAGAGCTTCTTCGAGACACCTTCACTTCCCTGGGC 1259
1307 TATGAAGTCCAGAAATCTTGCATCTCAGTATCCATGATATATCCAGATCTTGGCCAA 1366
1260 TATGAAGTCCAGAAATCTTGCATCTCAGTATCCATGATATATCCAGATCTTGGCCAA 1319
1367 TTTGCTGTATGATCCCGAGCACCCGAGACTACGACAGCTTTGTGTGTCTCTGTGAGCCGA 1426
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1320 TTTTGGCTGTATGCCGAGCACCAGAGACTACGACAGCTTGTGTGTCTCTGTGTGAGCCGA 1379
1427 GGAGGCTCCACAGAGTGTGTATGGTGGATCAGACTCACTCAGGCTCCCTCGATCAC 1486
1380 GGAGGCTCCACAGAGTGTGTATGGTGGATCAGACTCACTCAGGCTCCCTCGATCAC 1439
1487 ATCAGGAGGATGTTTCATGGGAGATTCATGCCCTTATCTAGCAGGGAAGCAAGATGTTT 1546
1440 ATCAGAGGATGTTTCATGGGAGATTCATGCCCTTATCTAGCAGGGAAGCAAGATGTTT 1499
1547 TTTTATTCAGAACTATGTGTGTGAGGCGGACAGTGGAGAAACAGACGCTCTTGGAGGTG 1606
1500 TTTTATTCAGAACTATGTGTGTGAGGCGGACAGTGGAGAAACAGACGCTCTTGGAGGTG 1559
1607 GATGGCCAGCAGATGAAGAATGTGGAATTTCAAGGCTCAGAAGCGAGGCTGTGCACAGTT 1666
1560 GATGGCCAGCAGATGAAGAATGTGGAATTTCAAGGCTCAGAAGCGAGGCTGTGCACAGTT 1619
1667 CACCGAAGCTGACTTCTTCTGGAGCCTGTGTACTGCGGACATGTCCCTGTGGAGCAG 1726
1620 CACCGAAGCTGACTTCTTCTGGAGCCTGTGTACTGCGGACATGTCCCTGTGGAGCAG 1679
1727 TCTCAGAGCTCACCCTCCCTGTACCTGCTCAGTGGCTTCCAGAAACTGAGACAAAGAA 1786
1680 TCTCAGAGCTCACCCTCCCTGTACCTGCTCAGTGGCTTCCAGAAACTGAGACAAAGAA 1739
1787 AAACGCCACTCCTGGATCTTCAATTTGAAGCTCAAGGCTCAGAAGCGAGGCTGTGCACAGC 1846
1740 AAACGCCACTCCTGGATCTTCAATTTGAAGCTCAAGGCTCAGAAGCGAGGCTGTGCACAGC 1799
1847 AGAGTTTCTCCCAAGAGAGAAATATATGTCTGGCTGCGAGCAGCACTGTGAGAAAGAACT 1906
1800 AGAGTTTCTCCCAAGAGAGAAATATATGTCTGGCTGCGAGCAGCACTGTGAGAAAGAACT 1859
1907 ATCTCTCTTACACATAAAGAAACCAAAAGCTTGGGCTAGTGGCTCACACCTGTAAATCCC 1966
1860 ATCTCTCTTACACATAAAGAAACCAAAAGCTTGGGCTAGTGGCTCACACCTGTAAATCCC 1919
1967 AGCACTTTGGAGGCCCAAGGAGGCGAGATCACTTCAGGTCAGGAGTTCGAGACCCAGCCTG 2026
1920 AGCACTTTGGAGGCCCAAGGAGGCGAGATCACTTCAGGTCAGGAGTTCGAGACCCAGCCTG 1979
2027 GCCAACATGTTAAACGC 2043
1980 GCCAACATGTTAAACGC 1996

RESULT 10
AAV50436
ID AAV50436 standard; cdNA; 2045 BP.
XX
AC AAV50436;
XX
DT 24-NOV-1998 (first entry)
XX
DE Human Casper gene.
XX
KW Casper gene; caspase-eight-related protein; human; apoptosis; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
CDS 511..1953
FT /*tag= a
XX
PN WO9833883-Al.
XX
PD 06-AUG-1998.
XX
PF 05-FEB-1998; 98WO-US02117.
XX
PR 05-FEB-1997; 97US-0795088.
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XX	(TULA-) TULARIK INC.
PA	Goeddel DV, Shu H;
XX	
PI	WPI: 1998-437440/37.
XX	P-FSDB; AAW69715.
DR	
DR	New Casper protein involved in regulation of apoptosis - used, e.g.
PT	to identify specific modulators, identify or isolate similar
PT	sequences and in gene therapy
XX	
PS	Claim 7; Page 21; 29pp; English.
XX	
CC	This CDNA clone includes a coding region for a novel human protein
CC	(see AAW69715), designated Casper (for caspase-eight-related protein),
CC	that is involved in regulation of apoptosis. The clone was
CC	isolated from a human expressed sequence tag database in a
CC	search for potential FADD-related genes. The isolated protein, or
CC	cells that express the protein, can be used to screen for agents,
CC	e.g. antibodies or T-cell receptors, that specifically modify the
CC	binding of Casper to a target, and thus its function. Nucleic acid
CC	sequences encoding Casper, or fragments of them, are used e.g. as
CC	probes and primers for diagnostic detection of Casper genes and
CC	their transcripts, for isolation of related sequences and for
CC	identification of wild-type or mutant alleles, also in gene therapy
CC	to modulate expression of active Casper protein (using antisense or
CC	sense sequences). They are also used for recombinant production of
CC	Casper and to generate transgenic animals for testing candidate
CC	drugs for Casper-associated diseases.
XX	
SQ	Sequence 2045 BP; 551 A; 475 C; 560 G; 459 T; 0 other;

Query Match	87.0%;	Score 1952.2;	DB 19;	Length 2045;
Best Local Similarity	99.8%;	Pred. No. 0;		
Matches 1965;	Conservative	0;	Mismatches	3; Indels
				1; Gaps

Qy	48	GCGAGCTTGCAAGCCTCACGACGTATCCGACGAGTCCTCAACTAAAGGGAGCTCCC	CGGAGCTTAGGGGTGG	107
Dd	78	GAGAGCTTGCAAGCCTCACGACGAGTCCTCAACTAAAGGGAGCTCCC	CGGAGCTTAGGGGTGG	137
Qy	108	GGACTCGGCCTCACACAGTGAAGTCGGGCTATTGGACTTTTGTCAGTGACAGCTGAGAC	167	
Dd	138	GGACTCGGCCTCACACAGTGAAGTCGGGCTATTGGACTTTTGTCAGTGACAGCTGAGAC	197	
Qy	168	AACAAGACCACGGAGGAGGTGTAGGAGAAGCGCCGCCAACAGCATCCCCAGGAC	227	
Dd	198	AACAAGACCACGGAGGAGGTGTAGGAGAAGCGCCGCCAACAGCATCCCCAGGAC	257	
Qy	228	CAAGTCGGCTTCCAGGCTTTCGGTTTCTTTGCTCCATCTTTGGGTGCGCTTCCCGGGT	287	
Dd	258	CAAGTCGGCTTCCAGGCTTTCGGTTTCTTTGCTCCATCTTTGGGTGCGCTTCCCGGGT	317	
Qy	288	CTAGGGAGCGAAGCGCTAGGTGCGCGGACGAGAGCTCCGGCCGCCNACAGGAGCACT	347	
Dd	318	CTAGGGAGCGAAGCGCTAGGTGCGCGGACGAGAGCTCCGGCCGCCNACAGGAGCACT	377	
Qy	348	CCCCACTGGAAGGATTTCTCAAAGAAATGAAGTCAGCCCTCAGAAAATGAAGTTGACATGC	407	
Dd	378	CCCCACTGGAAGGATTTCTCAAAGAAATGAAGTCAGCCCTCAGAAAATGAAGTTGACATGC	437	
Qy	408	CTGCTGGCTTTCCTGTTGATGCGCCCGGAGCTGTACTGCAAGACCCCTTGTGAGCTTCCT	467	
Dd	438	CTGCTGGCTTTCCTGTTGATGCGCCCGGAGCTGTACTGCAAGACCCCTTGTGAGCTTCCT	496	
Qy	468	AGTCTAAGAGTAGATGCTCTGCTGAAGTCATCCATCAGGTTGAAGAAGCACTTGTATACAG	527	
Dd	497	AGTCTAAGAGTAGATGCTCTGCTGAAGTCATCCATCAGGTTGAAGAAGCACTTGTATACAG	556	
Qy	528	ATGAGAAGGAGATCTGCTCTTTTTGTCGCGGGATGTTGCTATAGATCTGGTTCCACCTTA	587	
Dd	557	ATGAGAAGGAGATCTGCTCTTTTTGTCGCGGGATGTTGCTATAGATCTGGTTCCACCTTA	616	

QY	1223	AGCAAGCCCTAGGAATCTGCTGATATCGATTGCAATGGCAATGAGACAGAGCTTCTT	1282
Db	1246	AGCAAGCCCTAGGAATCTGCTGATATCGATTGCAATGGCAATGAGACAGAGCTTCTT	1305
QY	1283	CGAGACACTTCACATTCCTCGGCTATGAAGTCCAGAAATCTTCATCTCAGTATGAT	1342
Db	1306	CGAGACACTTCACATTCCTCGGCTATGAAGTCCAGAAATCTTCATCTCAGTATGAT	1365
QY	1343	GATATATCCAGATTCCTTGGCAATTTGCTGTATGCCGAGCACCCGAGACTACACAGC	1402
Db	1366	GATATATCCAGATTCCTTGGCAATTTGCTGTATGCCGAGCACCCGAGACTACACAGC	1425
QY	1403	TTTGTGTGTCTGCTGGTGAGCCGAGAGGCTCCAGAGTGTGTATGATGATGATGAT	1462
Db	1426	TTTGTGTGTCTGCTGGTGAGCCGAGAGGCTCCAGAGTGTGTATGATGATGATGAT	1485
QY	1463	CACTCAGGCTCCCTCTGCATCATCAGGAGGATGTTTCATGGGAGATTCATGCCCTTAT	1522
Db	1486	CACTCAGGCTCCCTCTGCATCATCAGGAGGATGTTTCATGGGAGATTCATGCCCTTAT	1545
QY	1523	CTAGCAGGGAAGCCAAAGATGTTTTTATTCAGAACTATGTGTGTCTCAGAGGGCCAGCTG	1582
Db	1546	CTAGCAGGGAAGCCAAAGATGTTTTTATTCAGAACTATGTGTGTCTCAGAGGGCCAGCTG	1605
QY	1583	GAGACAGAGCCTCTTGAGGTGGATGGCCAGCGATGAAGAATGTGAATTCAGGCT	1642
Db	1606	GAGACAGAGCCTCTTGAGGTGGATGGCCAGCGATGAAGAATGTGAATTCAGGCT	1665
QY	1643	CAGACAGAGGCTGTGCACACTTCACGAGAGCTGACTTCTTCTGGAGCTGTACT	1702
Db	1666	CAGACAGAGGCTGTGCACACTTCACGAGAGCTGACTTCTTCTGGAGCTGTACT	1725
QY	1703	GCGGACATGTCCTCTGAGCAGCTCACAGCTCACCGTCCCTGTACTCGAGTGCCTC	1762
Db	1726	GCGGACATGTCCTCTGAGCAGCTCACAGCTCACCGTCCCTGTACTCGAGTGCCTC	1785
QY	1763	TCCGAGAACTGAGACAGAAAGAAAGCCCACTCTGATCTTCATATGAATCAAT	1822
Db	1786	TCCGAGAACTGAGACAGAAAGAAAGCCCACTCTGATCTTCATATGAATCAAT	1845
QY	1823	GGCTACATGTATGATTGGAACAGCAGAGTTTCTGCCAAGGAGAAATATATCTCTGGCTG	1882
Db	1846	GGCTACATGTATGATTGGAACAGCAGAGTTTCTGCCAAGGAGAAATATATCTCTGGCTG	1905
QY	1883	CAGCAGCTCTGAGAAAGAACTTATCTCTCTACACATAGAAACCAAGGCTGGGC	1942
Db	1906	CAGCAGCTCTGAGAAAGAACTTATCTCTCTACACATAGAAACCAAGGCTGGGC	1965
QY	1943	GTAGTGGCTCACACCTGTATCCAGCAGCTTTGGGAGGCCAGGAGGAGATCACTCA	2002
Db	1966	GTAGTGGCTCACACCTGTATCCAGCAGCTTTGGGAGGCCAGGAGGAGATCACTCA	2025
QY	2003	GCTCAGGAGTTCGAGACAGCCTGGCCACATGTTAAAGCTGTCCCTAGTAAAAATGC	2061
Db	2026	GCTCAGGAGTTCGAGACAGCCTGGCCACATGTTAAAGCTGTCCCTAGTAAAAATAC	2084

RESULT 12
AAV74136

ID AAV74136 standard; cdna; 1750 BP.

XX AAV74136;

AC AAV74136;

XX 12-APR-1999 (first entry)

XX Human FLAME-1 cdna.

XX FLAME-1; FADD-like apoptotic/anti-apoptotic molecule; human;

XX apoptosis; HIV; infection; Alzheimer's disease; cancer; therapy;

XX ds.

XX Homo sapiens.

XX

Key	Location/Qualifiers
CDS	413..1750
	/*tag= a
PN	WO9852963-A1.
XX	26-NOV-1998.
PD	
XX	20-MAY-1998; 98WO-US10200.
PF	
XX	20-MAY-1997; 97US-0859167.
PR	
XX	(UYJE-) UNIV JEFFERSON THOMAS.
PA	
PI	Alnemri ES;
XX	
DR	WPI: 1999-045296/04.
DR	P-PSDB; AAW90107.
XX	
PT	New isolated FADD-like anti-apoptotic molecules - used to develop
PT	apoptotic and anti-apoptotic agents for treating, e.g. HIV
PT	infection, Alzheimer's disease or neoplastic conditions
PS	Claim 12; Page 36-38; 68pp; English.
XX	
CC	This cdna sequence codes for human FLAME-1 (see AAW90107), or
CC	FADD-like apoptotic/anti-apoptotic molecule 1. FLAME-1 is a novel
CC	anti-apoptotic protein that interacts specifically with FADD, Mch4,
CC	Mch5 and FLAME-2. It is recruited to the Fas receptor complex and
CC	can abrogate Fas/TNF-induced apoptosis upon expression in
CC	Fas/TNF-sensitive MCF-7 cells. The full-length FLAME-1 gene was mapped to
CC	chromosome 2q33-34. The full-length FLAME-1 cdna was isolated from
CC	a Jurkat cdna library using a partial FLAME-1 cdna probe that had
CC	itself been generated from the Jurkat library using primers (see
CC	AAV84139-42) based on an isolated EST clone. Host cells, recombinant
CC	vectors, and methods of using FLAME-1 to identify substrates,
CC	activators or inhibitors of FLAME-1 are provided. FLAME-1,
CC	FLAME-2 (see AAW90108) and agonists can be used to inhibit apoptosis,
CC	e.g. for treating HIV infection or Alzheimer's disease. Inhibitors
CC	of the polytypeptides can be used as apoptotic agents. FLAME nucleic
CC	acid molecules can be used for gene therapy, e.g. antisense
CC	oligonucleotides can be used in vivo for antineoplastic purposes.
XX	
SQ	Sequence 1750 BP; 465 A; 400 C; 476 G; 409 T; 0 other;
Query Match	72.2%; Score 1619.2; DB 20; Length 1750;
Best Local Similarity	94.1%; Pred No. 0;
Matches 1747; Conservative	0; Mismatches 3; Indels 106; Gaps 2;
QY	69 CGAGTCTCAACTAAAGGAGCTCCCGAGAGCTAGGGGTGGGACTCGGCTTCACAGTGA 128
Db	1 CGAGTCTCAACTAAAGGAGCTCCCGAGAGCTAGGGGTGGGACTCGGCTTCACAGTGA 60
QY	129 GTGCCGGCTATTTGGACTTTTGTCCAGTGCAGCTGACAGCTAGACAGGACACGGAGGAGG 188
Db	61 GTGCCGGCTATTTGGACTTTTGTCCAGTGCAGCTGACAGCTAGACAGGACACGGAGGAGG 120
QY	189 TGTAGGAGAGAGCCCGCAACAGCAGATCGCCAGCAGCAGCAAGTCCGCTTCAGGCTTTC 248
Db	121 TGTAGGAGAGAGCCCGCAACAGCAGATCGCCAGCAGCAGCAAGTCCGCTTCAGGCTTTC 180
QY	249 GGTTCCTTTGCTCCATCTTTGGGTGCGCTTCCCGGCGTCTTAGGGAGGAGGAGGCTGAGG 308
Db	181 GGTTCCTTTGCTCCATCTTTGGGTGCGCTTCCCGGCGTCTTAGGGAGGAGGAGGCTGAGG 240
QY	309 TGGCAGCGGAGGAGAGTCCCGCCGAGCAGACAGCACTCCCGCTTCAGGAGGATTCG 368
Db	241 TGGCAGCGGAGGAGAGTCCCGCCGAGCAGACAGCACTCCCGCTTCAGGAGGATTCG 300
QY	369 AAAGAATGAAGTCAAGCTCAGAAATGAAGTTGACTGCCTGCTGGCTTCTCTGTTGACT 428
Db	301 AAAGAATGAAGTCAAGCTCAGAAATGAAGTTGACTGCCTGCTGGCTTCTCTGTTGACT 359

QY	429	GGCCCCGAGGTGTACTGCAAGACCCCTGTGTAGAGTCTCCCTTAGTCTCAAGAGTAGGATGTCTG	488
Db	360	GGCCCCGAGGTGTACTGCAAGACCCCTGTGTAGAGTCTCCCTTAGTCTCAAGAGTAGGATGTCTG	419
QY	489	CTCAAGCTCATCCATCAGTGTGAAGAAGCACTTGATACAGATCAGAGGAGAGATGCTGCTCT	548
Db	420	CTGAAGTCACTCCATCAGGTGAAGAAGCACTTGATACAGATCAGAGGAGAGATGCTGCTCT	479
QY	549	TTTTTGTCCGGGATGTGTCTATAGATGTGTTTCCACCTAATGTCAGGGACCTTCTTGGATA	608
Db	480	TTTTTGTCCGGGATGTGTCTATAGATGTGTTTCCACCTAATGTCAGGGACCTTCTTGGATA	539
QY	609	TTTTTACGGGAAAGAGTAAGCTGTGTGTCGGGACTTGCTGAACTGCTCTACAGAGTGA	668
Db	540	TTTTTACGGGAAAGAGTAAGCTGTGTGTCGGGACTTGCTGAACTGCTCTACAGAGTGA	599
QY	669	GGCGATTTGACCTGCTCAACAGTATCTTGAAGATGGACAGAAAAGCTGTGGAGACCCACC	728
Db	600	GGCGATTTGACCTGCTCAACAGTATCTTGAAGATGGACAGAAAAGCTGTGGAGACCCACC	659
QY	729	TGCTCAGGAACCCCTCACCCTGTGTTCCGACTATAGAGTGTCTGATGGCAGAGATTTGTGAGG	788
Db	660	TGCTCAGGAACCCCTCACCCTGTGTTCCGACTATAGAGTGTCTGATGGCAGAGATTTGTGAGG	719
QY	789	ATTTGGATAAATCTGATGTCTCTCATTAATTTTCCATGAAGGATTAACATGGGCCGAG	848
Db	720	ATTTGGATAAATCTGATGTCTCTCATTAATTTTCCATGAAGGATTAACATGGGCCGAG	779
QY	849	GCAAGATAACCAAGGAGAGAGTTTCTTGACCTTGTGGTGTAGTTGGAGAACTAAAT	908
Db	780	GCAAGATAACCAAGGAGAGAGTTTCTTGACCTTGTGGTGTAGTTGGAGAACTAAAT	839
QY	909	TGTTTGCCCCCAGATCAACTGCATTTATTAGAAAATGCCTAAAGAACATCCACAGAAATAG	968
Db	840	TGTTTGCCCCCAGATCAACTGCATTTATTAGAAAATGCCTAAAGAACATCCACAGAAATAG	899
QY	969	ACCTGAAGACAAAATCCAGAAGTACAAGCAGTCTGTTCAAGGAGCAGGACCAAGTTACA	1028
Db	900	ACCTGAAGACAAAATCCAGAAGTACAAGCAGTCTGTTCAAGGAGCAGGACCAAGTTACA	959
QY	1029	GGATGTCTCCAGCAGCAATCCAAAAGTCTCAAGGATCCTTCAAACTCACTTCAGGC	1088
Db	960	GGATGTCTCCAGCAGCAATCCAAAAGTCTCAAGGATCCTTCAAACTCACTTCAGGC	1017
QY	1089	TCCATAATGGGAGAAAGTAAAGACAAAGACTTAAGGAACAGTGTGGCGTCAACAAGAAC	1148
Db	1018	-----	1017
QY	1149	CAGTGAAGAAATCCATTCAGGAATCAGAACTTTTTCCTTCAGAGCATACCTGAAGAGA	1208
Db	1018	-----GAGCATACCTGAAGAGA	1034
QY	1209	GATACAAGATGAAGAGCAAGCCCTAGGAATCTGCCTGATAATCGATTGCAATTTGGCAATG	1268
Db	1035	GATACAAGATGAAGAGCAAGCCCTAGGAATCTGCCTGATAATCGATTGCAATTTGGCAATG	1094
QY	1269	AGACAGAGCTTCTTCGAGACACCTTCACTTCCCTGGCTATGAAGTCCAGAAATTTCTGC	1328
Db	1095	AGACAGAGCTTCTTCGAGACACCTTCACTTCCCTGGCTATGAAGTCCAGAAATTTCTGC	1154
QY	1329	ATCTCAGTATGATGGTATATCCAGATTTCTTGCCCAATTTGCCTGTATGCCCGAGCACCC	1388
Db	1155	ATCTCAGTATGATGGTATATCCAGATTTCTTGCCCAATTTGCCTGTATGCCCGAGCACCC	1214
QY	1389	GAGACTAGCAGACTTTGTGTGTGTCCTGTGTAGCCGAGAGGCTCCACAGTGTGTATG	1448
Db	1215	GAGACTAGCAGACTTTGTGTGTGTCCTGTGTAGCCGAGAGGCTCCACAGTGTGTATG	1274
QY	1449	GTGTGGATCAGACTCACTCAGGCTCCCTCGCATCATCAGAGGATGTTTCATGGGAG	1508
Db	1275	GTGTGGATCAGACTCACTCAGGCTCCCTCGCATCATCAGAGGATGTTTCATGGGAG	1334
QY	1509	ATTTCATGCCCTTATCTACGAGGGAAGCAAGATGTTTTTTATTTCAGAACTATGTGGTGT	1568

Db	1335	ATTCATGCCCTTA	CTATCAGAGGAGCCAAAGATGTTTTTATTCAGAACTATGTGGTGT	1394
QY	1569	CAGAGGGCCAGCTGGAGAAACAGCAGCCTCTTTGGAGGTGGATGGGCCAGCGATGAAGAATG	1628	
Db	1395	CAGAGGGCCAGCTGGAGGACAGCAGCCTCTTTGGAGGTGGATGGGCCAGCGATGAAGAATG	1454	
QY	1629	TGGAATTCAGGCTCAGACGAGGGGTGTGCACAGTTACCCAGAGAAGCTGACTTCTTCT	1688	
Db	1455	TGGAATTCAGGCTCAGAGAAGGGGTGTGCACAGTTACCCAGAGAAGCTGACTTCTTCT	1514	
QY	1689	GGAGCCTGTGTACTGCGGCACATGTCCTGCTGGAGCAGTCTCACAGCTCACCGTCCCTGT	1748	
Db	1515	GGAGCCTGTGTACTGCGGCACATGTCCTGCTGGAGCAGTCTCACAGCTCACCGTCCCTGT	1574	
QY	1749	ACCTGCAGTGCCTCTCCAGAAACTGAGACAAGAAAGAAAACGCCCACTCCTCGATCTTC	1808	
Db	1575	ACCTGCAGTGCCTCTCCAGAAACTGAGACAAGAAAGAAAACGCCCACTCCTCGATCTTC	1634	
QY	1809	ACATTGAACTCAAATGGCTACATGTTATGATTGGAACAGCAGAGTTTCTGCGCAAGGAGAAAT	1868	
Db	1635	ACATTGAACTCAAATGGCTACATGTTATGATTGGAACAGCAGAGTTTCTGCGCAAGGAGAAAT	1694	
QY	1869	ATTATGTTCTGGCTGCAGCACACTCTGAGAAGAAACTTATCTCTCTACACATAA	1924	
Db	1695	ATTATGTTTGGCTGCAGCACACTCTGAGAAGAAACTTATCTCTCTACACATAA	1750	
RESULT 13				
AAD43202				
ID	AAD43202 standard; cDNA; 1750 BP.			
XX	AAD43202;			
DT	14-NOV-2002 (first entry)			
XX	Human FLAME-1 cDNA.			
DE	Human; FADD-like apoptotic/anti-apoptotic protein; Alzheimer's disease;			
KW	gene therapy; human immunodeficiency virus; HIV infection; apoptosis;			
KW	FLAME-1; gene; ss.			
XX	Homo sapiens.			
OS	Homo sapiens.			
XX	Key Location/Qualifiers			
FH	CDS 413..1750			
FT	/*tag= a			
FT	/product= "Human FLAME-1 protein"			
XX	US2002086983-A1.			
XX	04-JUL-2002.			
XX	22-AUG-2001; 2001US-0935223.			
XX	28-OCT-1997; 97US-0959167.			
PR	26-MAR-1999; 99US-0276993.			
PR	28-NOV-2000; 2000US-0723450.			
XX	(UYJE-) UNIV JEFFERSON THOMAS.			
PA	Alnemri ES;			
XX	WPI; 2002-642259/69.			
PI	P-PSDB; AAE26086.			
XX	Novel FADD-like apoptotic/anti-apoptotic proteins useful for inhibiting			
DR	apoptosis, treating diseases characterized by apoptosis e.g. HIV			
DR	infection and Alzheimer's disease, and for identifying modulators of			
XX	the protein			
XX	Claim 7; Page 12-14; 35pp; English.			
PS				
XX				

CC The invention relates to FADD-like apoptotic/anti-apoptotic proteins
CC (FLAME 1 or 2) and nucleic acid molecules encoding such proteins.
CC FLAME sequences are useful for inhibiting apoptosis and for gene
CC therapy of diseases characterised by apoptosis including HIV
CC infection and Alzheimer's disease. FLAME inhibitors are useful as
CC apoptotic agents and activators are useful as anti-apoptotic agents.
CC FLAME-1 is useful as a substrate for caspase in assays to identify
CC caspase inhibitors. The present sequence is human FLAME-1 cDNA.
xx

SO Sequence 1750 BP; 465 A; 400 C; 476 G; 409 T; 0 other;

Query Match 72.2%; Score 1619.2; DB 24; Length 1750;
Best Local Similarity 94.1%; Pred. No. 0;
Matches 1747; Conservative 0; Mismatches 3; Indels 106; Gaps 2;

Qy	69	CGAGTCTCAACTAAAGGGACTCCCGGAGCTAGGGTGGGACCTCGGCTCACACAGTGA	128
Db	1	CGAGTCTCAACTAAAGGGACTCCCGGAGCTAGGGTGGGACCTCGGCTCACACAGTGA	60
Qy	129	GTGCGGGCTATTGGACTTTTGTCCAGTGACAGCTGAGACAAAGAGCAGCGGAGGAGG	188
Db	61	GTGCGGGCTATTGGACTTTTGTCCAGTGACAGCTGAGACAAAGAGCAGCGGAGGAGG	120
Qy	189	TGTAGGAGAGAGCGCGGAGACAGCGATGCCAGCACCAAGTCCGCTTCCAGGCTTC	248
Db	121	TGTAGGAGAGAGCGCGGAGACAGCGATGCCAGCACCAAGTCCGCTTCCAGGCTTC	180
Qy	249	GGTTTCTTGGCTCCATCTTGGGTGGGCTTCCCGGCTCTAGGGGAGCGAAGCTGAGG	308
Db	181	GGTTTCTTGGCTCCATCTTGGGTGGGCTTCCCGGCTCTAGGGGAGCGAAGCTGAGG	240
Qy	309	TGGCAGCGGAGAGAGTCCGGCGGACAGAGCAACTCCCCCACTGGAAAGATTCTG	368
Db	241	TGGCAGCGGAGAGAGTCCGGCGGACAGAGCAACTCCCCCACTGGAAAGATTCTG	300
Qy	369	AAAGAAATGAGTCAGCCCTCAGAAATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT	428
Db	301	AAAGAAATGAGTCAGCCCTCAGAAATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT	359
Qy	429	GGCCCGGAGCTGTACTGCAAGACCTTGTGAGCTTCCCTAGTCTAAGAGTAGGATGCTG	488
Db	360	GGCCCGGAGCTGTACTGCAAGACCTTGTGAGCTTCCCTAGTCTAAGAGTAGGATGCTG	419
Qy	489	CTGAAGTCATCCATCAGGTTGAAGACACTTTGATACAGATGAGAGAGATGCTGCT	548
Db	420	CTGAAGTCATCCATCAGGTTGAAGACACTTTGATACAGATGAGAGAGATGCTGCT	479
Qy	549	TTTTGTGCGGGATGTTGCTATAGATGTGTTCCACCTAATGTCAGGAGCCTTCTGGATA	608
Db	480	TTTTGTGCGGGATGTTGCTATAGATGTGTTCCACCTAATGTCAGGAGCCTTCTGGATA	539
Qy	609	TTTTACGGGAAGAGGTAAGTGTCTGTGCGGGACTTGGCTGAAGTGTCTACAGAGTGA	668
Db	540	TTTTACGGGAAGAGGTAAGTGTCTGTGCGGGACTTGGCTGAAGTGTCTACAGAGTGA	599
Qy	669	GGCGATTGACCTGCTCAAGAGTATCTGAAGATGGACAGAAAAGCTGTGGAGACCCACC	728
Db	600	GGCGATTGACCTGCTCAAGAGTATCTGAAGATGGACAGAAAAGCTGTGGAGACCCACC	659
Qy	729	TGCTCAGGAACCTCACCCTGTTTCGGACTATAGTGTCTGATGCGCAGAGATTGGTAGG	788
Db	660	TGCTCAGGAACCTCACCCTGTTTCGGACTATAGTGTCTGATGCGCAGAGATTGGTAGG	719
Qy	789	ATTTGGATAATCTGATGTGCTTCAATTAATTTTCCATGAAGGATTACATGGCCGAG	848
Db	720	ATTTGGATAATCTGATGTGCTTCAATTAATTTTCCATGAAGGATTACATGGCCGAG	779
Qy	849	GCAAGATAAGCAAGAGAGAGTCTTCTGGACCTTGTGGTGTGAGTGGAGAACTAAAT	908
Db	780	GCAAGATAAGCAAGAGAGAGTCTTCTGGACCTTGTGGTGTGAGTGGAGAACTAAAT	839
Qy	909	TGGTGGCCCGAGATCACTGGATTATTTAGAAAAATGCCTAAGAACTCCACAGATAG	968

Db	840	TGGTGGCCCGAGATCAACTGGATTATTAGAAAAATGCCTAAAGAACATCCACAGATAG	899
Qy	969	ACCTGAAGACAAAAATCCAGAAGTACAGCAGTCTGTTCAAGAGGACGGGACAAAGTTACA	1028
Db	900	ACCTGAAGACAAAAATCCAGAAGTACAGCAGTCTGTTCAAGAGGACGGGACAAAGTTACA	959
Qy	1029	GGATGTTCTCCAAGCAGCAATCCAAAAGAGTCTCAAGGATCCTTCAATTAACCTCAGGC	1088
Db	960	GGATGTTCTCCAAGCAGCAATCCAAAAGAGTCTCAAGGATCCTTCAATTAACCTCAG--	1017
Qy	1089	TCCATAATGGGAGAAGTAAAGAACAAAGACTTAAGGAACAGCTTGGCGCTCAACAAGAAC	1148
Db	1018	-----	1017
Qy	1149	CAGTGAAGAAATCCATTCCAGGAATCAGAAAGCTTTTTTGCCTCAGAGCATACCTGAAGAGA	1208
Db	1018	-----GAGCATACCTGAAGAGA	1034
Qy	1209	GATACAAGATGAAGAGCAGCCCTAGGAATCTGCCTGATATATCGATTGCAATTTGGCAATG	1268
Db	1035	GATACAAGATGAAGAGCAGCCCTAGGAATCTGCCTGATATATCGATTGCAATTTGGCAATG	1094
Qy	1269	AGACAGAGCTTCTTCGAGACACCTTCACTTCCCTGGGCTATCAAGTCCAGAAATCTTTGC	1328
Db	1095	AGACAGAGCTTCTTCGAGACACCTTCACTTCCCTGGGCTATCAAGTCCAGAAATCTTTGC	1154
Qy	1329	ATCTCAGTATGCATGGTATATCCAGATTTCTTGGCAATTTTGCCTGTATGCCGAGCACC	1388
Db	1155	ATCTCAGTATGCATGGTATATCCAGATTTCTTGGCAATTTTGCCTGTATGCCGAGCACC	1214
Qy	1389	GAGACTAGCAGAGCTTGTGTGTCTGTGAGCGGAGGAGGCTTCCAGAGTGTGTATG	1448
Db	1215	GAGACTAGCAGAGCTTGTGTGTCTGTGAGCGGAGGAGGCTTCCAGAGTGTGTATG	1274
Qy	1449	GTGTGGATGACACTCAGCTCAGCGCTTCCCTGTCATCATCAGCAGGAGTGTTCATGGAG	1508
Db	1275	GTGTGGATGACACTCAGCTCAGCGCTTCCCTGTCATCATCAGCAGGAGTGTTCATGGAG	1334
Qy	1509	ATTCATGCCCCCTTATAGCAGGAGGAAAGCAAGATGTTTTTTATTCAGAACTATGTGTGT	1568
Db	1335	ATTCATGCCCCCTTATAGCAGGAGGAAAGCAAGATGTTTTTTATTCAGAACTATGTGTGT	1394
Qy	1569	CAGAGGCGCAGCTGGAGACAGCAGCTTCTTGGAGGTGGATGGGCCAGGATGAAGATG	1628
Db	1395	CAGAGGCGCAGCTGGAGACAGCAGCTTCTTGGAGGTGGATGGGCCAGGATGAAGATG	1454
Qy	1629	TGGAATTCAGGCTCAGAAAGCAGGCTGTGCACAGTTTCACGAGAGCTGACTTCTTCT	1688
Db	1455	TGGAATTCAGGCTCAGAAAGCAGGCTGTGCACAGTTTCACGAGAGCTGACTTCTTCT	1514
Qy	1689	GGAGCCTGTGTACTGCGGACATGTCCCTGTCTGGAGCAGTCTCAGAGCTCAGCCTCCCTGT	1748
Db	1515	GGAGCCTGTGTACTGCGGACATGTCCCTGTCTGGAGCAGTCTCAGAGCTCAGCCTCCCTGT	1574
Qy	1749	ACCTGAGTGCCTCTCCAGAACTTGACAGAAAGAAAGAAAGCCCACTCTCTGGATCTTC	1808
Db	1575	ACCTGAGTGCCTCTCCAGAACTTGACAGAAAGAAAGAAAGCCCACTCTCTGGATCTTC	1634
Qy	1809	ACATTTGAATCAATGGCTTACATGATGATTTGGAACAGCAGATTTCTCCCAAGGAGAAAT	1868
Db	1635	ACATTTGAATCAATGGCTTACATGATGATTTGGAACAGCAGATTTCTCCCAAGGAGAAAT	1694
Qy	1869	ATTATGTCTGGCTGAGCAGCACTCTGAGAAAGAAACTTATCTCTCTCTACACATAA	1924
Db	1695	ATTATGTCTGGCTGAGCAGCACTCTGAGAAAGAAACTTATCTCTCTCTACACATAA	1750

RESULT 14

AAA54301

ID AAA54301 standard; cDNA; 1517 BP.

XX AAA54301;

AC AAA54301;

XX

DT 26-FEB-2001 (first entry)

XX FLIP with detectable amino acid coding sequence.

XX Chimeric protein; fusion protein; FLICE like inhibitor protein;

XX FLIP; Fas; TNF; apoptosis; caspase-8; ligand; T cell; thymocyte;

KW tumour specific antigen; immune response; therapy; prophylaxis;

KW diagnosis; HIV; human immunodeficiency syndrome; AIDS;

KW acquired immune deficiency syndrome; human; ds.

XX Homo sapiens.

OS Synthetic.

OS Key

PH Location/Qualifiers

FT 8..1483

FT /tag= a

FT /product= FLICE like inhibitor protein and

FT detectable peptide tag

XX W0200059935-A1.

XX 12-OCT-2000.

XX 05-APR-2000; 2000WO-US09002.

XX 05-APR-1999; 99US-0127867.

XX 06-APR-1999; 99US-0128021.

XX (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.

PA (PAPA-) PAPA C.

PA (ALGE/) ALGECIRAS-SCHMINICH A.

XX PAPA C, Algeciras-Schminich A;

XX WPT: 2000-564988/64.

DR P-PSDB; AAB03964.

XX Fusion polypeptide useful for inhibiting ligand-induced apoptosis,

PT comprises portion of anti-apoptotic polypeptide linked to a transport

PT group

XX Disclosure; Page 83; 89pp; English.

XX A chimeric group or fusion peptide which comprises a portion of an

CC anti-apoptotic polypeptide which inhibits apoptosis of lymphocytes in

CC combination with a transport group is described. The transport group

CC is capable of transporting the chimeric group or fusion peptide

CC across the cell membrane. The anti-apoptotic polypeptide is FLICE-like

CC inhibitor protein (FLIP) which inhibits Fas and TNF mediated apoptosis

CC by inhibiting binding of Caspase-8 to the Fas receptor complex, thus

CC shutting off the downstream Fas signalling pathway. The chimeric group

CC and fusion peptide are useful for inhibiting ligand-induced apoptosis

CC by bringing them into contact with T cells. The chimeric group is

CC useful for expanding T cells in vitro e.g. T cells specific for

CC particular antigens such as tumour-specific antigen, for enhancing

CC immune response and to inhibit the apoptosis of chronically activated

CC T cells e.g. activated CD4+ T cells in HIV infected patients. The

CC chimeric group is also useful for therapeutic, prophylactic or

CC diagnosis of intracellular delivery of small molecules and

CC macromolecules such as anti-apoptotic polypeptides and nucleic

CC acids encoding such polypeptides.

XX Sequence 1517 BP; 441 A; 326 C; 384 G; 366 T; 0 other;

SQ

Query Match 64.28; Score 1439.2; DB 21; Length 1517;

Best Local Similarity 99.88; Pred. No. 0;

Matches 1441; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 482 ATGCTGCTGAAGTCATCCATCAGGTTGAAGAACGACCTTGATACAGATGAGAGGAGATG 541

|||||

DB 41 ATGCTGCTGAAGTCATCCATCAGGTTGAAGAACGACCTTGATACAGATGAGAGGAGATG 100

|||||

QY 542 CTGCTCTCTTTTGTGCGGGATGTTGCTATAGATGTTGCCACCTAATGTCAGGGACCTT 601

|||||

101 CTGCTCTCTTTTGTGCGGGATGTTGCTATAGATGTTGCCACCTAATGTCAGGACCTT 160

|||||

602 CTGGAATATTTACGGGAAAGAGGTAAGCTGTCTGTGCGGAGCTTGGCTGAATGCTCTAC 661

|||||

161 CTGGAATATTTACGGGAAAGAGGTAAGCTGTCTGTGCGGAGCTTGGCTGAATGCTCTAC 220

|||||

662 AGAGTGAGGCGATTTGACCTGCTCAAACTATCTTGAAGATGACAGAAAGAGCTGTGAG 721

|||||

221 AGAGTGAGGCGATTTGACCTGCTCAAACTATCTTGAAGATGACAGAAAGAGCTGTGAG 280

|||||

722 ACCCAGCTGCTCAGGAACCCCTCACCTGTTTCCGAGCTATAGAGTCTGATGCGAGATTT 781

|||||

281 ACCCAGCTGCTCAGGAACCCCTCACCTGTTTCCGAGCTATAGAGTCTGATGCGAGATTT 340

|||||

782 GGTGAGGATTTGGAATAATCTGATGTCCTCAATTAATTTCTCATGAAGATGATGATG 841

|||||

341 GGTGAGGATTTGGAATAATCTGATGTCCTCAATTAATTTCTCATGAAGATGATGATG 400

|||||

842 GCGGAGGCAAGATGAAGCAAGAGAGTTTCTTGAGCTTGTGGTGTGAGTTGAGAGAA 901

|||||

401 GCGGAGGCAAGATGAAGCAAGAGAGTTTCTTGAGCTTGTGGTGTGAGTTGAGAGAA 460

|||||

902 CTAAATTTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 961

|||||

461 CTAAATTTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 520

|||||

962 AGAATAGACCTGAAGCAAAATCCAGAGTACAGAGTCTGTTCAAGAGAGCAGGACA 1021

|||||

521 AGAATAGACCTGAAGCAAAATCCAGAGTACAGAGTCTGTTCAAGAGAGCAGGACA 580

|||||

1022 AGTTACAGGATTTCTTCCAGCAGCAATCCAAAGAGTCTCAAGATCTTCAANTAAC 1081

|||||

581 AGTTACAGGATTTCTTCCAGCAGCAATCCAAAGAGTCTCAAGATCTTCAANTAAC 640

|||||

1082 TTCAGGCTCCATTAATGGGAGAGTAAAGCAAAAGACTTAAGGAACAGCTTGGCCTCAA 1141

|||||

641 TTCAGGCTCCATTAATGGGAGAGTAAAGCAAAAGACTTAAGGAACAGCTTGGCCTCAA 700

|||||

1142 CAAGAACCACTGAAGAAATCCATTCAGGAATCAGAACTTTTGGCTCAGAGCATACT 1201

|||||

701 CAAGAACCACTGAAGAAATCCATTCAGGAATCAGAACTTTTGGCTCAGAGCATACT 760

|||||

1202 CAAGAGAGATACAGATGAAGAGAGCCCTAGGAATCTGCTGATAATTCATTGCAAT 1261

|||||

761 GAAGAGAGATACAGATGAAGAGAGCCCTAGGAATCTGCTGATAATTCATTGCAAT 820

|||||

1262 GGCAATCAGACAGAGCTTCTTCGACACACCTTCACTTCCCTGGCTATCAAGTCCAGAAA 1321

|||||

821 GGCAATCAGACAGAGCTTCTTCGACACACCTTCACTTCCCTGGCTATCAAGTCCAGAAA 880

|||||

1322 TTCCTGATCTCAGTATGATGATATCCAGATTTCTTGGCAATTTGCTGTATGCTT 1381

|||||

881 TTCCTGATCTCAGTATGATGATATCCAGATTTCTTGGCAATTTGCTGTATGCTT 940

|||||

1382 GAGCACCGAGACTACGACAGCTTTGTGTGTCTGCTGAGCCGAGAGGCTCCAGAGT 1441

|||||

941 GAGCACCGAGACTACGACAGCTTTGTGTGTCTGCTGAGCCGAGAGGCTCCAGAGT 1000

|||||

1442 GTGTATGTTGATCAGACTCACTCAGGGCTCCCTGCTGATCAGATCAGAGGAGTGTTC 1501

|||||

1001 GTGTATGTTGATCAGACTCACTCAGGGCTCCCTGCTGATCAGATCAGAGGAGTGTTC 1060

|||||

1502 ATGGAGATTCATGCTTATCTAGCAGGAGAGCAAGATGTTTATTCAGAGATAT 1561

|||||

1061 ATGGAGATTCATGCTTATCTAGCAGGAGAGCAAGATGTTTATTCAGAGATAT 1120

|||||

1562 GTGTGTGTCAGAGGCCAGCTGAGAACAGAGCTTGTGTGTGAGGTGAGTGGCCAGGATG 1621

|||||

1121 GTGTGTGTCAGAGGCCAGCTGAGAACAGAGCTTGTGTGTGAGGTGAGTGGCCAGGATG 1180

|||||

1622 AAGATGTGGAATTCAGAGCTCAGAGAGGAGGCTGTGTCACAGTTCACCGAGAGCTGAC 1681

|||||

Db 1181 AAGATGTGGATTCAAGGCTCAGACGAGGCGTGTGCACAGTTTCCACGAGAGCTGAC 1240
 Qy 1682 TTCTTCTGGAGCCTGTGTACTGGGACATGTCCTGCTGGAGCAGTGTCTACAGCTCACCG 1741
 Db 1241 TTCTTCTGGAGCCTGTGTACTGGGACATGTCCTGCTGGAGCAGTGTCTACAGCTCACCA 1300
 Qy 1742 TCCTGTACTGAGTCCCTCTCCAGAACTGAGACAAAGAAAGAAACGCCACCTCTG 1801
 Db 1301 TCCTGTACTGAGTCCCTCTCCAGAACTGAGACAAAGAAAGAAACGCCACCTCTG 1360
 Qy 1802 GATCTTCACATTTGAACCTCAATGGCTACATGTATGATTGGAAACAGCAGATTTCTGCCAAG 1861
 Db 1361 GATCTTCACATTTGAACCTCAATGGCTACATGTATGATTGGAAACAGCAGATTTCTGCCAAG 1420
 Qy 1862 GAGAAATATTATGTCTGGCTGCAGCACACTCTGAGAAAGAAACTTATCTCTCTCTACACA 1921
 Db 1421 GAGAAATATTATGTCTGGCTGCAGCACACTCTGAGAAAGAAACTTATCTCTCTCTACACA 1480
 Qy 1922 TAAG 1925
 Db 1481 TAAG 1484
 RESULT 15
 AAZ56988 standard; cDNA; 1389 BP.
 XX
 AC AAZ56988;
 XX
 DT 12-MAY-2000 (first entry)
 DE Usurin-beta polypeptide encoding cDNA.
 KW Usurin-alpha; death effector domain; DED; prodomain; usurin-beta;
 KW usurin-gamma; procaspase-8; CD95; apoptosis; cancer; immunosuppressive;
 KW caspase; cytostatic; antiparkinsonian; antidiabetic; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200003023-A1.
 XX
 PD 20-JAN-2000.
 XX
 PF 07-JUL-1999; 98WO-CA00615.
 XX
 PR 08-JUL-1998; 98US-0092005.
 XX
 PA (MERI) MERCK FROSST CANADA INC.
 XX
 PI Nicholson DW, Rasper DM, Xanthoudakis S, Roy S;
 XX
 DR WPI; 2000-160929/14.
 XX
 PT P-PSDB; AAY67419.
 XX
 PT Novel recombinant DNA molecules and polypeptides for treating apoptosis
 PT mediated diseases e.g. autoimmune diabetes, cancer and Parkinson's
 PT disease
 XX
 PS Claim 2; Fig 10A; 69pp; English.
 XX
 CC The invention provides recombinant nucleic acid molecules encoding
 CC usurin-alpha (lacking the first death effector domain (DED) or its
 CC prodomain), usurin-beta or usurin-gamma. Usurin polypeptides are
 CC useful for in vitro and in vivo identification of usurin-procaspase-8
 CC interaction inhibitor. Usurin is useful as modulator of the sensitivity
 CC of cells to CD95(Fas/Apo-1) mediated apoptosis. Modulation of apoptosis
 CC is useful for treating diseases like autoimmune diabetes, cancer and
 CC Parkinson's disease. Activators and inhibitors of usurin-procaspase-8
 CC interaction are also useful for treating various diseases mediated by
 CC apoptosis. Usurin provides an attractive model for modulating caspase
 CC activation. Sensitivity of cells bearing CD95(Fas/Apo-1) receptor can
 CC be regulated at several levels in the presence of usurin, conferring
 CC resistance to Fas-ligand cell death. The present sequence represents a

CC cDNA encoding the usurin-beta polypeptide.
 XX
 SQ Sequence 1389 BP; 393 A; 296 C; 364 G; 336 T; 0 other;
 Query Match 58.0%; Score 1300.8; DB 21; Length 1389;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1302; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 482 ATGCTGCTGAAATCATCATCAGTTGAAGAAGCAGCTTGTATACAGATGAGAAGGAGATG 541
 Db 1 ATGCTGCTGAAATCATCATCAGTTGAAGAAGCAGCTTGTATACAGATGAGAAGGAGATG 60
 Qy 542 CTGCTCTTTTGTGCGGGGATGTTGCTATAGATGTTGCTTCCACTATGTCAGGACCTT 601
 Db 61 CTGCTCTTTTGTGCGGGGATGTTGCTATAGATGTTGCTTCCACTATGTCAGGACCTT 120
 Qy 602 CTGATATTTTACGGGAAAGAGGTAACTGCTGTCGGGGACTTGGCTGAACCTGCTCTAC 661
 Db 121 CTGATATTTTACGGGAAAGAGGTAACTGCTGTCGGGGACTTGGCTGAACCTGCTCTAC 180
 Qy 662 AGAGTAGGGGATTTGACCTGCTCAAAAGATATCTTGAAGATGGACAGAAAGCTGTGGAG 721
 Db 181 AGAGTAGGGGATTTGACCTGCTCAAAAGATATCTTGAAGATGGACAGAAAGCTGTGGAG 240
 Qy 722 ACCCAGCTGCTCAGGAAACCTTCACTTGTGTCGACTATAGATGCTGATGGCAGAGATT 781
 Db 241 ACCCAGCTGCTCAGGAAACCTTCACTTGTGTCGACTATAGATGCTGATGGCAGAGATT 300
 Qy 782 GGTGAGGATTTGGATAAATCTGATGTCCTCATTAATTTTCCTCATGAAGGATTACATG 841
 Db 301 GGTGAGGATTTGGATAAATCTGATGTCCTCATTAATTTTCCTCATGAAGGATTACATG 360
 Qy 842 GGCCGAGGCAAGATAAGCAAGGAGAGATTTCTTGGACCTTGTGGTGGTGGAGAAA 901
 Db 361 GGCCGAGGCAAGATAAGCAAGGAGAGATTTCTTGGACCTTGTGGTGGTGGAGAAA 420
 Qy 902 CTAATTTGTTGCCCGAGATCAACTGGATTTATTAGAAAAATGCTTAAAGAAATCCAC 961
 Db 421 CTAATTTGTTGCCCGAGATCAACTGGATTTATTAGAAAAATGCTTAAAGAAATCCAC 480
 Qy 962 AGAATAGACCTGAAGACAAAAATCCAGAGTACAGAGTCTGTTTCAAGAGAGAGGACA 1021
 Db 481 AGAATAGACCTGAAGACAAAAATCCAGAGTACAGAGTCTGTTTCAAGAGAGAGGACA 540
 Qy 1022 AGTTACAGGATGTTCTCCAGCAGCAATCCAAAGAGTCTCAAGGATCCTTCAATTAAC 1081
 Db 541 AGTTACAGGATGTTCTCCAGCAGCAATCCAAAGAGTCTCAAGGATCCTTCAATTAAC 600
 Qy 1082 TTCAGGCTCCATAATGGGAGAAAGTAAAGAACAAAGACTTAAAGAACAGCTTGGCGCTCAA 1141
 Db 601 TTCAGGCTCCATAATGGGAGAAAGTAAAGAACAAAGACTTAAAGAACAGCTTGGCGCTCAA 660
 Qy 1142 CAAGAACCAGTGAAGAAATCCATTCAGGAATCAGAAAGCTTTTTCCTCAGAGCATACCT 1201
 Db 661 CAAGAACCAGTGAAGAAATCCATTCAGGAATCAGAAAGCTTTTTCCTCAGAGCATACCT 720
 Qy 1202 GAAGAGATACAGATGAAGCAAGCCCTTAGGAATCGCTCATATGATGATTCATT 1261
 Db 721 GAAGAGATACAGATGAAGCAAGCCCTTAGGAATCGCTCATATGATGATTCATT 780
 Qy 1262 GGCATGAGACAGAGCTTCTTCGAGACACCTTCACTTCCCTGGGCTATGAGTCCAGAAA 1321
 Db 781 GGCATGAGACAGAGCTTCTTCGAGACACCTTCACTTCCCTGGGCTATGAGTCCAGAAA 840
 Qy 1322 TTCTTGCATCTCAGTATGATGATGATATATCCAGATTTCTTGGCAATTTGCTGTATGCC 1381
 Db 841 TTCTTGCATCTCAGTATGATGATGATATATCCAGATTTCTTGGCAATTTGCTGTATGCC 900
 Qy 1382 GAGCAGCAGACTACAGAGCTTTGCTGTCTCTGTTGGTGGCCGAGGAGGCTCCAGAGT 1441
 Db 901 GAGCAGCAGACTACAGAGCTTTGCTGTCTCTGTTGGTGGCCGAGGAGGCTCCAGAGT 960
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Search completed: August 22, 2003, 07:51:26
 Job time : 633.438 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model.

Run on: August 22, 2003, 05:37:21 ; Search time 8370.31 Seconds
(without alignments)
10962.592 Million cell updates/sec

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Perfect score: 2243
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues
Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_hgt.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
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- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
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- 29: em_vl.*
- 30: em_htg_hum.*
- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htg_mus.*
- 34: em_htg_pln.*
- 35: em_htg_rod.*
- 36: em_htg_mam.*
- 37: em_htg_vrt.*
- 38: em_sy.*
- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	2243	100.0	2243	6	A86556	A86556 Sequence 1
2	2243	100.0	2243	6	BD105908	BD105908 CASH(Casp
3	2243	100.0	2243	9	HSY14039	Y14039 Homo sapien
4	2124	94.7	2143	6	A84918	A84918 Sequence 9
5	2124	94.7	2143	6	BD107658	BD107658 FLIP gene
6	2124	94.7	2143	9	U97074	U97074 Homo sapten
7	2005.8	89.5	2034	6	BD056976	BD056976 I-FLICE,
8	2000.4	89.2	2025	9	BC001602	BC001602 Homo sapi
9	1991	88.8	2040	6	AR194324	AR194324 Sequence
10	1991	88.8	2040	9	AF005774	AF005774 Homo sapi
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12	1952.2	87.0	2045	6	AR156902	AR156902 Sequence
13	1922	85.7	2056	9	AF009616	AF009616 Homo sapi
14	1711.8	76.3	2084	9	AF015450	AF015450 Homo sapi
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17	1454.8	64.9	1458	9	AF041458	AF041458 Homo sapi
18	1438.2	64.1	1443	6	A84924	A84924 Sequence 3
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20	1438.2	64.1	1443	9	HSU85059	HSU85059 Human prote
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ALIGNMENTS

RESULT 1
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LOCUS A86556 Sequence 1 from Patent WO9839435.
DEFINITION A86556
ACCESSION A86556
VERSION A86556.1 GI:6735154
KEYWORDS
SOURCE unidentified
ORGANISM unclassified
REFERENCE 1 (bases 1 to 2243)
AUTHORS Wallach,D. and Goltsev,Y.
TITLE CASH (CASPAE HOMOLOGUE) WITH DEATH EFFECTOR DOMAIN, MODULATORS OF
THE FUNCTION OF FAS RECEPTORS
JOURNAL Patent: WO 9839435-A 1 11-SEP-1998;

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VERSION A84918.1 GI:6733758
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 2143)
AUTHORS Schroeder, M. and Steiner, V.
TITLE FLIP GENE AND FLIP PROTEIN
JOURNAL Patent: WO 9844104-A 9 08-OCT-1998;
SCHROEDER MICHAEL (CH); STEINER VERONIQUE (CH)
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ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

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FLIP gene and FLIP protein.
BD107658
BD107658.1 GI:23202476
JP 2002501371-A/2.
unidentified
unclassified.
1 (bases 1 to 2143)
Tschopp,J., Thome,M., Burns,K., Irmeler,M., Hahne,M., Schroter,M.,
Schneider,P., Bodmer,J.L., Steiner,V., Rimoldi,D., Hofmann,K. and
French,L.E.
Patent: JP 2002501371-A 2 15-JAN-2002;
APOTECH SA
OS Homo sapiens, long version of FLIP-DNA
PN JP 2002501371-A/2
PD 15-JAN-2002
PF 31-MAR-1998 JP 1998541154
PR 01-APR-1997 DE 197 13 393.2
PI JURG TSCHOPP, MARGOT THOME, KIMBERLY BURNS, MARTIN IRMLER, MICHAEL

PI HAHNE,
PI MICHAEL SCHROTER, PASCAL SCHNEIDER, JEAN LUC BODMER, VERNIQUE
PI STEINER,
PI DONATA RIMOLDI, KAY HOFMANN, LARS E FRENCH
PC C12N15/12, C07K14/47, C12N5/10, G01N33/68
CC Strandedness: Single;
CC Topology: Linear;
CC FLIP gene and FLIP protein
FH Key Location/Qualifiers
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1. .2143
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BASE COUNT 590 a 482 c 576 g 495 t
ORIGIN

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Best Local Similarity 99.7%; Pred. No. 0;
Matches 2138; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

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QY 339 GGACGACTCCCGGCTGGAAGGATTCGAAAGAAATGAAGTCAAGCTCAGACCTCAGAAATGAA 398
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QY 1419 TGAGCCGAGGAGGCTCCAGAGTGTGTATGGTGTGATCAGACTCACTCAGGGCTCCCCC 1478
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Query Match 89.5%; Score 206.8; DB 6; Length 2034;									
Best Local Similarity 99.68; Pred. No. 0; Mismatches 7; Indels 1; Gaps 1;									
Matches 2022; Conservative 0;									
Qy	214	CGATCGCCACGACCAAGTCCGCTCCAGCTTTCGAGCTTCGTTTTCGCTCCATCTGGGTG	273						
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Qy	394	ATGAAGTTGACTGCTGCTGCTTTCGCTTTCGCTGAGTGGCCCGGAGCTGTACTCAAGACC	453						
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Db	300	AGCACTTGATACAGATGAGAAGGAGATGCTGCTTTCGCTGCGGAGTTCCTATAGA	359						
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Qy	634	TGTCGGGAGCTTGCTGCACTGCTCTACAGAGTGAAGGAGTGAAGCTGCTCAACGAT	693						
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Qy	694	CTTGAAGATGGACAAAGGCTGAGAGACCCAGCTGCTCAGGAACCCCTCACCTTGTTTC	753						
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RESULT 8
BC001602
LOCUS

DEFINITION Homo sapiens, Similar to CASP8 and FADD-like apoptosis regulator,

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Db	1740	CACCTGTAATCCAGCAGCTTGGGAGGCCAAGGAGGAGGAGGAGGAGGAGGAGG	1799						
Qy	2014	CGAGACAGCCTGGCCAACTGTAACGCTGCTCCCTAGTAAATAATGCAAAAAATAG	2073						
Db	1800	CGAGACAGCCTGGCCAACTGTAACGCTGCTCCCTAGTAAATAATGCAAAAAATAG	1859						
Qy	2074	GCTGTGGGTGGTACCTGTTCCAGTACTTGGGAGGCTGAGGTGGGAGGAGTCTTT	2133						
Db	1860	GCTGTGGGTGGTACCTGTTCCAGTACTTGGGAGGCTGAGGTGGGAGGAGTCTTT	1919						
Qy	2134	TGAACCCAGGAGTTCAGGGTCATAGCATGCTGATTGCTGCTGCTGCTGCTGCTG	2193						
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Qy	2194	ACCAACCTGGCAGTATAGCAAGATCCCTCTCTTTAAAAAATAAAAAA 2243							
Db	1980	ACCAACCTGGCAGTATAGCAAGATCCCTCTCTTTAAAAAATAAAAAA 2029							

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

clone MGC:2044 IMAGE:3542993, mRNA, complete cds.

BC001602

BC001602.1 GI:12804400

MGC.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Strausberg,R.

Direct Submission

Submitted (03-JAN-2001)

National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgapbs-remail.nih.gov

Tissue procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)

DNA Sequencing by: Genome Sequence Centre,

BC Cancer Agency, Vancouver, BC, Canada

info@bcgsc.bc.ca

Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,

Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,

Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo

Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven

Ness, Pawan Pandoh, Anna-Lisa Prabhu, Parvaneh Saeedi, Jacqueline

Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,

Michael Thorne, Miranada Tsai, Marasja van den Bosch, Jill Vardy,

George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNLN at: <http://image.llnl.gov>

Series: IRAL Plate: 8 Row: 1 Column: 12

This clone was selected for full length sequencing because it

passed the following selection criteria: matched mRNA gi: 2653415.

Location/Qualifiers

1..2025

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/note="Vector: pOTB7"

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regulator"

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BASE COUNT
ORIGIN

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Best Local Similarity 99.7%; Pred. No. 0;

Matches 2015; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

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DB 121 CGAACTCCCCACTCGAAAGGATTCGAAAGAAATGAAGTCAAGCCCTCAGAAATGAAGTT 180

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QY 402 GACTGCTGCTGGCTTTCTCTGTTGACTGCGCGGAGCTGTAAGTCAAGCCCTCAGAAATGAAGTT 461

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DEFINITION mRNA, alternatively spliced, complete cds.
ACCESSION AF005774
VERSION AF005774.1 GI:2286144
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2040)
AUTHORS Inohara, N., Koseki, T., Hu, Y., Chen, S. and Nunez, G.
TITLE Clarp, a death effector domain-containing protein interacts with
caspase-8 and regulates apoptosis
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 94 (20), 10717-10722 (1997)
MEDLINE 98021435
PUBMED 9380701
REFERENCE 2 (bases 1 to 2040)
AUTHORS Inohara, N., Koseki, T., Hu, Y., Chen, S. and Nunez, G.
TITLE Direct Submission
JOURNAL Submitted (28-MAY-1997) Department of Pathology, University of
Michigan Medical School, 1150 W. Medical Center Dr., C558 MSRBII,
Ann Arbor, MI 48109, USA
FEATURES
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LOCUS AF010127 Homo sapiens Casper mRNA, complete cds.
DEFINITION AF010127 Homo sapiens Casper mRNA, complete cds.
ACCESSION AF010127
VERSION AF010127.1 GI:2281475

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 2039)
AUTHORS Shu,H.B., Halpin,D.R. and Goeddel,D.V.
TITLE Casper is a FADD- and caspase-related inducer of apoptosis
JOURNAL Immunity 6 (6), 751-763 (1997)
MEDLINE 97352452
PUBMED 9208847
REFERENCE 2 (bases 1 to 2039)
AUTHORS Shu,H.B., Halpins,D.R. and Goeddel,D.V.

Direct Submission
Submitted (23-JUN-1997) Biology, Tularik, Inc., Two Corporate Dr.,
South San Francisco, CA 94080, USA
Location/Qualifiers
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RESULT 12
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LOCUS      2045 bp      DNA      linear      PAT 08-AUG-2001
DEFINITION Sequence 1 from patent US 6242569.
ACCESSION AR156902
VERSION AR156902.1 GI:15125606
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unclassified.
REFERENCE 1 (bases 1 to 2045)
AUTHORS      Shu, H.-B. and Goeddel, D.V.
TITLE      Regulators of apoptosis
JOURNAL      Patent: US 6242569-A 1 05-JUN-2001;
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BASE COUNT 551 a 475 c 560 g 459 t
ORIGIN

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DEFINITION Homo sapiens FLAME-1 mRNA, complete cds.
ACCESSION AF009616
VERSION AF009616.1 GI:2429153
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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1 (bases 1 to 2056)
Srinivasula,S.M., Ahmad,M., Ohtsuka,S., Bullrich,F., Banks,S.,
Fernandes-Alnemri,T., Croce,C.M., Litwack,G., Tomaselli,K.J.,
Armstrong,R.C. and Alnemri,E.S.
FLAME-1, a novel FADD-like anti-apoptotic molecule that regulates
Fas/TNFR1-induced apoptosis
J. Biol. Chem. 272 (30), 18542-18545 (1997)
97373543
PUBMED 9228018
REFERENCE 2 (bases 1 to 2056)
Alnemri,E.S.
Direct Submission
Submitted (18-JUN-1997) Microbiology and Immunology, Thomas,
Jefferson University, Kimmel Cancer Institute, 233 S. Tenth,
Street, Philadelphia, PA 19107, USA
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Roy,S. and Nicholson,D.W.			
Cell death attenuation by 'Usurpin', a mammalian DED-caspase			
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Hornung,F., Lenardo,M.J., Xanthoudakis,S., Roy,S. and			
Nicholson,D.W.			
Direct Submission			
Submitted (22-JUL-1997) Biochemistry and Molecular Biology, Merck			
Frost Centre for Therapeutic Research, P.O. Box 1005, Pointe			
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ORGANISM
Unknown.

Unclassified.	
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Job time : 8385.31 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 22, 2003, 07:06:39 ; Search time 4907.18 Seconds
(without alignments)
11109.213 Million cell updates/sec

Title: US-09-380-546A-1

Perfect score: 2243

Sequence: 1 ggacgtcgagcattacaat.....cttttaaaaaaaaaaaaaa 2243

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: em_estin.*

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8: em_htc.*

9: gb_est1.*

10: gb_est2.*

11: gb_htc.*

12: gb_est3.*

13: gb_est4.*

14: gb_est5.*

15: em_estfun.*

16: em_estom.*

17: em_gss_hum.*

18: em_gss_inv.*

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20: em_gss_vrt.*

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23: em_gss_mus.*

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29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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3	904.4	40.3	1201	9	AL551989
4	879	39.2	929	13	BQ706783

5	857.2	38.2	1004	12	BM555216	BM555216 AGENCOURT
6	836	37.3	927	13	BQ712545	BQ712545 AGENCOURT
7	829.8	37.0	915	13	BQ709107	BQ709107 AGENCOURT
8	794	35.4	896	13	BX353373	BX353373 BX353373
9	781.6	34.8	1201	9	AL552025	AL552025 AL552025
10	767	34.2	982	13	BQ644010	BQ644010 AGENCOURT
11	759	33.8	902	13	BX457155	BX457155 BX457155
12	756	33.7	1054	12	BM928334	BM928334 AGENCOURT
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15	714.2	31.8	901	13	BQ722885	BQ722885 AGENCOURT
16	707.4	31.5	757	12	B1819620	B1819620 603034156
17	688.6	30.7	898	13	BQ898388	BQ898388 AGENCOURT
18	686.6	30.6	698	14	CD368455	CD368455 UI-H-FT1 -
19	681.8	30.4	690	14	CA394435	CA394435 C851e06.y
20	678.2	30.2	898	13	BX353372	BX353372 BX353372
21	675.2	30.1	704	13	BU685902	BU685902 UI-CF-DU1
22	672.4	30.0	697	14	CB242360	CB242360 UI-CF-FN0
23	672.4	30.0	700	12	B1548057	B1548057 603196567
24	664.2	29.6	1106	10	BE786211	BE786211 601474339
25	663.6	29.6	962	10	BG118195	BG118195 602349977
26	663.4	29.6	699	10	BG431627	BG431627 602499221
27	650	29.0	830	12	B1871546	B1871546 603396018
28	637.4	28.4	788	14	CD521046	CD521046 AGENCOURT
29	632.8	28.2	667	10	AW855857	AW855857 RC3-CT027
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41	602.4	26.9	727	10	BE304652	BE304652 601106166
42	601.4	26.8	701	9	AI132915	AI132915 HAI497.Hu
43	599	26.7	611	14	CB158243	CB158243 K-EST0217
44	587.6	26.2	647	10	AW856737	AW856737 RC3-CT029
45	583.6	26.0	637	9	AI921624	AI921624 wo27h03.x

ALIGNMENTS

RESULT 1
AL526318
LOCUS
DEFINITION AL526318 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
CDNA clone CS0DC016Y006 5-PRIME, mRNA sequence.
ACCESSION AL526318
VERSION AL526318.2 GI:31064178
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT On Feb 13, 2001 this sequence version replaced gi:12789811.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 1297.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DC016BH030P1&cluster=1297.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :

BASE COUNT	296 a		228 c		295 g		244 t		8 others	
	ORIGIN									
Query Match		43.8%	Score	982.2;	DB 9;	Length	1071;			
Best Local Similarity		98.8%	Pred. No.	4.6e-23;						
Matches 1003; Conservative			6;	Mismatches	4;	Indels	2;	Gaps	2;	
QY	101	GGGTGGGGACTCGGCCTCACACAGTGAAGTGGCGGGCTATTGGACTTTTGTCTCAGTGACAG	160							
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QY	161	CTGAGACAAACAGGACCACCGGAGGAGGTGTAGAGAGAGAAGCGCCGACAGACGATCGC	220							
DB	119	CTGAGACAAACAGGACCACCGGAGGAGGTGTAGAGARAAGCGCCGCAACAGCGATCGC	178							
QY	221	CCAGACCAACTCCGCTTCCAGAGCTTTCGGTTTCTTTTGGCTCCATCTTGGGTGCGCCTTC	280							
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QY	281	CCGGCGTCTAGGGAGCGAAGCTGTAGGTTGGCAGCGCAGGAGAGTCCGGCCGCGACAGG	340							
DB	239	CCGGCGTCTAGGGAGCGAAGCTGTAGTGGCAGCGCAGGAGAGTCCGGCCGCGACAGG	298							
QY	341	ACGAACTCCCCACTGGAAAGGATTCGAAAGAAATGAAGTACGCCCTCAGAAATGAAGT	400							
DB	299	ACGAACTCCCCACTGGAAAGGATTCGAAAGAAATGAAGTACGCCCTCAGAAATGAAGT	358							
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DB	478	GATACAGATGAAGAAGAGATCCTCTCTTTTGTGCGGGATGTTGCTATAGATGTGGTT	537							
QY	581	CCACCTAATGTCAGGACCTCTCGGATATTTTCGGGAAGAGGTAGCTGCTCTGTCGGG	640							
DB	538	CCACCTAATGTCAGGACCTCTCGGATATTTTCGGGAAGAGGTAGCTGCTCTGTCGGG	597							
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DB	598	GACTTGGCTGAACCTGCTCTACAGAGTAGGCGATTTTGACCTGCTCAACAGTATCTTGAAG	657							
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DB	658	ATGGACAGAAAAGCTGTGGAGACCACCTGCTCAGGAACCCCTCACCTGTGTTTCGGACTAT	717							
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DB	718	AGAGTCTCATGGCAGAGATTGGTGAGGATTTGGATAAATCTGATGTGTCCTCATTAAT	777							
QY	821	TTCTCTCATGAAGGATTACATGCGCCGAGGCAAGATATACCAAGGAGAGAGATTTCTTGGAC	880							
DB	778	TTCTCTCATGAAGGATTACATGCGCCGAGGCAAGATATACCAAGGAGAGATTTCTTGGAC	837							

QY 601 TCTGATATTTACGGGAAGAGGTAAGCTGTCTCGGGACCTTGGCTGAACCTCTCTA 660
Db 121 TCTGATATTTACGGGAAGAGGTAAGCTGTCTCGGGACCTTGGCTGAACCTCTCTA 180
QY 661 CAGAGTGAGGCGATTTGACCTGCTCAAAAGCTATCTTGAAGATGGACAGAAAAGCTGTGA 720
Db 181 CAGAGTGAGGCGATTTGACCTGCTCAAAAGCTATCTTGAAGATGGACAGAAAAGCTGTGA 240
QY 721 GACCCACCTGCTCAGGAACCCCTACCTTGTTCGGCATATAGAGTGTCTGATGGCAGAGAT 780
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Db 301 TGGTGAGGATTTGGATAATCTGATGTCTCTCATTAATTTCTTCATGAAGGATTACAT 360
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Db 361 GGGCCGAGCAAGATAAGCAAGGAGAAGTGTCTTGGACCTTGTGGTGTAGTTGGAGAA 420
QY 901 ACTAAATTTGGTGGCCGAGATCAACTGGATTTATTAGAAAAATCCCTAAAGAACATCCA 960
Db 421 ACTAAATCTGTTGGCCGAGATCAACTGGATTTATTAGAAAAATCCCTAAAGAACATCCA 480
QY 961 CAGATAGACCTGAAGACAAAATCCAGAGTACAGAGTGTCTTCAAGGAGGAGGAC 1020
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Db 541 AAGTTACAGGATGTCTTCCAGAGCAATCAAAAGAGTCTCAAGGATCCCTCAAAATAA 600
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Db 841 ATCTTGTGATCTCAGTATGCTATGATATCCAGATTTCTTGGCCAAATTTGCCGTATGCC 900
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Db 901 CGAGCAGGAGACTACGACAGCTTTGTGTGTGTCTCGTGTGAGCGGAGGAGGCTCCCA 960
QY 1438 GAGTGTGTATGTTGGATACAGACTCCTC-----AGGGCTCCCTCCCTGCATCAC 1486
Db 961 GAGGCTGTATTGGTGTGGATTACAGACTCCACTCAGGGGCTCCCTCCCTGCATCAC 1015

RESULT 3
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LOCUS AL551989 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CS0D1060Yell 3-PRIME, mRNA sequence.
ACCESSION AL551989
VERSION AL551989.2 GI:31273805
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 1201)
Li.W.B., Gruber.C., Jessee.J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
On Feb 15, 2001 this sequence version replaced gi:12890457.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 1297.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0D1060AC06NP1&cluster=1297.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0D1060AC06NP1.

FEATURES
source

1. 1201
/organism="Homo sapiens"
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/note="1st strand cDNA was primed with a NotI-oligo(dT)
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digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT 268 a 262 c 258 g 353 t 60 others
ORIGIN

Query Match 40.3%; Score 904.4; DB 9; Length 1201;
Best Local Similarity 96.6%; Pred. No. 1.1e-20;
Matches 952; Conservative 11; Mismatches 19; Indels 4; Gaps 4;
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460	TCTTGGAGGTGGATGGCCAGCGGATGAAGAAATGTGAATTCAGGCTCAGAAGCGAGGGC	401
1656	TGTGCACAGTTACCCAGAGAGCTGACTTCTCTCGGAGCCTGTGTACTGC - GGACATGTCC	1714
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1715	CTGCTGGAGCAGTCTCACAGCTCACCGTCCCTGACTGCAGTGCCTCTCTCCAGAAACTG	1774
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1775	AGACAAGAAGAAAGCCGCCACTCCTGGATCTTTCACATTGAACATCAATGGCTACATGTAT	1834
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220	GATTGGAAACAGCAGAGTTTCTGCCAAGGAGAAATATATGTCTGGCTGCAGCAGCACTCTG	161
1895	AGAAAGAACTTATCCTCTCCTACATAAGAAACCAAAAGGCTGGCGGTAGTGGCTCAC	1954
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1955	ACCTGTAATCCCAGCACTTTGGGAGGCCAAGGAGGCGAGATCACTTCAGTTCAGGAGTTC	2014
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RESULT 4
BQ706783
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BQ706783 929 bp mRNA linear EST 16-JUL-2002
AGENCOURT_7975998 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6214879
5', mRNA sequence.
BQ706783
BQ706783.1 GI:21845682
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 929)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-f@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2382 row: o column: 08
High quality sequence stop: 669.
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/clone="IMAGE:6214879"
/lab_host="DH10B (phage-resistant)"
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/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using Zap-cDNA synthesis kit (Stratagene) and

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Superscript II RT (Life Technologies).. Note: this is a NIH_MGC Library."									
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ORIGIN									
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DB	660	ATGGGCGGCGCAGATTAAGCAAGGAGAGAGTTCCTTGACACCTGTGGTTGAGTTGGAG	719						
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RESULT 5
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LOCUS
DEFINITION
AGENCY: 6541158 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:5550264
5' mRNA sequence.
BM555216
EST.
BM555216.1 GI:18795496
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1004)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM12262 row: c column: 01
High quality sequence stop: 713.
FEATURES
Location/Qualifiers
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/clone="IMAGE:5550264"
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_88"
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enriched for full-length clones and constructed by Life
Technologies. Note: this is a NIH_MGC Library."
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Best Local Similarity 97.6%; Pred. No. 3.4e-19;
Matches 932; Conservative 0; Mismatches 16; Indels 7; Gaps 6;
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QY 222 CAGCACCAGTCCGCTTCCAGGCTTTCGGTTTTCGCTTCCATCTTGGTGGCGCTTCC 281
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DB 301 CGAAGTCCCGGAGGAGGAGTCTGAAAGAAATGAAGTACGCTCAGAAATGAAGT 360
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DB 660 TGGACAGAAAAGCTGTGGAGACCCACTGCTCAGGAACCTCACCCTGTTTTCGGACTATA 719
QY 762 GAGTGTGATGCGCAGAGATTTGGTGGAGTATTTGGATAAATCTGATGTCTCTCAATTAATT 821
DB 720 GAGTGTGATGCGCAGAGATTTGGTGGAGTATTTGGATAAATCTGATGTCTCTCAATTAATT 779
QY 822 TCCTCATGAGGATTTACATGGCCGAGGCAAGATTAAGCAAGGAGAGAGTTTC-TTGGAG 880
DB 780 TCCTCATGAGGATTTACATGGCCGAGGCAAGATTAAGCAAGGAGAGAGTTTC-TTGGAG 839
QY 881 CTGTGTGTTGAGTTGGAGAACTATAATTTGGTTGGCC-CAGATCAACT-GGATTTATTAG 938
DB 840 CTGTGTGTTGAGTTGGAGAACTATAATCTGTTGGCCNCAGATCAACTGGGATTTATTAG 899
QY 939 AAAAATG-CCTAAAGAACATCCACAGAA--TAGACCTGAAGCAAAAATCCAGAA 990
DB 900 AAAAATGCCCTAAAGAACATCCACAGAAATAGACCCCTGAAGACNAAATTCANGA 954
RESULT 6
BM12545
LOCUS
DEFINITION
AGENCY: 8495301 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6302007
5' mRNA sequence.
BM12545
VERSION
BM12545.1 GI:21851444
EST.
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 927)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM2518 row: m column: 16
High quality sequence start: 4
High quality sequence stop: 632.
FEATURES
Location/Qualifiers
1..927
/organism="Homo sapiens"
/mol_type="mRNA"
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/db_xref="taxon:9606"
/clone="IMAGE:6302007"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_113"
/notes="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dt priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
BASE COUNT      246 a  203 c  263 g  215 t
ORIGIN
Query Match      37.3%; Score 836; DB 13; Length 927;
Best Local Similarity 97.3%; Pred. No. 1.6e-18;
Matches 903; Conservative 0; Mismatches 20; Indels 5; Gaps 5;
QY 160 GCTGAGACAAAGACGACGAGGAGGTGTAGGAGAGAGCGCGCAACAGCGATCG 219
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QY 220 CCCAGCACCAAGTCCGCTTCAGGCTTTCGGTTTCTTTCCTCCATCTTGGGTGCGCCTT 279
DB 61 CCCAGCACCAAGTCCGCTTCAGGCTTTCGGTTTCTTTCCTCCATCTTGGGTGCGCCTT 120
QY 280 CCCGGGCTCTAGGGAGGAGGAGGCTGAGTGGCGGAGGAGGAGGAGGAGGAGGAGGAG 339
DB 121 CCCGGGCTCTAGGGAGGAGGAGGCTGAGTGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
QY 340 GACGAACCTCCCGACCTGAAAGAGGATCTGAAAGAAATGAATCAGCCCTCAGAAATGAAG 399
DB 181 GACGAACCTCCCGACCTGAAAGAGGATCTGAAAGAAATGAATCAGCCCTCAGAAATGAAG 240
QY 400 TTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 459
DB 241 TTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 299
QY 460 GCTTCCCTTAGTCTAAGAGTAGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 519
DB 300 GCTTCCCTTAGTCTAAGAGTAGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 359
QY 520 TGATACAGATGAGAGGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 579
DB 360 TGATACAGATGAGAGGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 419
QY 580 TCCACTTAATGTCAGGAGCTTCTGATATTTAGGGGAAAGAGGAGTGTGCTGCTGCTGCTGCTG 639
DB 420 TCCACTTAATGTCAGGAGCTTCTGATATTTAGGGGAAAGAGGAGTGTGCTGCTGCTGCTGCTG 479
QY 640 GGACTTGGCTGAACCTGCTCTACAGAGTGGGCGGATTTGACCTGCTCAACACCTATCTTGA 699
DB 480 GGACTTGGCTGAACCTGCTCTACAGAGTGGGCGGATTTGACCTGCTCAACACCTATCTTGA 539
QY 700 GATGGACAGAAAGCTGTGGAGACCCACCTGCTCAGGAGCCCTGCTGCTGCTGCTGCTGCTGCT 759
DB 540 GATGGACAGAAAGCTGTGGAGACCCACCTGCTCAGGAGCCCTGCTGCTGCTGCTGCTGCTGCT 599
QY 760 TAGAGTGTGATGGGAGAGATTTGAGGATTTGATTAATCTGATGCTGCTGCTGCTGCTGCTGCT 819
DB 600 TAGAGTGTGATGGGAGAGATTTGAGGATTTGATTAATCTGATGCTGCTGCTGCTGCTGCTGCT 659
QY 820 TTTCCCTCATGAGGATTTACATGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 878
DB 660 TTTCCCTCATGAGGATTTACATGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 719
QY 879 ACCTTGTGTTGATGGAGAACTAAATTTGGTGGCCCGGAGGAGGAGGAGGAGGAGGAGGAGG 938
DB 720 ACCTTGTGTTGATGGAGAACTAAATTTGGTGGCCCGGAGGAGGAGGAGGAGGAGGAGGAGG 779
QY 939 AAAAATGCCCTAAAGAACATCCACAGAAATAGACCT-GAAGACAAAAATCCAGAGATACAG 997

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780 AAAAATGCCCTAAAGAACATCCACAGAAATAGACCTGGAGAGCAAAAAATCCCGAAGTACAG 839
998 CAGTCTGTTCAGGAGGAGGAGGAGGAGTTCACAGGAGTTCCTCCAGGAGCAAT-CCAAAA 1056
840 CAGTCTGTTCAGGAGGAGGAGGAGGAGTTCACAGGAGTTCCTCCAGGAGCAATCCCAAAA 899
1057 GAGTCT-CAAGGATCCTTCAATAACTT 1083
900 GAGTCTCCAGGAGTCTTCAATAACTT 927

RESULT 7
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LOCUS AGENCOURT_8484859 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6301179
5', mRNA sequence.
ACCESSION BO709107
VERSION BO709107.1 GI:21848019
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 915)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.,
Email: cgapbs@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LICM2516 row: k column: 04
High quality sequence stop: 709.
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6301179"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dt priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
BASE COUNT 242 a 199 c 258 g 214 t 2 others
ORIGIN
Query Match 37.08; Score 829.8; DB 13; Length 915;
Best Local Similarity 98.5%; Pred. No. 2.5e-18;
Matches 868; Conservative 0; Mismatches 9; Indels 4; Gaps 3;
QY 179 CGGAGGAGGAGTGTAGGAGAGAGCGCGCAACAGCGATCGCCAGCAACAGTCCGCTT 238
DB 1 CGGAGGAGGAGTGTAGGAGAGAGCGCGCAACAGCGATCGCCAGCAACAGTCCGCTT 60
QY 239 CCAGGCTTTCGGTTTCTTTCCTCCATCTTGGGTGCGCTTCCCGGCGCTTAGGGAGCG 298
DB 61 CCAGGCTTTCGGTTTCTTTCCTCCATCTTGGGTGCGCTTCCCGGCGCTTAGGGAGCG 120
QY 299 AAGGCTGAGTGGGAGGAGGAGGAGTCCCGCGCGGAGGAGGAGTCCCGCGGAGGAGGAGGAG 358
DB 121 AAGGCTGAGTGGGAGGAGGAGGAGTCCCGCGCGGAGGAGGAGTCCCGCGGAGGAGGAGGAG 180

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QY 359 AAGGATTCTGAAGAAATGAAGTCAGCCCTCAGAAATGAAGTGTGACTGCTGGCTTT 418
Db 181 AAGGATTCTGAAGAAATGAAGTGTGACTGCTGGCTTT 240
QY 419 CTGTTGACTGCGCCGGAGCTGTACTGCAAGACCTTGTGAGCTTCCCTAGTCTAAGAGT 478
Db 241 -CTGTTGACTGCGCCGGAGCTGTACTGCAAGACCTTGTGAGCTTCCCTAGTCTAAGAGT 299
QY 479 AGGATGCTGTGAAGTCAATCCATCAGGTTGAAGAAGACATTTGATACAGATGAGAAGGAG 538
Db 300 AGGATGCTGTGAAGTCAATCCATCAGGTTGAAGAAGACATTTGATACAGATGAGAAGGAG 359
QY 539 ATGCTGCTCTTTTGTGCGGGAGTGTCTATAGATGTGTTCCACCTAATGTACAGGAC 598
Db 360 ATGCTGCTCTTTTGTGCGGGAGTGTCTATAGATGTGTTCCACCTAATGTACAGGAC 419
QY 599 CTTCTGGATATTTACGGGAAGAGTAAGTGTGTGTCGGGGACTTGGCTGAACCTGTC 658
Db 420 CTTCTGGATATTTACGGGAAGAGTAAGTGTGTGTCGGGGACTTGGCTGAACCTGTC 479
QY 659 TACAGATGAGCGGATTTGACCTGCTCAACGTAFTCTTGAAGATGGACAGAAAAGCTGTG 718
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QY 719 GAGACCCACCTGCTCAGAACCCCTCACCTTCTTCCGACTATAGATGCTGATGCCAG 778
Db 540 GAGACCCACCTGCTCAGAACCCCTCACCTTCTTCCGACTATAGATGCTGATGCCAG 599
QY 779 ATTGTGAGGATTTGGATAAATCTGATGTGCTCATTAATTTTCTCATGAAGGATAC 838
Db 600 ATTGTGAGGATTTGGATAAATCTGATGTGCTCATTAATTTTCTCATGAAGGATAC 659
QY 839 ATGGCCCGAGGACAGATAAGCAAGAGAGTGTCTTGGACCTTGTGGTGTGAGTTGGAG 898
Db 660 ATGGCCCGAGGACAGATAAGCAAGAGAGTGTCTTGGACCTTGTGGTGTGAGTTGGAG 719
QY 899 AAATCTAAATTTGGTGTGCCCCAGATCAACTGATTTATTAGAAAATGCTTAAAGAACATC 958
Db 720 AAATCTAAATTTGGTGTGCCCCAGATCAACTGATTTATTAGAAAATGCTTAAAGAACATC 779
QY 959 CACAGATAGACCTGAAGACAAAATCCAGAGTACAGACGAGTCTGTTCAGAGGACA -GG 1017
Db 780 CACAGATAGACCTGAAGACAAAATCCAGAGTACAGAGTACAGACGAGTCTGTTCAGAGGACGG 839
QY 1018 GACAGTTACAGG--AATGTTCTTCAACGACAGAAATCCAAA 1056
Db 840 GACAGTTACAGGAAATGTTCTTCAACGACAGAAATCCAAA 880
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RESULT 8

BX353373

LOCUS

DEFINITION

BX353373 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens

CDNA clone CS0DC005Y016 5-PRIME, mRNA sequence.

BX353373.1 GI:30383781

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 896)

L.I.W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

Unpublished

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 1297.f For

more information about this cluster, see

http://www.genoscope.cns.fr/

COMMENT

FEATURES

source

cgi-bin/cluster.cgi?seq=CS0DC005BH080P1&cluster=1297.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DC005BH080P1.

Location/Qualifiers

1..896

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS0DC005Y016"

/tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"

/clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo(dT)

primer. Five prime end enriched, double-strand cDNA was

digested with Not I and cloned into the Not I and EcoR V

sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT 251 a 184 c 238 g 219 t 4 others

ORIGIN

Query Match 35.4%; Score 794; DB 13; Length 896;

Best Local Similarity 98.8%; Pred. No. 3.3e-17;

Matches 806; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

274 CGCCTTCCCGGCTAGGGAGCGAAGGCTGAGTGGCAGCGGAGGAGTCCGGCG 333

13 CGGGATCCCGGCTAGGGAGCGAAGGCTGAGTGGCAGCGGAGGAGTCCGGCG 72

334 CCACAGGACGAACTCCCGACTGGAAAGGATCTGAAAGAAATGAAGTCAGCCCTCAGAA 393

73 CGACAGGACGAACTCCCGACTGGAAAGGATCTGAAAGAAATGAAGTCAGCCCTCAGAA 132

394 ATGAAGTTGACTGCTGCTGGCTTCTGTTGACTGGCCCGGAGTGTACTGCAAGACCC 453

133 ATGAAGTTGACTGCTGCTGGCTTCTGTTGACTGGCCCGGAGTGTACTGCAAGACCC 191

454 TTGTGAGCTTCCCTAGTCTAAGAGTGGATGCTGCTGAAGTCATCATCATGAGTTGAAGA 513

192 TTGTGAGCTTCCCTAGTCTAAGAGTGGATGCTGCTGAAGTCATCATCATGAGTTGAAGA 251

514 AGCACTTGATACAGATGAGAGGAGATGCTGCTCTTTTGTGCCGGGATGTTGCTATAGA 573

252 AGCACTTGATACAGATGAGAGGAGATGCTGCTCTTTTGTGCCGGGATGTTGCTATAGA 311

574 TGTGTTCCACCTAATGTGTCAGGACCTTCTGATGATTTTACGGGAAGAGGTAAGCTGTC 633

312 TGTGTTCCACCTAATGTGTCAGGACCTTCTGATGATTTTACGGGAAGAGGTAAGCTGTC 371

634 TGTGCGGACCTGGCTGAACCTGCTACAGAGTGGAGGATTTGACCTGCTCAACAGTAT 693

372 TGTGCGGACCTGGCTGAACCTGCTACAGAGTGGAGGATTTGACCTGCTCAACAGTAT 431

694 CTTGAAGATGGACAGAAAGCTGTGGAGACCCACCTGCTCAGAGAACCTCACCCTTGTTC 753

432 CTTGAAGATGGACAGAAAGCTGTGGAGACCCACCTGCTCAGAGAACCTCACCCTTGTTC 491

754 GGACTATAGAGTGTGATGGCAGAGATTTGGTGTGAGATTTGGATAAATCTGATGTCTC 813

492 GGACTATAGAGTGTGATGGCAGAGATTTGGTGTGAGATTTGGATAAATCTGATGTCTC 551

814 ATTAATTTTCTCATGAAGGATTTACATGGCCGAGGCAAGATAAGCAAGAGAGAGTTT 873

552 ATTAATTTTCTCATGAAGGATTTACATGGCCGAGGCAAGATAAGCAAGAGAGAGTTT 611

874 CTTGGACCTTGTGTTGAGTTGGAGAACTAAATTTGTTGTTGCCAGATCAACTGGATTT 933

612 CTTGGACCTTGTGTTGAGTTGGAGAACTAAATTTGTTGTTGCCAGATCAACTGGATTT 671

934 ATTAGAAAATGCTTAAAGAACATCCACAGATAGACTGAGACAAAATCCAGAGAGTA 993

672 ATTAGAAAATGCTTAAAGAACATCCACAGATAGACTGAGACAAAATCCAGAGAGTA 731

994 CAAGCAGTCTGTTCAAGGAGGAGGCAAGTGTACAGGATTTCTTCCCAAGCAGCAATCA 1053

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Qy	1014	CAGGACAAGTTACAGGAATGTTCTCCAAAGCAGCAATCCAAAAGAGTCTCAAGGATCCCTT	1073
Db	725	CAGGACAAGTTACAGGAATGTTCTCCAAAGCAGCAATCCAAAAGAGTCTCAAGGATCCCTT	784
Qy	1074	CAATACTTTCAGGCT	1089
Db	785	TCATAACTTCAGAT	800
RESULT 11			
LOCUS	1		
DEFINITION	1		
ACCESSION	1		
VERSION	1		
KEYWORDS	1		
SOURCE	1		
ORGANISM	1		
REFERENCE	1		
AUTHORS	1		
TITLE	1		
JOURNAL	1		
COMMENT	1		
FEATURES	1		
source	1		
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ORIGIN			
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Best Local Similarity	98.3%	Pred. No. 3.9e-16;	
Matches 798;	Conservative	1; Mismatches 11;	Indels 3; Gaps 3;
Qy	29	CAGGCCATACATGAACACGAGAGCTTGGACGCTCACCGAGAGTCTCAACTAAAAGGGA	88
Db	91	CAAGCCATAGCAGGAACACGAGAGCTTGGACGCTCACCGAGAGTCTCAACTAAAAGGGA	150
Qy	89	CTCCCGAGCTAGGGTGGGAGCTCGGCCTCACACAGTGTAGTCCCGGCTATTGGACTTTT	148
Db	151	CTCCCGAGCTAGGGTGGGAGCTCGGCCTCACACAGTGTAGTCCCGGCTATTGGACTTTT	210
Qy	149	GTCCAGTGTAGAGCTGAGACAACAGGACACACGGGAGGAGTGTAGGAGAGAGCGCCGCG	208
Db	211	GTCCAGTGTAGAGCTGAGACAACAGGACACACGGGAGGAGTGTAGGAGAGAGCGCCGCG	270
Qy	209	AACAGGATCGCCAGCAGCAACATCGCGTTCAGGCTTTTCGGTTTTCCTCCCTCCATCTT	268
Db	271	AACAGGATCGCCAGCAGCAACATCGCGTTCAGGCTTTTCGGTTTTCCTCCCTCCATCTT	330


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QY 1078 TAACTTCAGGCT 1089
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Db 781 TAACTTCAAGAT 792

RESULT 13
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DEFINITION MAMMAL Homo sapiens CDNA clone MAMMA1001850 5', mRNA
sequence.
ACCESSION AUI22196
VERSION AUI22196.1 GI:10937431
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 795)
AUTHORS Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saiko,K., Kawai,Y.,
Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
Isogai,T.
TITLE HRI human cDNA project
JOURNAL Unpublished
COMMENT Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.

FEATURES
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/db_xref="taxon:9606"
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/note="Vector: pME18SFL3"
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Best Local Similarity 98.5%; Pred. No. 2.4e-15;
Matches 782; Conservative 0; Mismatches 8; Indels 4; Gaps 4;

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Db 1 AACAAAGCACCGGAGGAGGTGTAGGAGAGAAGCGCGCAACAGCGATCGCCAGCAC 60

QY 228 CAAGTCGCTCCAGCGTTTCGGTTTCTTTCCTCCATCTTGGGTGGCGCTTCCCGGGT 287
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Db 61 CAAGTCGCTCCAGCGTTTCGGTTTCTTTCCTCCATCTTGGGTGGCGCTTCCCGGGT 120

QY 288 CTAGGGAGCGAAGCTCAGTGGCGAGGAGAGTCCGGCCGCGACAGGAGCAACT 347
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Db 121 CTAGGGAGCGAAGCTCAGTGGCGAGGAGAGTCCGGCCGCGACAGGAGCAACT 180

QY 348 CCCCACCTGGAAGGATTCTGAAGAAATGAAGTCAGCCCTCAGAAATGAAGTTGACTGC 407
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Db 181 CCCCACCTGGAAGGATTCTGAAGAAATGAAGTCAGCCCTCAGAAATGAAGTTGACTGC 240

QY 408 CTGCTGGCTTTCCTGTTGACGTGGCCCGGAGCTGTACTGCAAGACCCCTTGTAGCTTCCCT 467
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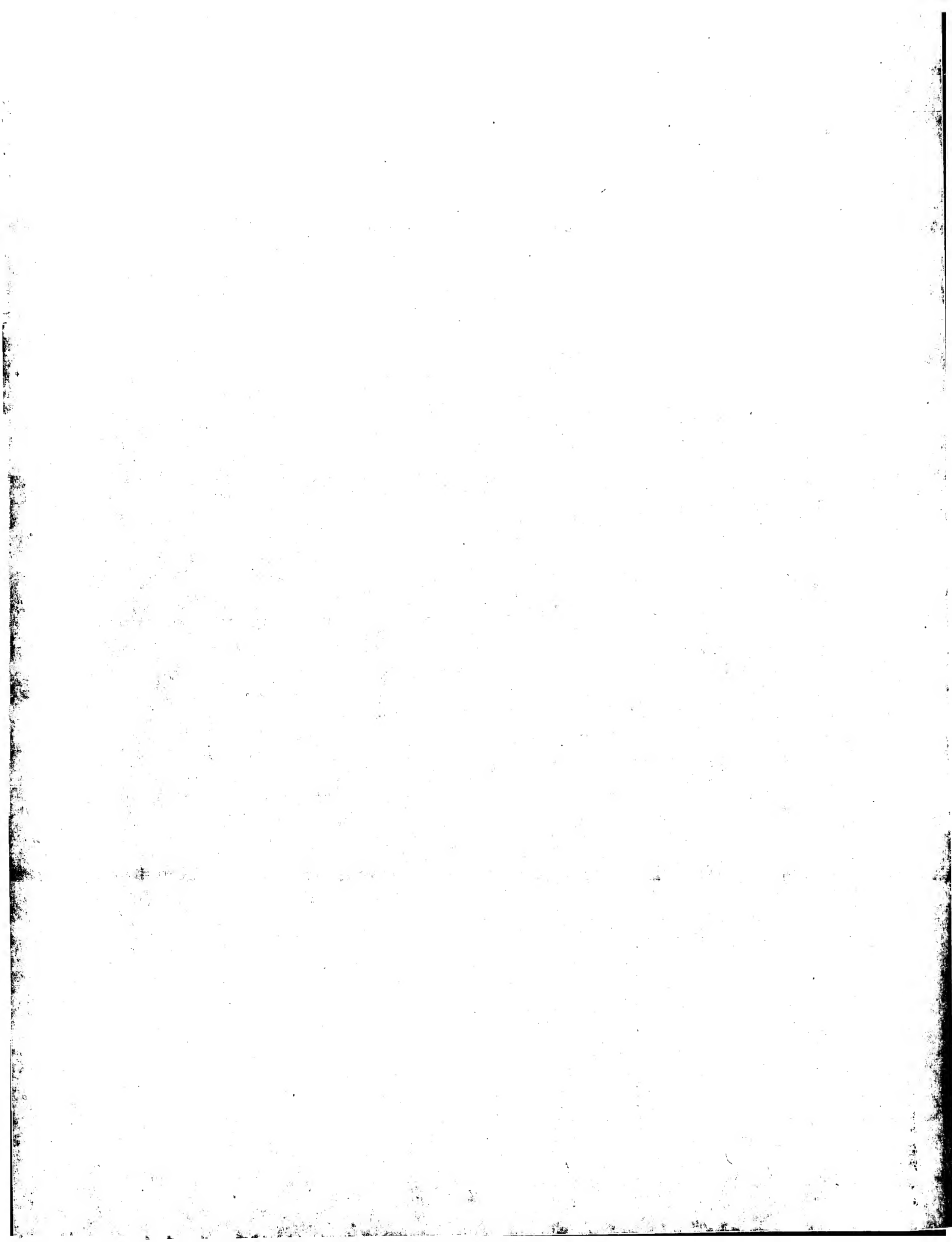
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Db 360 ATGAGAAGGAGATGCTGCTCTTTTGTCCGGGATGTTGCTATAGATGTTGGTTCCACCTA 419
588 ATGTCAGGGACCTTCTGGATATTTTACGGGAAGAGGTAAGCTGTCTGTCTCGGGGACTTGG 647
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708 GAAAAAGCTGTGGAGACCCACCTGCTCAGGAACCCCTCACCTTCTTTCGGGACTATAGAGTGC 767
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660 TGAAGGATTACATGGGCGGCGGAGCAAGATAAAGCAAGGAGAGAGTTCCTTGAACCTTGT 719
886 GGTTGAGTTGGAGAACTAAATTTGG-TTGGCCCGAGATCAACTGGATTTATTAGAAAAAT 944
720 GGGTANTTGGAGAACTAAATCTGGCTGTCGCCAGATCAACTGGGTTTATTAGAAAAAT 779
945 GCGTAAAGCAATC 958
780 GCGTAAAGCAATC 793

RESULT 14
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DEFINITION CD388330 900 bp mRNA linear EST 30-MAY-2003
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VERSION CD388330.1 GI:31226484
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 900)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: c9apbs-remail.nih.gov
Tissue Procurement: Dr. Jamie Thompson, University of WI
cDNA Library Arrayed by: Gina Zastrow-Hayes
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDKM77 row: 1 column: 09
High quality sequence start: 29
High quality sequence stop: 646.
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Qy		1115	AGACTTTAAGGAACAGCTTGCGCTCA	ACAAGAACCACTGGAAGAAATCCATT	CAGGAATCA 1174
Db		421	AGACTTAAGGAACAGCTTGCGCTCA	ACAAGAACCACTGGAAGAAATCCATT	CAGGAATCA 480
Qy		1175	GAACTTTTTTGGCTCAGAGCATACCT	TGAAGAGAGATACAAAGATGAAGACAG	CCCCCTA 1234
Db		481	GAACTTTTTTGGCTCAGAGCATACCT	TGAAGAGAGATACAAAGATGAAGACAG	CCCCCTA 540
Qy		1235	GGAATCTGCCGTGATAATCGATTGC	ATGGSAAATGAGACAGAGCTTCTCG	AGACACCTTC 1294
Db		541	GGAATCTGCCGTGATAATCGATTGC	ATGGSAAATGAGACAGAGCTTCTCG	AGACACCTTC 600
Qy		1295	ACTTCCCT - GGGCTATGAAGTCC	CAGAAAATCTTTGCATCTCAGTAT	CGATGGTATATCCCA 1353
Db		601	ACTTCCCTGGGGCTATGAAGTCC	CAGAAAATCTTTGCATCTCAGTAT	CGATGGTATATCCCA 660
Qy		1354	GATTCTTTGGCCAATTTGCCGTGTA	TGCCGAGCACCCAGAGACTAGCACAG	- CTTTGTGTGTG 1412
Db		661	GATTCTTTGGCCAATTTGCCGTGTA	TGCCGAGCACCCAGAGACTAGCACAG	CGCTTTGTGTGTG 720
Qy		1413	TCCTGG - TGAGCCGAGGAGCTCCC	AGA - - - - GTGTGTATGTGTGTG	ATGGATCAGACTC 1466
Db		721	TCCTGGTTGAGCCGAGGAGCTCC	AGANAGTGTGGGGGATGTGGGGG	ATTCAAACTCACT 780
Qy		1467	CAGGGCTCCCC		1478
Db		781	CAGGGGCTCCCC		792

Search completed: August 22, 2003, 13:49:38
Job time : 4919.18 secs



Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	1991	88.8	2040	4	US-09-069-023-33	Sequence 33, Appl
2	1952.2	87.0	2045	3	US-08-795-088A-1	Sequence 1, Appl
3	1619.2	72.2	1750	3	US-08-859-167-1	Sequence 1, Appl
4	1619.2	72.2	1750	3	US-09-109-273-1	Sequence 1, Appl
5	1619.2	72.2	1750	3	US-09-276-993-1	Sequence 1, Appl
6	1619.2	72.2	1750	4	US-09-723-450-1	Sequence 1, Appl
C 7	175	7.8	14581	4	US-08-520-373D-4	Sequence 4, Appl
C 8	175	7.8	22481	4	US-08-367-841A-3	Sequence 43, Appl
C 9	175	7.8	22481	5	PCR-US95-07201-43	Sequence 43, Appl
C 10	175	7.8	22484	4	US-09-875-223-2	Sequence 2, Appl
11	174.8	7.8	17327	1	US-07-906-871-15	Sequence 15, Appl
C 12	171.2	7.6	24707	4	US-09-740-027-3	Sequence 3, Appl
C 13	170.6	7.6	35060	3	US-08-814-095-7	Sequence 7, Appl
C 14	169.8	7.6	72928	3	US-09-009-913-1	Sequence 1, Appl
C 15	169.6	7.6	17493	4	US-09-804-471A-3	Sequence 3, Appl
C 16	169.2	7.5	6990	4	US-09-620-312D-155	Sequence 155, Appl
C 17	168.4	7.5	3867	3	US-09-347-114A-81	Sequence 81, Appl
C 18	168.2	7.5	36741	3	US-09-301-665-3	Sequence 3, Appl
19	168.2	7.5	87350	3	US-08-781-891-79	Sequence 79, Appl
20	168.2	7.5	87350	4	US-09-618-166-79	Sequence 79, Appl
21	168.2	7.5	87543	4	US-09-791-211-3	Sequence 3, Appl
22	168	7.5	1175	4	US-09-489-847-105	Sequence 105, Appl
C 23	167	7.4	2923	1	US-08-480-449-1	Sequence 1, Appl
C 24	167	7.4	2923	2	US-08-660-542-1	Sequence 1, Appl
C 25	167	7.4	2923	4	US-08-479-603-1	Sequence 1, Appl
C 26	167	7.4	2923	4	US-08-939-107-1	Sequence 1, Appl
C 27	167	7.4	2923	4	US-08-931-764-1	Sequence 1, Appl

Db 361 CCTGCTGGCTTCTGTGTAGCTGGCCGGAGCTGTACTGCAAGACCTTTGTGACCTCC 420
QY 467 TAGCTAAGAGTAGAGTGTCTGTGTAAGTCAATCCATCAGGTTCAGGAAGACACTTGTATACA 526
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QY 527 GATCAGAAAGAGATGCTGCTCTTTTGTGTCGGGATGTGCTATAGATGTGGTTCACCT 586
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QY 1667 CACGAGAAAGCTGACTTCTTCTGGAGCCTGTGTACTGCGGACATGTCCCTGCTGGAGCAG 1726
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Db 1861 ATCCTCTCTACACATAAGAAACCAAGAGCTGCGCTGCTGCTCACACTGTAAATCCC 1920
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Db 1921 AGCACTTTGGAGGCCAAGGAGGAGCAGATCACTTCAAGTTCAGGAGTTCGAGACCGCTG 1980
QY 2027 GCCAACATGTATAAGCTGCTCCCTAGTAAATAATGCAAAATA 2069
Db 1981 GCCAACATGTATAAGCTGCTCCCTAGTAAATAATGCAAAATA 2023

RESULT 2

US-08-795-088A-1
; Sequence 1, Application US/08795088A
; Patent No. 6242569
; GENERAL INFORMATION:
; APPLICANT: Sul, Hong-Bing
; APPLICANT: Goeddel, David V.
; TITLE OF INVENTION: Regulators of Apoptosis
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Science & Technology Law Group
; STREET: 75 Denise Drive
; CITY: Hillsborough
; STATE: California
; COUNTRY: USA
; ZIP: 94010
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,088A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 343-4341
; TELEFAX: (650) 343-4342
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:

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; LENGTH: 2045 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-795-088A-1

Query Match      87.0%; Score 1952.2; DB 3; Length 2045;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1965; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

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Qy 108 GGACTCGGCTCACACAGTGAAGTCCGCGCTATTGGACTTTTGTCCAGTGAAGCTGAGAC 167
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Qy 228 CAAGTCCGCTTCCAGGCTTTCGGTTTCTTTGCTTCCATCTTTGGGTGGCGCTTCCCGCGT 287
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Qy 318 CTAGGGAGGAGGAGTGTAGTGGTGGCGGAGAGTCCGGCGGAGAGGAGTCCCGCGGAGGAGT 377
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Qy 348 CCCCCACTGGAAGGATCTGAAAGAAATGAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 407
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Qy 378 CCCCCACTGGAAGGATCTGAAAGAAATGAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 437
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Db 1637 ATGGGCGAGCGATGAAGAAATGGAATTCAGAGGCTCAGAGGAGGAGGAGGAGGAGGAGGAGG 1696
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Db 1757 CTCAGAGTCAAGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1816
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Db 1937 TCCCTCTCTACACATTAAGAAACCAAGGCTGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1996
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Db 1997 GCACCTTTGGGAGGCGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2045
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: Sequence 1, Application US/08859167
: Patent No. 6037461
: GENERAL INFORMATION:
: APPLICANT: Alnemri, Emad S.
: APPLICANT: Fernandez-Alnemri, Teresa
: TITLE OF INVENTION: FADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF
: TITLE OF INVENTION: USING THE SAME, AND COMPOSITIONS FOR AND METHODS OF
: NUMBER OF SEQUENCES: 17
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6037461rlis
: STREET: One Liberty Place, 46th floor
: CITY: Philadelphia
: STATE: PA
: COUNTRY: USA
: ZIP: 19103
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: WINDOWS
: SOFTWARE: WordPerfect
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/859,167
: FILING DATE:
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: DeLuca, Mark
: REGISTRATION NUMBER: 33,229
: REFERENCE/DOCKET NUMBER: TJU-
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (215) 568-3100
: TELEFAX: (215) 568-3439
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1750 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: both
: MOLECULE TYPE: CDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 413..1750
: US-08-859-167-1

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Query Match	72.2%	Score 1619.2	DB 3	Length 1750
Best Local Similarity	94.1%	Pred. No. 0		
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			Indels	106
			Gaps	2
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QY	129	GTGCGGGCTAATGCACTTTTGTCCAGTGACAGCTGAGACAACAGGACACGGGAGGAGG	188	
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QY	189	TGTAGGAGAGAGCGCGCAACAGCGATCGCCAGCACCAAGTCCGCTTCCAGGCTTTC	248	
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QY	249	GGTTTCTTTGCTCCATCTTTGGGTGGGCTTCCCGGCGCTCTAGGGAGCGAAGCTGAGG	308	
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QY	309	TGGCAGCGGAGGAGAGTCCGGCCGCGACGAGCAACTCCCCACATGGAAAGGATTCG	368	
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Db	301	AAAGAAATGAAGTCAGCCCTCAGAAATGAAGTTGACTGCCTGCCTGCTTTCCTGTTGACT	359	
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Qy 1869 ATTATGCTGGCTGCAGCACACTCTGAGAAAGAACTTATCCTCTCTCTACACATAA 1924
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RESULT 4

US-09-109-273-1
; Sequence 1, Application US/09109273
; Patent No. 6063760
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: FADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF
; TITLE OF INVENTION: USING THE SAME, AND COMPOSITIONS FOR AND METHODS
; TITLE OF INVENTION: OF MAKING THE SAME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6063760rls
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: WINDOWS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/109,273
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/859,167
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: RJU-
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1750 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; NAME/KEY: CDS

; LOCATION: 413..1750
US-09-109-273-1
Query Match 72.2%; Score 1619.2; DB 3; Length 1750;
Best Local Similarity 94.1%; Pred. No. 0;
Matches 1747; Conservative 0; Mismatches 3; Indels 106; Gaps 2;
Qy 69 CGAGTCTCAACTAAAGGGACTCCCGAGCTAGGGGTGGGACTCGCCCTCACACAGTGA 128
Db 1 CGAGTCTCAACTAAAGGGACTCCCGAGCTAGGGGTGGGACTCGCCCTCACACAGTGA 60
Qy 129 GTCCCGGCTATTGGACTTTTGTCCAGTGCAGCTGACACAACAGGACCACGGAGGAGG 188
Db 61 GTCCCGGCTATTGGACTTTTGTCCAGTGCAGCTGACACAACAGGACCACGGAGGAGG 120
Qy 189 TGTAGGAGAGAAGCGCCGCAACAGCGATCGCCAGCACCAAGTCCCTTCCAGGCTTTC 248
Db 121 TGTAGGAGAGAAGCGCCGCAACAGCGATCGCCAGCACCAAGTCCCTTCCAGGCTTTC 180
Qy 249 GGTTCCTTTCCTCCATCTTGGGTGCGCCTTCCCGGCGTCTAGGGGAGCGAAGCTGAGG 308
Db 181 GGTTCCTTTCCTCCATCTTGGGTGCGCCTTCCCGGCGTCTAGGGGAGCGAAGCTGAGG 240
Qy 309 TGGCAGCGGAGGAGAGTCCGGCGCGCACAGGAGCAACTCCCCCACTGGAAGAGTTCG 368
Db 241 TGGCAGCGGAGGAGAGTCCGGCGCGCACAGGAGCAACTCCCCCACTGGAAGAGTTCG 300
Qy 369 AAGAAATGAAGTCAGCCCTCAGAAATGAAGTTGACTGCCTGCTGGCTTCTCTTCTGACT 428
Db 301 AAGAAATGAAGTCAGCCCTCAGAAATGAAGTTGACTGCCTGCTGGCTTCTCTTCTGACT 359
Qy 429 GGCCCGGAGCTGTACTGCAAGACCCCTTGTGAGCTTCCCTAGTCTTAAGAGTAGGATGCTG 488
Db 360 GGCCCGGAGCTGTACTGCAAGACCCCTTGTGAGCTTCCCTAGTCTTAAGAGTAGGATGCTG 419
Qy 489 CTGAAGTCATCCATCAGGTTTGAAGAAGCACTTGATACAGATGACGAAGAGAGATGCTGCT 548
Db 420 CTGAAGTCATCCATCAGGTTTGAAGAAGCACTTGATACAGATGACGAAGAGAGATGCTGCT 479
Qy 549 TTTTGTCCCGGAGTGTGCTATAGATGTGGTTCACCTTAATGTTCAGGAGACCTTCTGGATA 608
Db 480 TTTTGTCCCGGAGTGTGCTATAGATGTGGTTCACCTTAATGTTCAGGAGACCTTCTGGATA 539
Qy 609 TTTTACGGGAAAGAGGTAAGCTGCTGTCCGGGAGCTTGGCTGAACTGCTCTACAGAGTGA 668
Db 540 TTTTACGGGAAAGAGGTAAGCTGCTGTCCGGGAGCTTGGCTGAACTGCTCTACAGAGTGA 599
Qy 669 GGCGATTTGACCTGCTCAAGAGTATCTTGAAGTGGACAGAAAAGCTGTGGAGACCCACC 728
Db 600 GGCGATTTGACCTGCTCAAGAGTATCTTGAAGTGGACAGAAAAGCTGTGGAGACCCACC 659
Qy 729 TGCTCAGGAACCCCTCAGCTTGTTCGGACTATAGAGTGTGATGGCAGAGATTGGTGAGG 788
Db 660 TGCTCAGGAACCCCTCAGCTTGTTCGGACTATAGAGTGTGATGGCAGAGATTGGTGAGG 719
Qy 789 ATTTGGATAAATCTGATGTCCTCAATTAATTTTCCATGAAGAGATTACATGGCCCGAG 848
Db 720 ATTTGGATAAATCTGATGTCCTCAATTAATTTTCCATGAAGAGATTACATGGCCCGAG 779
Qy 849 GCAAGATAAGCAAGGAGAGATTTCCTGGACCTTGTGGTGTGAGTTGGAGAACTAAATT 908
Db 780 GCAAGATAAGCAAGGAGAGATTTCCTGGACCTTGTGGTGTGAGTTGGAGAACTAAATC 839
Qy 909 TGGTTGCCCCAGATCAACTGGATTATTATAGAAAAATGCTTAAGAACTCCACAGAATAG 968
Db 840 TGGTTGCCCCAGATCAACTGGATTATTATAGAAAAATGCTTAAGAACTCCACAGAATAG 899
Qy 969 ACCTGAAGACAAAAATCCAGAAGTACAGCAGTCTGTTCAAGGAGGAGGACAAAGTTACA 1028
Db 900 ACCTGAAGACAAAAATCCAGAAGTACAGCAGTCTGTTCAAGGAGGAGGACAAAGTTACA 959
Qy 1029 GGAATGTTCTCCAAAGCAGCAATCCAAAGAGTCTCAAGGATCCTTCAAACTAACCTCAGGC 1088
|||||

Db 960 GGAATGTTCTCCAGCAGCAATCCAAAAGAGTCTCAAGGATCCTTCAAAATAACTTCAG-- 1017
QY 1089 TCATAATGGGAGAGTAAAGAACAAAGACTTAAGGAACAGCTTGCGCTCACAGAAC 1148
Db 1018 ----- 1017
QY 1149 CAGTGAAGAAATCCATTTCAGGAATCAGAAAGCTTTTTCCTCAGAGATACCTGGAAG 1208
Db 1018 -----GAGCATACCTGAAGAGA 1034
QY 1209 GATACAGATGAAGACCAAGCCCTAGGAATCTGCTGTATATCGATTGATGCGCAATG 1268
Db 1035 GATACAGATGAAGACCAAGCCCTAGGAATCTGCTGTATATCGATTGATGCGCAATG 1094
QY 1269 AGACAGAGCTTCTTCGAGACACCTTCACATTCCTGCTGCTATGAAGTCCAGAAATCTTTCG 1328
Db 1095 AGACAGAGCTTCTTCGAGACACCTTCACATTCCTGCTGCTATGAAGTCCAGAAATCTTTCG 1154
QY 1329 ATCTCAGTATGCATGTATATCCAGATTCCTTGGCCAAATTCGCTGTATGCCCCGAGACCC 1388
Db 1155 ATCTCAGTATGCATGTATATCCAGATTCCTTGGCCAAATTCGCTGTATGCCCCGAGACCC 1214
QY 1389 GAGACTACGACAGCTTGTGTCTGCTGCTGAGCGGAGGCTCCAGAGTGTGTATG 1448
Db 1215 GAGACTACGACAGCTTGTGTCTGCTGCTGAGCGGAGGCTCCAGAGTGTGTATG 1274
QY 1449 GTGTGATCAGACTCACTCAGGCTCCCTGCTGCTATCATCAGAGGATGTTTCATGGGAG 1508
Db 1275 GTGTGATCAGACTCACTCAGGCTCCCTGCTGCTATCATCAGAGGATGTTTCATGGGAG 1334
QY 1509 ATTCATGCCCTTATCTAGCAGGAAGCCAAAGATCTTTTATTCAGAACTATGTGTGT 1568
Db 1335 ATTCATGCCCTTATCTAGCAGGAAGCCAAAGATCTTTTATTCAGAACTATGTGTGT 1394
QY 1569 CAGAGGGCAGCTGGAGACACAGCAGCTTCTGGAGTGGATGGGCGCAGGATGAAGAATG 1628
Db 1395 CAGAGGGCAGCTGGAGACACAGCAGCTTCTGGAGTGGATGGGCGCAGGATGAAGAATG 1454
QY 1629 TGAATTCAGCTCAGAGCGAGGCTGTGCACAGTTCACCGAGAACTGACTTCTTCT 1688
Db 1455 TGAATTCAGCTCAGAGCGAGGCTGTGCACAGTTCACCGAGAACTGACTTCTTCT 1514
QY 1689 GGAGCTGTGTACTCGGACATGTCCTGCTGGAGCAGTTCACAGCTCACCGTCCCTGCT 1748
Db 1515 GGAGCTGTGTACTCGGACATGTCCTGCTGGAGCAGTTCACAGCTCACCGTCCCTGCT 1574
QY 1749 ACCTGAGTGCCTTCCAGAACTGAGACAAAGAAAGAAAGCCCACTCCTGATCTTC 1808
Db 1575 ACCTGAGTGCCTTCCAGAACTGAGACAAAGAAAGAAAGCCCACTCCTGATCTTC 1634
QY 1809 ACATTGAATCAATGGCTACATGATGATTGGAACAGAGTTCCTGCCAAGGAGAAAT 1868
Db 1635 ACATTGAATCAATGGCTACATGATGATTGGAACAGAGTTCCTGCCAAGGAGAAAT 1694
QY 1869 ATTATGCTGCTGAGCAGACTCTGAGAAAGAAACTTATCTCTCTCTACACATAA 1924
Db 1695 ATTATGTTGGCTGAGCAGACTCTGAGAAAGAAACTTATCTCTCTCTACACATAA 1750

RESULT 5
US-09-276-993-1
; Sequence 1, Application US/09276993
; Patent No. 6207801
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: FADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF
; TITLE OF INVENTION: USING THE SAME, AND COMPOSITIONS FOR AND METHODS
; TITLE OF INVENTION: OF MAKING THE SAME
; NUMBER OF INVENTIONS: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6207801ris
; STREET: One Liberty Place, 46th floor

CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: WINDOWS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/276,993
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/859,167
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1750 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: both
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 413..1750
US-09-276-993-1

Query Match 72.2%; Score 1619.2; DB 3; Length 1750;
Best Local Similarity 94.1%; Pred. No. 0;
Matches 1747; Conservative 0; Mismatches 3; Indels 106; Gaps 2;
QY 69 CGAGTCTCACTAAAGGGAGTCCCGGAGCTAGGGTGGGAGCTCGGCCTCACACAGTGA 128
Db 1 CGAGTCTCACTAAAGGGAGTCCCGGAGCTAGGGTGGGAGCTCGGCCTCACACAGTGA 60
QY 129 GTGCCGCTATTGGACTTTTGTCCAGTGACAGCTGAGACAAAGGACCAAGGAGGAGG 188
Db 61 GTGCCGCTATTGGACTTTTGTCCAGTGACAGCTGAGACAAAGGACCAAGGAGGAGG 120
QY 189 TGTAGGAGAGAGCGCGCGAAGCAGGATCGCCAGCAGCAAGTCCGCTTCCAGGCTTC 248
Db 121 TGTAGGAGAGAGCGCGCGAAGCAGGATCGCCAGCAGCAAGTCCGCTTCCAGGCTTC 180
QY 249 GGTTCCTTTCCCTCCATCTTTGGTGGCGCTTCCCGGCTAGGGAGCGAAGGCTGAGG 308
Db 181 GGTTCCTTTCCCTCCATCTTTGGTGGCGCTTCCCGGCTAGGGAGCGAAGGCTGAGG 240
QY 309 TGGCAGCGGAGAGAGTCCCGCGGACAGGAGCAACTCCCCACTTGGAAAGGATTCG 368
Db 241 TGGCAGCGGAGAGAGTCCCGCGGACAGGAGCAACTCCCCACTTGGAAAGGATTCG 300
QY 369 AAAGAAATGAAGTCAGCCCTCAGAAATGAAGTGGCTGCTGCTGCTTCTGTTGACT 428
Db 301 AAAGAAATGAAGTCAGCCCTCAGAAATGAAGTGGCTGCTGCTGCTTCTGTTGACT 359
QY 429 GGCCCGGAGCTGTACTGCAAGACCTTGTGAGCTTCCCTAGTCTAAGAGTAGGATCTCG 488
Db 360 GGCCCGGAGCTGTACTGCAAGACCTTGTGAGCTTCCCTAGTCTAAGAGTAGGATCTCG 419
QY 489 CTGAAGTCTATCCATCAGGTTGAAGAGCACTTGATACATGAGAGGAGATGCTCTCT 548
Db 420 CTGAAGTCTATCCATCAGGTTGAAGAGCACTTGATACATGAGAGGAGATGCTCTCT 479
QY 549 TTTTGTCCGGGATGTTGCTATAGATGTGTTCCACCTAATGTACAGGAGCTTCTTGATA 608
|||||

Db 480 TTTTGTCCCGGATGTTGCTATAGATGTGTTCCACCTTAATGTGTCAGGAGCCTTCTGGATA 539
Qy 609 TTTTACGGGAAAGAGTGAAGTCTGTCTGGGGACTTGGCTGAACCTCTACAGAGTGA 668
Db 540 TTTTACGGGAAAGAGTGAAGTGTCTGTGGGGACTTGGCTGAACCTCTACAGAGTGA 599
Qy 669 GGGGATTTGACCTGCTCAACAGTATCTTGAAGATGGACAGAAAAGCTGTGGAGCCACC 728
Db 600 GGGGATTTGACCTGCTCAACAGTATCTTGAAGATGGACAGAAAAGCTGTGGAGCCACC 659
Qy 729 TGTCTAGGAACCTCACCTTGTTCGGACTATAGAGTGTGATGGCAGAGATGGTGAGG 788
Db 660 TGTCTAGGAACCTCACCTTGTTCGGACTATAGAGTGTGATGGCAGAGATGGTGAGG 719
Qy 789 ATTTGGATAAATCTGATGTCTCTCAATTAATTTTCCTCATGAAGATTAACATGGGCCGAG 848
Db 720 ATTTGGATAAATCTGATGTCTCTCAATTAATTTTCCTCATGAAGATTAACATGGGCCGAG 779
Qy 849 GCAAGATAAGCAGGAGAGTTCCTTGACCTTGGCTTGAGTTGGAGAACTAAAT 908
Db 780 GCAAGATAAGCAGGAGAGTTCCTTGACCTTGGCTTGAGTTGGAGAACTAAATC 839
Qy 909 TGGTTGCCCGAGATCAACTGGATTTATTAGAAAAATGCCTAAAGAACATCCACAGATAG 968
Db 840 TGGTTGCCCGAGATCAACTGGATTTATTAGAAAAATGCCTAAAGAACATCCACAGATAG 899
Qy 969 ACCTGAAGCAAAAATCCAGAGTACAAAGCAGTCTGTTCAAGGAGCAGGACAAAGTTACA 1028
Db 900 ACCTGAAGCAAAAATCCAGAGTACAAAGCAGTCTGTTCAAGGAGCAGGACAAAGTTACA 959
Qy 1029 GGAATGTCTCCAGCAGCAATCCAAAGAGTCTCAAGGATCTTCAATTAACCTTCAGC 1088
Db 960 GGAATGTCTCCAGCAGCAATCCAAAGAGTCTCAAGGATCTTCAATTAACCTTCAGC 1017
Qy 1089 TCCATAATGGGAGAGTAAAGAACAAAGACTTAAGGAACAGCTTGGCGCTCAACAGAAC 1148
Db 1018 ----- 1017
Qy 1149 CAGTGAAGAAATCCATTACAGGAATCAGAACTTTTTCCTCAGAGCATACCTGAAGAGA 1208
Db 1018 -----GAGCATACCTGAAGAGA 1034
Qy 1209 GATACAGATGAAGAGCAAGCCCTAGGAATCTGCCTGATGAATCGATTCGATGGCAATG 1268
Db 1035 GATACAGATGAAGAGCAAGCCCTAGGAATCTGCCTGATGAATCGATTCGATGGCAATG 1094
Qy 1269 AGACAGAGCTTCTTCGAGACACCTTCACTTCCCTGGGCTATGAAGTCCAGAAATCTTGC 1328
Db 1095 AGACAGAGCTTCTTCGAGACACCTTCACTTCCCTGGGCTATGAAGTCCAGAAATCTTGC 1154
Qy 1329 ATCTCAGTATGCATGATATCCAGATTTCTTGCCCAATTTGGCTGTATGCCCGAGCACC 1388
Db 1155 ATCTCAGTATGCATGATATCCAGATTTCTTGCCCAATTTGGCTGTATGCCCGAGCACC 1214
Qy 1389 GAGACTACGACAGCTTGTGTGTCTGTCTGTGAGCCGAGAGGCTCCAGAGTGTGTATG 1448
Db 1215 GAGACTACGACAGCTTGTGTGTCTGTGTGTGAGCCGAGAGGCTCCAGAGTGTGTATG 1274
Qy 1449 GTGTGGATCAGACTCACTCAGGGCTCCCTCGATCATCATCAGGAGATGTTCATGGGAG 1508
Db 1275 GTGTGGATCAGACTCACTCAGGGCTCCCTCGATCATCATCAGGAGATGTTCATGGGAG 1334
Qy 1509 ATTCATGCCCTTATCTACAGGAGGAGCAAGATGTTTTTATTCAGAACTATGTGTGT 1568
Db 1335 ATTCATGCCCTTATCTACAGGAGGAGCAAGATGTTTTTATTCAGAACTATGTGTGT 1394
Qy 1569 CAGAGGCCAGCTGGAGAACAGCAGCTCTTGGAGTGGATGGGCCAGCGATGAAGATG 1628
Db 1395 CAGAGGCCAGCTGGAGAACAGCAGCTCTTGGAGTGGATGGGCCAGCGATGAAGATG 1454
Qy 1629 TGGAAATCAAGGCTCAGAAAGGAGGCTGTGCACAGTTTCCCGAGAGAGCTGACTTCTCT 1688
Db 1455 TGGAAATCAAGGCTCAGAAAGGAGGCTGTGCACAGTTTCCCGAGAGAGCTGACTTCTCT 1514

RESULT 6

US-09-723-450-1

: Sequence 1, Application US/09723450

: Patent No. 6576751

: GENERAL INFORMATION:

: APPLICANT: Alnemrl, Emad S.

: TITLE OF INVENTION: Padd-Like Anti-Apoptotic Molecules, Methods Of Using The Same,

: FILE OF INVENTION: Compositions For And Methods Of Making The Same

: FILE REFERENCE: TJU2445

: CURRENT APPLICATION NUMBER: US/09/723.450

: PRIOR FILING DATE: 2000-11-28

: PRIOR APPLICATION NUMBER: 09/276,993

: PRIOR FILING DATE: 1999-03-26

: PRIOR APPLICATION NUMBER: 08/859,167

: PRIOR FILING DATE: 1997-05-20

: NUMBER OF SEQ ID NOS: 17

: SOFTWARE: PatentIn version 3.0

: SEQ ID NO 1

: LENGTH: 1750

: TYPE: DNA

: ORGANISM: Artificial Sequence

: FEATURE:

: NAME/KEY: misc.feature

: OTHER INFORMATION: No. 6576751el Sequence

: NAME/KEY: CDS

: LOCATION: (413)..(1750)

US-09-723-450-1

Query Match 72.2%; Score 1619.2; DB 4; Length 1750;

Best Local Similarity 94.1%; Pred. No. 0;

Matches 1747; Conservative 0; Mismatches 3; Indels 106; Gaps 2;

Qy 69 CGAGTCTCAACTAAAGGGACTCCCGGAGCTAGGGGTGGGACTCGGCCCTCACAGTGA 128

Db 1 CGAGTCTCAACTAAAGGGACTCCCGGAGCTAGGGGTGGGACTCGGCCCTCACAGTGA 60

Qy 129 GTCCCGGCTATTGGACATTTGTCAGTGCAGCTGAGACACACAGGACCACGGAGGAGG 188

Db 61 GTCCCGGCTATTGGACATTTGTCAGTGCAGCTGAGACACACAGGACCACGGAGGAGG 120

Qy 189 TGTAGGAGAGAAAGCCCGCAACAGCGATCCCGCAGCACCAAGTCCCGCTTCAGGCTTTC 248

Db 121 TGTAGGAGAGAAAGCCCGCAACAGCGATCCCGCAGCACCAAGTCCCGCTTCAGGCTTTC 180

Qy 249 GGTTCCTTTGCCCTCCATCTTGGGTGCGCCTTCCCGGCGTCTAGGGGAGCGAAGGCTGAGG 308

Db 181 GGTTCCTTTGCCCTCCATCTTGGGTGCGCCTTCCCGGCGTCTAGGGGAGCGAAGGCTGAGG 240

Qy 309 TGGCAGCGGAGGAGAGTCCGGCCCGCACAGGAGCAACTCCCCACTGGAAAGGATTCGTG 368

Db 241 TGGCAGCGGAGGAGAGTCCGGCCCGCACAGGAGCAACTCCCCACTGGAAAGGATTCGTG 300

Qy 369 AAGAAATAGAGTACGCCCTCAGAAATGAAGTTGACTTCGCTGCTGGCTTCTCTGACT 428

Db 301 AAGAAATAGAGTACGCCCTCAGAAATGAAGTTGACTTCGCTGCTGGCTTCTCTGACT 359

QY	429	GGCCCGGAGCTGTACTCAAGACCCCTTGTGAGCTTCCCTAGTCTAAAGATAGGATGCTGTG	488
DB	360	GGCCCGGAGCTGTACTCAAGACCCCTTGTGAGCTTCCCTAGTCTAAAGATAGGATGCTGTG	419
QY	489	CTGAAGTCATCCATCAGGTTGAAGAAGCACTTGATACAGATGAGAAGAGATGCTGCTCT	548
DB	420	CTGAAGTCATCCATCAGGTTGAAGAAGCACTTGATACAGATGAGAAGAGATGCTGCTCT	479
QY	549	TTTTTGTCGGGGATGTGCTATAGATGTGGTTCCACCTAATGTCAGGAGCCTTCTGGATA	608
DB	480	TTTTTGTCGGGGATGTGCTATAGATGTGGTTCCACCTAATGTCAGGAGCCTTCTGGATA	539
QY	609	TTTTACGGGAAAGAGTGAAGTGCTCTCGGGGACTTGGCTGAACCTCTACAGACTGA	668
DB	540	TTTTACGGGAAAGAGTGAAGTGCTCTCGGGGACTTGGCTGAACCTCTACAGACTGA	599
QY	669	GGCGATTGACCTGCTCAAAAGTATCTTGAAGATGGACAGAAAAAGCTGTGGAGACCCACC	728
DB	600	GGCGATTGACCTGCTCAAAAGTATCTTGAAGATGGACAGAAAAAGCTGTGGAGACCCACC	659
QY	729	TGCTCAGGAACCCCTACCTTGTTCGGACATATAGAGTCTGATGGCAGAGATTTGGTCAGG	788
DB	660	TGCTCAGGAACCCCTACCTTGTTCGGACATATAGAGTCTGATGGCAGAGATTTGGTCAGG	719
QY	789	ATTTGGATTAATCTGATGTGCTCTCAATTAATTTCCCTCATGAAGGATTTACATGGCGCAG	848
DB	720	ATTTGGATTAATCTGATGTGCTCTCAATTAATTTCCCTCATGAAGGATTTACATGGCGCAG	779
QY	849	GCAAGATAAGCAAGGAGAAGAGTTCTCTGGACCTTGTGGTTGAGTTGGAGAAACTTAATT	908
DB	780	GCAAGATAAGCAAGGAGAAGAGTTCTCTGGACCTTGTGGTTGAGTTGGAGAAACTTAATT	839
QY	909	TGGTTGCCCGAGATCAACTGGATTTATAGAAAAATGCCCTAAAGAACATCCACAGAAATG	968
DB	840	TGGTTGCCCGAGATCAACTGGATTTATAGAAAAATGCCCTAAAGAACATCCACAGAAATG	899
QY	969	ACCTGAAGACAAAAATCCAGAGTACAAAGCAGTCTGTTCAAGGACGAGGACAGTTTACA	1028
DB	900	ACCTGAAGACAAAAATCCAGAGTACAAAGCAGTCTGTTCAAGGACGAGGACAGTTTACA	959
QY	1029	GGAAATGTTCCAAAGCAGCAATCCAAAGAGTCTCAAGGATCCTTCAAAATACTTCAGGC	1088
DB	960	GGAAATGTTCCAAAGCAGCAATCCAAAGAGTCTCAAGGATCCTTCAAAATACTTCAGGC	1017
QY	1089	TCCATAATGGGAGAAGTAAAGACAAAGACTTAAGGAACAGCTTGGCGCTCAACAGAAC	1148
DB	1018	-----	1017
QY	1149	CAGTGAAGAAATCCATTCAGGAATCAGAAGCTTTTTCCTCAGAGCATACCTGAAGAGA	1208
DB	1018	-----GAGCATACCTGAAGAGA	1034
QY	1209	GATCAAGATGAAGACAGACCCCTAGGAATCTGCCTGATTAATCGATTGATGGCAATG	1268
DB	1035	GATCAAGATGAAGACAGACCCCTAGGAATCTGCCTGATTAATCGATTGATGGCAATG	1094
QY	1269	AGACAGAGCTTCTTCGAGACACCTTCACCTTCCCTGGGCTATGAAGTCCAGAAATCTTGC	1328
DB	1095	AGACAGAGCTTCTTCGAGACACCTTCACCTTCCCTGGGCTATGAAGTCCAGAAATCTTGC	1154
QY	1329	ATCTCAGTATGCGATGGTATATCCAGATTTCTTGGCCAAATTTGGCTGTATGCCGAGCACC	1388
DB	1155	ATCTCAGTATGCGATGGTATATCCAGATTTCTTGGCCAAATTTGGCTGTATGCCGAGCACC	1214
QY	1389	GAGACTACGACAGCTTTGTGTGTCTGTGTGAGCCGAGGAGGCTCCACAGTGTGTATG	1448
DB	1215	GAGACTACGACAGCTTTGTGTGTCTGTGTGAGCCGAGGAGGCTCCACAGTGTGTATG	1274
QY	1449	GTGTGATCAGACTCACTCAGGCGTCCCTCGATCAATCAGAGAGATGTTCAATGGGAG	1508
DB	1275	GTGTGATCAGACTCACTCAGGCGTCCCTCGATCAATCAGAGAGATGTTCAATGGGAG	1334

Qy	1509	ATT	CATGCCCTT	ATCTAGCAGGG	AAGCCAAAGATGTTTTT	TATTCAGAACTATGTGGTGT	1568
Db	1335	ATT	CATGCCCTT	ATCTAGCAGGG	AAGCCAAAGATGTTTTT	TATTCAGAACTATGTGGTGT	1394
Qy	1569	CAGAGGCC	AGCTGGAGAA	CAGCAGCCTCTTGGAGGT	GGATGGGCCAGCCATGAAGAA	TCG 1628	
Db	1395	CAGAGGCC	AGCTGGAGAG	CAGCAGCCTCTTGGAGGT	GGATGGGCCAGCCATGAAGAA	TCG 1454	
Qy	1629	TGGAATTC	AAGGCTCAGAAG	CGAGGGGTGTGCACAGTTT	CACCGAGAGCTGACTCTCTCT	1688	
Db	1455	TGGAATTC	AAGGCTCAGAAG	CGAGGGGTGTGCACAGTTT	CACCGAGAGCTGACTCTCTCT	1514	
Qy	1689	GGAGCCTGT	GTACTGCGG	ACATGTCCCTGCTGGAGCAGT	CTCAGAGCTCACCCGTCCCTGT	1748	
Db	1515	GGAGCCTGT	GTACTGCGG	ACATGTCCCTGCTGGAGCAGT	CTCAGAGCTCACCCGTCCCTGT	1574	
Qy	1749	ACCTGCA	GTGCCCTCCAGAA	ACTGAGACAAAGAAAACGGCC	ACTCCTCGATCTTC 1808		
Db	1575	ACCTGCA	GTGCCCTCCAGAA	ACTGAGACAAAGAAAACGGCC	ACTCCTCGATCTTC 1634		
Qy	1809	ACATTGA	ACTCAATGGCTACATGTAT	GATTGGAACACAGAGTTTCT	TGCCCAAGGAGAAAT 1868		
Db	1635	ACATTGA	ACTCAATGGCTACATGTAT	GATTGGAACACAGAGTTTCT	TGCCCAAGGAGAAAT 1694		
Qy	1869	ATTATG	CTGGCTGCAGC	ACACTCTGAGAAGAACTTAT	TCCTCTCTCTACACATAA 1924		
Db	1695	ATTATG	CTGGCTGCAGC	ACACTCTGAGAAGAACTTAT	TCCTCTCTCTACACATAA 1750		

RESULT 7

RESULT 7
 US-08-520-373D-4/c
 ; Sequence 4, Application US/08520373D
 ; Patent No. 6451763
 ; GENERAL INFORMATION:
 ; APPLICANT: Tombran-Tink, Joyce
 ; APPLICANT: Steele, Fintan R
 ; APPLICANT: Chader, Gerald J
 ; APPLICANT: Becerra, Sofia P
 ; APPLICANT: Johnson, Lincoln V
 ; APPLICANT: Rodriguez, Ignacio R
 ; TITLE OF INVENTION: RETINAL PIGMENTED EPITHELIUM DERIVED NEUROTROPIC FACTOR
 ; FILE REFERENCE: 2026-4203US1
 ; CURRENT APPLICATION NUMBER: US/08/520,373D
 ; CURRENT FILING DATE: 1995-08-29
 ; PRIOR APPLICATION NUMBER: 08/377,710
 ; PRIOR FILING DATE: 1995-01-25
 ; PRIOR APPLICATION NUMBER: 08/279,979
 ; PRIOR FILING DATE: 1994-07-25
 ; PRIOR APPLICATION NUMBER: 07/894,215
 ; PRIOR FILING DATE: 1992-06-04
 ; PRIOR APPLICATION NUMBER: 07/952,796
 ; PRIOR FILING DATE: 1992-09-24
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 4
 ; LENGTH: 14581
 ; TYPE: DNA
 ; ORGANISM: HUMAN
 ; FEATURE:
 ; OTHER INFORMATION: mRNA: 6683; EXON: 6683-6790; EXON 11584-11675;
 ; OTHER INFORMATION: EXON: 14539-14581; INTRON: 6791-11583; INTRON:
 ; OTHER INFORMATION: 11676-14538; CDS: 11584-11675; 14539-14580
 US-08-520-373D-4

	Query Match	7.98;	Score 175;	DB 4;	Length 14581;
	Best Local Similarity	76.28;	Pred. No. 2.1e-42;		
	Matches 246;	Conservative	0;	Mismatches 65;	Indels 12; Gaps 2;
Qy	1921	ATAAGAAACCAAAAGCTGGCGCTAGTGGCTACACCTGTAAATCCAGCAGCACTTTGGAGG	1980		
Db	9834	AAAAAAAAAAAAAGCCAGGCCAGTGGCTAAACCTGTAAATCCAGCAGCACTTTGAGAG	9775		
Qy	1981	CAAAGGAGGCCAGATCACTTCAGGTACAGGAGTTTCGAGACCAAGCTGCCCAACATGG-TAA	2039		

Db 9774 CCGAGGCGGTAGTACCTGAGGTGAGAGTTTGGAGCCTCTGGCCCAACATGGAGAA 9715
QY 2040 ACCTGTCTCCCTAGTAAAAATGCAAAATAGCTGGGTGGGTGGGTACCTGTGTCTCC 2099
Db 9714 ACCCATCTCTACTAAAAATACAAAATAGCCGGGTGGTGGCCGATGCCGTGTATCC 9655
QY 2100 CAGTTACTTGGGAGGCTGAGGTGGGAGGATCTTTTGAACCCAGGAGTTTCAGGCTCATAGC 2159
Db 9654 CAGCTACTTGGGAGGCTAAGCCAGGAGGAATCACTTGAATCCAGGAAGTGGAGGTTCGAGT 9595
QY 2160 ATGCTGTGATGTGCTACGAATAGCCACTGCATACCAACCTCGGCAATATACGAAGATC 2219
Db 9594 GAGCTGAGATCG-----CGCCTGCTACTCAGGCTGGGCAACAGACAGACT 9546
QY 2220 CCATCTCTTTTAAAAAATAAAAAA 2242
Db 9545 CCATCTCAAAAAAATAAAAAA 9523

RESULT 8

US-08-367-841A-43/c
; Sequence 43, Application US/08367841A
; Patent No. 6315687
; GENERAL INFORMATION:
; APPLICANT: Chader, Gerald J.; Rodriguez,
; APPLICANT: Ignacio R.; Mazuruk, Krzysztof;
; APPLICANT: Tombran-Tink, Joyce
; TITLE OF INVENTION: PIGMENT EPITHELIUM
; TITLE OF INVENTION: DERIVED FACTOR: CHARACTERIZATION GENOMIC
; TITLE OF INVENTION: ORGANIZATION AND SEQUENCE OF THE PEDF GENE
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan
; STREET: 345 Park Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10154

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/367,841A
; FILING DATE: 30-DEC-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/257,963
; FILING DATE: 07-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/952,796
; FILING DATE: 24-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: DOROTHY R. AUTH
; REGISTRATION NUMBER: 36434
; REFERENCE/DOCKET NUMBER: 20264126US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22481 Base Pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Double
; TOPOLOGY: Unknown
; MOLECULE TYPE: Genomic DNA
; FEATURE:
; NAME/KEY: Pl-147
; LOCATION:
; IDENTIFICATION METHOD: full length genomic
; OTHER INFORMATION: full length genomic

; OTHER INFORMATION: sequence for PEDF plus flanking sequences.
US-08-367-841A-43

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Best Local Similarity 76.2%; Pred. No. 2.8e-42;
Matches 246; Conservative 0; Mismatches 55; Indels 12; Gaps 2;
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Db 9823 AAAAAAAAAAAAAAGCCAGGCGCAGTGGCTGCTAAACCTGTAAATCCAGCAGCTTTGAGAGG 9764
QY 1981 CCAAGGAGGCGCAGTCACTTCAAGTCAAGGAGTTTCAGACCCAGCAGCTGSCCAACATGG-TAA 2039
Db 9763 CCAGGCGGCTAGTACCTGAGGTGAGAGTTTGGAGCCATCTCTGGCCCAACATGGAGAA 9704
QY 2040 ACCTGTCTCCCTAGTAAAAATGCAAAATAGCTGGGTGGGTGGGTACCTGTGTCTCC 2099
Db 9703 ACCCATCTCTACTAAAAATACAAAATAGCCGGGTGGTGGCCGATGCCGTGTATCC 9644
QY 2100 CAGTTACTTGGGAGGCTGAGGTGGGAGGATCTTTTGAACCCAGGAGTTTCAGGCTCATAGC 2159
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QY 2160 ATGCTGTGATGTGCTACGAATAGCCACTGCATACCAACCTCGGCAATATACGAAGATC 2219
Db 9583 GAGCTGAGATCG-----CGCCTGCTACTCAGGCTGGGCAACAGACAGACT 9535
QY 2220 CCATCTCTTTTAAAAAATAAAAAA 2242
Db 9534 CCATCTCAAAAAAATAAAAAA 9512

RESULT 9

PCT-US95-07201-43/c
; Sequence 43, Application PC/TUS9507201
; GENERAL INFORMATION:
; APPLICANT: Chader, Gerald J.; Becerra, Sofia
; APPLICANT: Patricia; Schwartz, Joan P.;
; APPLICANT: Taniwaki, Takayuki
; TITLE OF INVENTION: PIGMENT EPITHELIUM
; TITLE OF INVENTION: DERIVED FACTOR: CHARACTERIZATION GENOMIC
; TITLE OF INVENTION: ORGANIZATION AND SEQUENCE OF THE PEDF GENE
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/07201
; FILING DATE: 06-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/367,841
; FILING DATE: 30-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/257,963
; FILING DATE: 07-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/952,796
; FILING DATE: 24-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: DOROTHY R. AUTH
; REGISTRATION NUMBER: 36434
; REFERENCE/DOCKET NUMBER: 20264126PCT
; TELECOMMUNICATION INFORMATION:

; NAME: Cimbal, Michele A
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 0627.2830004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)833-7533
; TELEFAX: (202)833-8716
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17327 base pairs
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; TOPOLOGY: linear
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; NAME/KEY: exon
; LOCATION: 16397..17327
US-07-906-871-15

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QY 2114 GCTGAGTGGGAGGATCTTTGAACCCAGGAGTTCAGGCTCATAGCATCTGTGATTGTG 2173
DB 7711 GCTGAGGAGGAGATCGCTTGAACCTGGAGGAGAGGTTCCAGTGAGCCAGATTGT- 7769

QY 2174 CCTACGAATAGCCACTGCATACCAACCTGGGCAATATAGCAAGATCCCATCTCTTTAAA 2233
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QY 2234 AAAAAAAA 2243
DB 7820 AAAAAAAA 7829

RESULT 12
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; Sequence 3, Application US/09740027
; Patent No. 6485939
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER COFACTOR
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER
; FILE REFERENCE: COFACTOR PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL001052
; CURRENT APPLICATION NUMBER: US/09/740,027
; CURRENT FILING DATE: 2000-12-20
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 3
; LENGTH: 24707
; TYPE: DNA
; ORGANISM: Human
US-09-740-027-3

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Best Local Similarity 76.8%; Pred. No. 4.2e-41;
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QY 2114 GCTGAGTGGGAGGATCTTTGAACCCAGGAGTTCAGGCTCATAGCATCTGTGATTGTG 2173
DB 16034 GCTGAGGAGGAGATCGCTTGAACCCAGGAGGAGGAGTTCAGTGTGGGATTGTG 15975

QY 2174 CCTACGAATAGCCACTGCATACCAACCTGGGCAATATAGCAAGATCCCATCTCTTTAAA 2233
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QY 2234 AAAAAAAA 2243
DB 15922 AAAAAACTAA 15913

RESULT 13
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; Sequence 7, Application US/08814095
; Patent No. 6025183
; GENERAL INFORMATION:
; APPLICANT: Soreq, Hermona
; APPLICANT: Zakut, Haim
; APPLICANT: Shani, Moshe
; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
; TITLE OF INVENTION: ANTI-CHOLINESTERASE SUBSTANCES
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KOHN & ASSOCIATES
; STREET: 30500 No. 6025183thwestern Highway, Suite 410
; CITY: Farmington Hills
; STATE: Michigan
; COUNTRY: U.S.
; ZIP: 48334
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/814,095
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Montgomery, Ilene N.
; REGISTRATION NUMBER: 38,972
; REFERENCE/DOCKET NUMBER: 2391.00066
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (248) 539-5050
; TELEFAX: (248) 539-5055
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35060 base pairs
; TYPE: nucleic acid

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MOLECULE TYPE: other nucleic acid
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ANTI-SENSE: NO
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Qy	2126	GGATCTTTTGAACCCAGGAGTTACAGGTCATAGCATGCTGTGTAATGTGCGCTACGAATGC	2185
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Qy	2186	CACGTGATACCAACCTGGGCAATATAGCAAGATCCCATCTCTTTTAAAAAATAAAAAA	2243
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Search completed: August 22, 2003, 13:53:40
Job time : 153.706 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 22, 2003, 11:36:53 ; Search time 509.885 Seconds
(without alignments)
9889.733 Million cell updates/sec

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Perfect score: 2243
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Scoring table: IDENTITY_NUC
Gapop 10_0 , Gapext 1.0

Searched: 1517243 seqs, 1124081882 residues

Total number of hits satisfying chosen parameters: 3034486

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_NA.*

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- 17: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2124	94.7	2143	9	US-09-410-194-16
3	2006.8	89.5	2034	11	US-09-009-893-1
4	1952.2	87.0	2045	9	US-09-861-270-1
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6	1209.6	53.9	1319	14	US-10-115-928-19
7	899.6	40.1	2597	11	US-09-009-893-5
8	849.6	37.9	2452	9	US-09-410-194-18
9	813.6	36.3	2770	13	US-10-005-921-1
10	731.8	32.6	1190	9	US-09-410-194-14
11	431.4	19.2	495	11	US-09-918-995-26998
12	423.2	18.9	479	11	US-09-918-995-37866
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15	345	15.4	443	11	US-09-918-995-35271
16	313.4	14.0	414	11	US-09-009-893-23

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c 18	292.6	13.0	309	11	US-09-009-893-25
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c 21	276	12.3	437	9	US-09-864-761-3120
c 22	259.8	11.6	430	9	US-09-864-761-1769
c 23	245.4	10.9	324	11	US-09-009-893-27
c 24	223.8	10.0	227	9	US-09-864-761-18522
c 25	215.4	9.6	308	11	US-09-009-893-29
c 26	213	9.5	389	10	US-09-783-590-4424
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c 28	206.4	9.2	297	11	US-09-009-893-30
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c 42	175	7.8	22484	10	US-09-880-107-3341
c 43	174.8	7.8	3553	13	US-10-027-632-115288
c 44	174.8	7.8	7737	9	US-09-764-887-453
c 45	174.8	7.8	7737	10	US-09-764-847-2001

ALIGNMENTS

RESULT 1
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; Sequence 2, Application US/09471749
; Publication No. US20030124113A1
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Patterson, Chandra
; APPLICANT: Baughn, Mariah
; TITLE OF INVENTION: HUMAN APOPTOSIS ASSOCIATED PROTEINS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/471,749
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/078,402
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cerrone, Michael C.
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0519 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:

Mon Aug 25 09:11:02 2003

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; LENGTH: 2352 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: THP1PLB02
; CLONE: 157658
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QY	436	AGCTGTACTGCAAGACCCCTGTGAGCTTCCCTAGTCTAAGACTAGAGTGTCTCTCAAGT	495	
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QY	496	CATCCATCAGGTGGAAGAGCACATGATACAGATGAGAAGAGATGCTCTTTTGTG	555	
DB	626	CATCCATCAGGTGGAAGAGCACATGATACAGATGAGAAGAGATGCTCTTTTGTG	685	
QY	556	CCGGATGTTGCTATAGATGTGGTTCCACCTAATGTCTAGGACCTCTTGATATTTACG	615	
DB	686	CCGGATGTTGCTATAGATGTGGTTCCACCTAATGTCTAGGACCTCTTGATATTTACG	745	
QY	616	GGAAGAGGTAGCTGTCTGCGGGAGCTTGGCTGAACTGCTCTACAGAGTAGGCGGATT	675	
DB	746	GGAAGAGGTAGCTGTCTGCGGGAGCTTGGCTGAACTGCTCTACAGAGTAGGCGGATT	805	
QY	676	TGACCTGCTCAACAGTATCTTGAAGATGGACAGAAAAGCTGTGGAGACCCAGCTGCTCAG	735	
DB	806	TGACCTGCTCAACAGTATCTTGAAGATGGACAGAAAAGCTGTGGAGACCCAGCTGCTCAG	865	
QY	736	GAACCCCTACCTTGTCTCGGACTATAGAGTGTGATGGCAGAGATTGGTAGGATTTGGA	795	
DB	866	GAACCCCTACCTTGTCTCGGACTATAGAGTGTGATGGCAGAGATTGGTAGGATTTGGA	925	
QY	796	TAAATCTGATGTGCTCATTAATTTTCTCATGAAGGATTACATGGCGCGAGCAGAT	855	
DB	926	TAAATCTGATGTGCTCATTAATTTTCTCATGAAGGATTACATGGCGCGAGCAGAT	985	
QY	856	AAGCAAGGAGAGAGTTTCTTGGACCTGTGTGTTGAGTTGGAGAACTAAATTTGGTTGC	915	
DB	986	AAGCAAGGAGAGAGTTTCTTGGACCTGTGTGTTGAGTTGGAGAACTAAATTTGGTTGC	1045	

QY	916	CCACGATCAACTGGGATTTTATTAGAAAAAATGCTTAAGAACAATCCACAGAAATAGACCTGAA	975
Db	1046	CCCGATCAACTGGGATTTATTAGAAAAAATGCTTAAGAACATCCACAGATAGACCTGAA	1105
QY	976	GACAAAAATCCAGAAAGTACAAAGCAGTCTGTTCAGGAGCAGGGACAAAGTTACAGGAATGT	1035
Db	1106	GACAAAAATCCAGAAAGTACAAAGCAGTCTGTTCAGGAGCAGGGACAAAGTTACAGGAATGT	1165
QY	1036	TTCTCAAGCAGCAATCCAAAAAGAGTCTCAAGGATCCCTTCAAAATACCTTCAGGCTCCATAA	1095
Db	1166	TTCTCAAGCAGCAATCCAAAAAGAGTCTCAAGGATCCCTTCAAAATACCTTCAGGCTCCATAA	1225
QY	1096	TGGGAGAACTAAAGAACAAAGACTTTAAGGAACAGCTTGGCGCTCAAAAGAACACAGTGAA	1155
Db	1226	TGGGAGAACTAAAGAACAAAGACTTTAAGGAACAGCTTGGCGCTCAAAAGAACACAGTGAA	1285
QY	1156	GAAATCCATTCAGGAATCAGAAAGCTTTTTTGCTCAGAGCATACCTGAAGAGAGATACAA	1215
Db	1286	GAAATCCATTCAGGAATCAGAAAGCTTTTTTGCTCAGAGCATACCTGAAGAGAGATACAA	1345
QY	1216	GATGAAGACCAAGCCCTAGGAATCTGCCTGATATCGATTGCATTGGCAATGAGACAGA	1275
Db	1346	GATGAAGACCAAGCCCTAGGAATCTGCCTGATATCGATTGCATTGGCAATGAGACAGA	1405
QY	1276	GCCTTCTTCGAGACACCTTCACCTTCCCTGGGCTATGAAGTCCAGAAATTTCTTGGCATCTCAG	1335
Db	1406	GCCTTCTTCGAGACACCTTCACCTTCCCTGGGCTATGAAGTCCAGAAATTTCTTGGCATCTCAG	1465
QY	1336	TATGCATGGTATATCCAGATCTTGGGCCAATTTGCCTGTATGCCGAGCACCAGACTA	1395
Db	1466	TATGCATGGTATATCCAGATCTTGGGCCAATTTGCCTGTATGCCGAGCACCAGACTA	1525
QY	1396	CGACAGCTTTGTGTGTCTCTGTGTGAGCCGAGGAGCTCCAGAGTGTGTATGGTGTGA	1455
Db	1526	CGACAGCTTTGTGTGTCTCTGTGTGAGCCGAGGAGCTCCAGAGTGTGTATGGTGTGA	1585
QY	1456	TCAGACTCACTCAGGGCTCCCTCTGCATCATACTCAGGAGGATGTTTCATGGGAGATTCATG	1515
Db	1586	TCAGACTCACTCAGGGCTCCCTCTGCATCATACTCAGGAGGATGTTTCATGGGAGATTCATG	1645
QY	1516	CCCTTATCTAGCAGGGGAAGCCAAAGATGTTTTTATTCAGAACTATGTGGTCTCAGAGGG	1575
Db	1646	CCCTTATCTAGCAGGGGAAGCCAAAGATGTTTTTATTCAGAACTATGTGGTCTCAGAGGG	1705
QY	1576	CCAGCTGGAGAACAGCAGCCTCTTGGAGTGGATGGCCAGCGGATGAAGAAATGTGGAAT	1635
Db	1706	CCAGCTGGAGAACAGCAGCCTCTTGGAGTGGATGGCCAGCGGATGAAGAAATGTGGAAT	1765
QY	1636	CAAGGCTCAGAAAGCAGGGCTGTGCAGTTACCGAGAGCTGACTTCTCTGGAGCCT	1695
Db	1766	CAAGGCTCAGAAAGCAGGGCTGTGCAGTTACCGAGAGCTGACTTCTCTGGAGCCT	1825
QY	1696	GTGTACTCGGACATGTCCCTGTGTGGAGCAGTCTCAGAGCTCACCGTCCCTGTACCTGCA	1755
Db	1826	GTGTACTCGGACATGTCCCTGTGTGGAGCAGTCTCAGAGCTCACCGTCCCTGTACCTGCA	1885
QY	1756	GTGGCTCTCCAGAAACTGAGACAAGAAAGAACGCCCACTCTGATCTTCCACATTTGA	1815
Db	1886	GTGGCTCTCCAGAAACTGAGACAAGAAAGAACGCCCACTCTGATCTTCCACATTTGA	1945
QY	1816	ACTCAATGGCTACATGTATGATTTGGAACAGCAGAGTTTCTGCCAAGGAGAAATATTATGT	1875
Db	1946	ACTCAATGGCTACATGTATGATTTGGAACAGCAGAGTTTCTGCCAAGGAGAAATATTATGT	2005
QY	1876	CTGGCTGCAGCACACTTGAGAAAGAAACTTATCCTCTCTACNCATAGAAGAACCCAAAG	1935
Db	2006	CTGGCTGCAGCACACTTGAGAAAGAAACTTATCCTCTCTACACATAAGAAACCCAAAG	2065
QY	1936	GTGTGGGCTAGTGGCTCACACTGTATPCCAGCACTTTGGGAGGCCCAAGGAGGGCAGAT	1995
Db	2066	GTGTGGGCTAGTGGCTCACACTGTATPCCAGCACTTTGGGAGGCCCAAGGAGGGCAGAT	2125
QY	1996	CACCTTCAGGTCAAGGATTCGAGACACAGCCTGGCCAAACATGFTAAACGCTGTCCCTAGTAA	2055

RESULT 3
 US-09-099-993-1
 ; Sequence 1, Application US/09009893
 ; Publication No. US20030087339A1
 ; GENERAL INFORMATION:
 ; APPLICANT: NI, JIAN
 ; APPLICANT: ROSEN, CRAIG A.
 ; APPLICANT: DIXIT, VISHVA M.
 ; APPLICANT: GENTZ, REINER L.
 ; APPLICANT: KENNY, JOSEPH J.
 ; TITLE OF INVENTION: I-FLICE, A NOVEL INHIBITOR OF TUMOR
 ; TITLE OF INVENTION: NECROSIS FACTOR RECEPTOR-1 AND CD-95 INDUCED APOPTOSIS
 ; NUMBER OF SEQUENCES: 32
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
 ; STREET: 1100 NEW YORK AVENUE, SUITE 600
 ; CITY: WASHINGTON
 ; STATE: DC

Query Match	89.5%;	Score 2006.8;	DB 11;	Length 2034;
Best Local Similarity	99.6%;	Pred: No. 0;		
Matches 2022;	Conservative	0;	Mismatches 7;	Indels 1; Gaps 1;
QY	214	CGATCGCCACGACCAAGTCCGCTTCCAGGCTTTCGGTTTCTTGGCTTCATCTTGGGTG	273	
Db	1	CGATCGCCACGACCAAGTCCGCTTCCAGGCTTTCGGTTTCTTGGCTTCATCTTGGGTG	60	
QY	274	CGCTTCCCGGCTCTAGGGGACGAAGGCTCAGCTGGCAGCGCAGGAGAGTCCGGCCG	333	
Db	61	CGCTTCCCGGCTCTAGGGGACGAAGGCTCAGCTGGCAGCGCAGGAGAGTCCGGCCG	120	
QY	334	CGACGAGCAACTCCCCACTGGAAAGATTCTGAAGAATGAAGTCAGCCCTCAGAA	393	
Db	121	CGACGAGCAACTCCCCACTGGAAAGATTCTGAAGAATGAAGTCAGCCCTCAGAA	180	
QY	394	ATGAAGTTGACTGCTGCTGGCTTTCCTCTGTGACTGGCCGGAGCTGTACTGCAAGACC	453	
Db	181	ATGAAGTTGACTGCTGCTGGCTTTCCTGTGTGACTGGCCGGAGCTGTACTGCAAGACC	239	
QY	454	TGTGAGCTTCCCTTAGTCTTAAGAGTAGGATGCTGCTGAAGTCATCCATCAGGTTGAGA	513	
Db	240	TGTGAGCTTCCCTTAGTCTTAAGAGTAGGATGCTGCTGAAGTCATCCATCAGGTTGAGA	299	
QY	514	AGCACTTGATACATACAGAGAGAGATGCTGCTTTTTTTGTCCGGGATGTTGCTATAGA	573	
Db	300	AGCACTTGATACATACAGAGAGAGATGCTGCTTTTTTTGTCCGGGATGTTGCTATAGA	359	
QY	574	TGTGTTTCCACCTAATGTCAGGGACCTTTCGGATATTTTACGGGAAGAGGTTAAGCTCTC	633	
Db	360	TGTGTTTCCACCTAATGTCAGGGACCTTTCGGATATTTTACGGGAAGAGGTTAAGCTCTC	419	
QY	634	TGTCGGGACCTTGCTGTAACCTGCTCTACAGAGTAGGCGGATTTTGACCTCTCTCAAACTAT	693	
Db	420	TGTCGGGACCTTGCTGTAACCTGCTCTACAGAGTAGGCGGATTTTGACCTCTCTCAAACTAT	479	
QY	694	CTTGAAGTAGGACAGAAAGCTGTGGAGCCCACTGCTCAGGAACCCCTCACCTTGTTC	753	

Db 480 CTTGAAGATGACAAAGCTGGAGACCCACCTGCTCAGGAACCCCTCACCTGTGTTTC 539
Qy 754 GGACTATAGAGTGTGATGGCAGAGATTGGTGGAGATTGGGATAAATCTGATGTGCTTC 813
Db 540 GGACTATAGAGTGTGATGGCAGAGATTGGTGGAGATTGGGATAAATCTGATGTGCTTC 599
Qy 814 ATTAATTTTCTCATGAAGGATTACATGGGCCGAGCAAGATAAGCAAGAGAGATTT 873
Db 600 ATTAATTTTCTCATGAAGGATTACATGGGCCGAGCAAGATAAGCAAGAGAGATTT 659
Qy 874 CTTGGACCTGTGCTTGGTGGAGAACTAAATTTGTTGGTCCGCCAGATCAACTGGATTT 933
Db 660 CTTGGACCTGTGCTTGGTGGAGAACTAAATTTGTTGGTCCGCCAGATCAACTGGATTT 719
Qy 934 ATTAGAAAAATGCCATAAGAACATCCACAGAATAAGACTGAAGCAAAAAATCCAGAAAGTA 993
Db 720 ATTAGAAAAATGCCATAAGAACATCCACAGAATAAGACTGAAGCAAAAAATCCAGAAAGTA 779
Qy 994 CAAGCAGTCTGTTCAAGAGAGAGGAGCAAGTTACAGGAATGTTCTCCAAGCAGCAATCCA 1053
Db 780 CAAGCAGTCTGTTCAAGAGAGAGGAGCAAGTTACAGGAATGTTCTCCAAGCAGCAATCCA 839
Qy 1054 AAACAGTCTCAAGGATCCTTCAATAACTTCCAGGCTCCATAATGGGAGAACTAAAGACA 1113
Db 840 AAACAGTCTCAAGGATCCTTCAATAACTTCCAGGCTCCATAATGGGAGAACTAAAGACA 899
Qy 1114 AAGACTTTAAGGAACAGCTTGGCGCTCAACAGAACCCAGTGAAGAAATCCATTCCAGGAATC 1173
Db 900 AAGACTTTAAGGAACAGCTTGGCGCTCAACAGAACCCAGTGAAGAAATCCATTCCAGGAATC 959
Qy 1174 AAGACTTTTGGCTCAGAGCATACCTGAAGAGAGATACAAAGATGAAGAGCAAGCCCT 1233
Db 960 AAGACTTTTGGCTCAGAGCATACCTGAAGAGAGATACAAAGATGAAGAGCAAGCCCT 1019
Qy 1234 AGGAATCTGCTGATAATCCATTGCAATGGCAATGAGACAGAGCTTCTCGACAGACCTT 1293
Db 1020 AGGAATCTGCTGATAATCCATTGCAATGGCAATGAGACAGAGCTTCTCGACAGACCTT 1079
Qy 1294 CACTTCCTCGGCTATGAAGTCCAGAAATTTCTGCATCTCAGTATGATGATATATCCCA 1353
Db 1080 CACTTCCTCGGCTATGAAGTCCAGAAATTTCTGCATCTCAGTATGATGATATATCCCA 1139
Qy 1354 GATTCTTGGCCAAATTTGCTGTATGCGCAGCACCAGACATACGACAGCTTTGTGTGT 1413
Db 1140 GATTCTTGGCCAAATTTGCTGTATGCGCAGCACCAGACATACGACAGCTTTGTGTGT 1199
Qy 1414 CTTGGTGGCCGAGGAGCTCCAGAGCTGTATGTTGGATCAGACTCACTCAGGCT 1473
Db 1200 CTTGGTGGCCGAGGAGCTCCAGAGCTGTATGTTGGATCAGACTCACTCAGGCT 1259
Qy 1474 CCCCCTGCATCAGAGGAGTGTTCATGGGAGATTTCATGCCCTTATCTAGCAGGAA 1533
Db 1260 CCCCCTGCATCAGAGGAGTGTTCATGGGAGATTTCATGCCCTTATCTAGCAGGAA 1319
Qy 1534 GCCAAAGATGTTTTTATTCAGAACTATGTGGTGTACAGGGCCAGCTGGAGAACAGAG 1593
Db 1320 GCCAAAGATGTTTTTATTCAGAACTATGTGGTGTACAGGGCCAGCTGGAGAACAGAG 1379
Qy 1594 CTTCTGGAGTGTGATGGCCAGGATGAAGAAATGTAAGTTCAAGGCTCAGAACGAGG 1653
Db 1380 CTTCTGGAGTGTGATGGCCAGGATGAAGAAATGTAAGTTCAAGGCTCAGAACGAGG 1439
Qy 1654 GCTGTGCACAGTTTCCAGCAGAGCTGACTTCTTCTGGAGCTGTGTACTGCGGACATGTC 1713
Db 1440 GCTGTGCACAGTTTCCAGCAGAGCTGACTTCTTCTGGAGCTGTGTACTGCGGACATGTC 1499
Qy 1714 CTTCTGGAGAGTCTCAGAGCTCAGCTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1773
Db 1500 CTTCTGGAGAGTCTCAGAGCTCAGCTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1559
Qy 1774 GAGACAAAGAAAGCCCACTTCTGGATCTTCACTTCACTCAATGGCTACATGTA 1833

Db 1560 GAGACAAGAAGAAACGCCCACTCTCTGGATCTTTCACATTTGAACATGAATGGCTACATGTA 1619
Qy 1834 TGATTGGAACAGCAGAGATTTCTGCAAGAGGAGAAATATTATGCTGGCTGCAGACACTCT 1893
Db 1620 TGATTGGAACAGCAGAGATTTCTGCAAGAGGAGAAATATTATGCTGGCTGCAGACACTCT 1679
Qy 1994 GAGAAAGAACTTATCTCTCTCTACATACATAGAAACCAAAAGGCTGGCGTGTGGCTCA 1953
Db 1680 GAGAAAGAACTTATCTCTCTCTACATACATAGAAACCAAAAGGCTGGCGTGTGGCTCG 1739
Qy 1954 CACCTGTAAATCCAGCAGCTTTGGGAGGCCAAGGAGGCGAGATCACTTCAAGTCAAGGATTT 2013
Db 1740 CACCTGTAAATCCAGCAGCTTTGGGAGGCCAAGGAGGCGAGATCACTTCAAGTCAAGGATTT 1799
Qy 2014 CGACACAGCCTGGCCCAACATGTTAAACGCTGCTCCCTAGTAAATAATGCAAAAAATAGCTG 2073
Db 1800 CGACACAGCCTGGCCCAACATGTTAAACGCTGCTCCCTAGTAAAGAGTGCNAANAATAGCTG 1859
Qy 2074 GGTGTGGTGTGGTACTGTTTCCAGCTTACTTGGGAGGCTGAGGTGGGAGGATCTTT 2133
Db 1860 GGTGTGGTGTGGTACTGTTTCCAGCTTACTTGGGAGGCTGAGGTGGGAGGATCTTT 1919
Qy 2134 TGAACCCAGAGTTTCAGGTCATAGCATGCTGATTTGCTGCTACGAATAGCCACTGCAT 2193
Db 1920 TGAACCCAGAGTTTCAGGTCATAGCATGCTGATTTGCTGCTACGAATAGCCACTGCAT 1979
Qy 2194 ACCAACCTGGCAATATAGCAAGATCCCATCTCTTTAAAAAATAAAAAA 2243
Db 1980 ACCAACCTGGCAATATAGCAAGATCCCATCTCTTTAAAAAATAAAAAA 2029

RESULT 4

US-09-861-270-1
; Sequence 1, Application US/09861270
; Patent No. US20020052474A1
; GENERAL INFORMATION:
; APPLICANT: Sui, Hong-Bing
; Goedel, David V.
; TITLE OF INVENTION: Regulators of Apoptosis
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Science & Technology Law Group
; STREET: 75 Denise Drive
; CITY: Hillsborough
; STATE: California
; COUNTRY: USA
; ZIP: 94010
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/861,270
; FILING DATE: 18-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/795,088
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 343-4341
; TELEFAX: (650) 343-4342
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2045 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 1:									
US-09-861-270-1									
Query Match 87.0%; Score 1952.2; DB 9; Length 2045;									
Best Local Similarity 99.8%; Pred. No. 0;									
Matches 1965; Conservative 0; Mismatches 3; Indels 1; Gaps 1;									
QY	48	GGAGCTTCACGCTCAGCGAGCTCACTAAAGAGGACTCCCGGAGCTTAGGGTGG	107						
DB	78	GAGAGCTTCAGCTCAGCGAGCTCACTAAAGAGGACTCCCGGAGCTTAGGGTGG	137						
QY	108	GGACTCGGCTCACACAGTGAAGTGGCGCTATTGGACTTTTTCAGTGCACAGCTGAGAC	167						
DB	138	GGACTCGGCTCACACAGTGAAGTGGCGCTATTGGACTTTTTCAGTGCACAGCTGAGAC	197						
QY	168	ACAAGGACACGGAGGAGTGTAGGAGAGAGCGCGCAACAGCGATCGCCACGAC	227						
DB	198	ACAAGGACACGGAGGAGTGTAGGAGAGAGCGCGCAACAGCGATCGCCACGAC	257						
QY	228	CAAGTCCGCTTCAGGCTTTCGGTTTCTTTGGCTCCATCTTGGTGGCGCTTCCGGGGT	287						
DB	258	CAAGTCCGCTTCAGGCTTTCGGTTTCTTTGGCTCCATCTTGGTGGCGCTTCCGGGGT	317						
QY	288	CTAGGGAGCGAAGGTGAGTGGCGAGCGGAGAGTCCGGCGCGACAGAGCACT	347						
DB	318	CTAGGGAGCGAAGGTGAGTGGCGAGCGGAGAGTCCGGCGCGACAGAGCACT	377						
QY	348	CCCCCACTGGAAGGATCTGAAAGAAATGAAGTCAGCCCTCAGAAATGAAGTTGACTGC	407						
DB	378	CCCCCACTGGAAGGATCTGAAAGAAATGAAGTCAGCCCTCAGAAATGAAGTTGACTGC	437						
QY	408	CTCCTGGCTTCTGTTGACTGGCCGGAGCTGTACTGCAAGACCCCTGTGAGCTTCCCT	467						
DB	438	CTCCTGGCTTCTGTTGACTGGCCGGAGCTGTACTGCAAGACCCCTGTGAGCTTCCCT	496						
QY	468	AGTCTAAGAGTACGATGTCTGCTGAAGTATCATCATCAGTGTGAAGAGCACCTGTATACAG	527						
DB	497	AGTCTAAGAGTACGATGTCTGCTGAAGTATCATCATCAGTGTGAAGAGCACCTGTATACAG	556						
QY	528	ATGAGAAGGAGTGTCTTTTGTGCGGGATGTGCTATAGATGTGGTTTCCACCTA	587						
DB	557	ATGAGAAGGAGTGTCTTTTGTGCGGGATGTGCTATAGATGTGGTTTCCACCTA	616						
QY	588	ATGTCAGGACCTTCGGATATTTTACGGGAAGAGGTGAAGCTGTCTGCGGGACTTGG	647						
DB	617	ATGTCAGGACCTTCGGATATTTTACGGGAAGAGGTGAAGCTGTCTGCGGGACTTGG	676						
QY	648	CTGAACCTGCTACAGAGTACGGGATTTGACCTGCTCAACCGTATCTTGAAGATGGACA	707						
DB	677	CTGAACCTGCTACAGAGTACGGGATTTGACCTGCTCAACCGTATCTTGAAGATGGACA	736						
QY	708	GAAAGCTGTGGAGACCCCTGCTCAGGAACCCCTCACCTTGTTCGGACTATAGAGTGC	767						
DB	737	GAAAGCTGTGGAGACCCCTGCTCAGGAACCCCTCACCTTGTTCGGACTATAGAGTGC	796						
QY	768	TGATGGCAGAGATTGGTACAGATTGGATAAATCTGATGTCTCTCAATTAATTTCTCTCA	827						
DB	797	TGATGGCAGAGATTGGTACAGATTGGATAAATCTGATGTCTCTCAATTAATTTCTCTCA	856						
QY	828	TGAAGGATTACATGGCGGAGGCAAGATAAGCAAGAGAGAGTTTCTTGGACCTTGTGG	887						
DB	857	TGAAGGATTACATGGCGGAGGCAAGATAAGCAAGAGAGAGTTTCTTGGACCTTGTGG	916						
QY	888	TTGAGTTGGAGAACTAAATTTGGTTGCCCGAGATCAACTGGATTATTAAGAAAATGCC	947						
DB	917	TTGAGTTGGAGAACTAAATTTGGTTGCCCGAGATCAACTGGATTATTAAGAAAATGCC	976						
QY	948	TAAAGACATCCACAGATAGACCTGAGACAAATCCAGAACTCAACAGCTCTCTTC	1007						
DB	977	TAAAGACATCCACAGATAGACCTGAGACAAATCCAGAACTCAACAGCTCTCTTC	1036						
QY	1008	AAGGAGGAGGACAAAGTTACAGGAATGTCTTCCAGCAGCAATCCAAAAGAGTCTCAAGG	1067						

RESULT 5
US-10-103-313-34
; Sequence 34, Application US/10103313
; Publication No. US20030082758A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.

134 CTGGACCTGTTGGTGGAGGAACTAATCTGGTGGCCGACGATCACTGGATT 193
 934 ATTAGAAAATGCTTAAGAACATCCACAGATAGACCTGAAGCAAAATCCAGAGTA 993
 194 ATTAGAAAATGCTTAAGAACATCCACAGATAGACCTGAAGCAAAATCCAGAGTA 253
 994 CAAGAGCTGTTCAAGGAGGAGGACAGTACAGGATGTTCCAGAGCAGCAATCA 1053
 254 CAAGAGCTGTTCAAGGAGGAGGACAGTACAGGATGTTCCAGAGCAGCAATCA 313
 1054 AAAGAGCTCTCAAGATCTTCAAAATCACTGAGGCTCCATAATGGAGAGTAAGAA 1113
 314 AAAGAGCTCTCAAGATCTTCAAAATCACTGAGGCTCCATAATGGAGAGTAAGAA 373
 1114 AAAGAGCTCTCAAGATCTTCAAAATCACTGAGGCTCCATAATGGAGAGTAAGAA 1173
 374 AAAGAGCTCTCAAGATCTTCAAAATCACTGAGGCTCCATAATGGAGAGTAAGAA 433
 1174 AAAGAGCTCTCAAGATCTTCAAAATCACTGAGGCTCCATAATGGAGAGTAAGAA 1233
 434 AAAGAGCTCTCAAGATCTTCAAAATCACTGAGGCTCCATAATGGAGAGTAAGAA 493
 1234 AAAGAGCTCTCAAGATCTTCAAAATCACTGAGGCTCCATAATGGAGAGTAAGAA 1293
 494 AAAGAGCTCTCAAGATCTTCAAAATCACTGAGGCTCCATAATGGAGAGTAAGAA 553
 1294 AAAGAGCTCTCAAGATCTTCAAAATCACTGAGGCTCCATAATGGAGAGTAAGAA 1353
 554 AAAGAGCTCTCAAGATCTTCAAAATCACTGAGGCTCCATAATGGAGAGTAAGAA 613
 1354 AAAGAGCTCTCAAGATCTTCAAAATCACTGAGGCTCCATAATGGAGAGTAAGAA 1413
 614 AAAGAGCTCTCAAGATCTTCAAAATCACTGAGGCTCCATAATGGAGAGTAAGAA 673
 1414 AAAGAGCTCTCAAGATCTTCAAAATCACTGAGGCTCCATAATGGAGAGTAAGAA 1473
 674 AAAGAGCTCTCAAGATCTTCAAAATCACTGAGGCTCCATAATGGAGAGTAAGAA 733
 1474 AAAGAGCTCTCAAGATCTTCAAAATCACTGAGGCTCCATAATGGAGAGTAAGAA 1533
 734 AAAGAGCTCTCAAGATCTTCAAAATCACTGAGGCTCCATAATGGAGAGTAAGAA 793
 1534 AAAGAGCTCTCAAGATCTTCAAAATCACTGAGGCTCCATAATGGAGAGTAAGAA 1593
 794 AAAGAGCTCTCAAGATCTTCAAAATCACTGAGGCTCCATAATGGAGAGTAAGAA 853
 1594 AAAGAGCTCTCAAGATCTTCAAAATCACTGAGGCTCCATAATGGAGAGTAAGAA 1653
 854 AAAGAGCTCTCAAGATCTTCAAAATCACTGAGGCTCCATAATGGAGAGTAAGAA 913
 1654 AAAGAGCTCTCAAGATCTTCAAAATCACTGAGGCTCCATAATGGAGAGTAAGAA 1713
 914 AAAGAGCTCTCAAGATCTTCAAAATCACTGAGGCTCCATAATGGAGAGTAAGAA 973
 1714 AAAGAGCTCTCAAGATCTTCAAAATCACTGAGGCTCCATAATGGAGAGTAAGAA 1773
 974 AAAGAGCTCTCAAGATCTTCAAAATCACTGAGGCTCCATAATGGAGAGTAAGAA 1033
 1774 AAAGAGCTCTCAAGATCTTCAAAATCACTGAGGCTCCATAATGGAGAGTAAGAA 1833
 1034 AAAGAGCTCTCAAGATCTTCAAAATCACTGAGGCTCCATAATGGAGAGTAAGAA 1093
 1834 AAAGAGCTCTCAAGATCTTCAAAATCACTGAGGCTCCATAATGGAGAGTAAGAA 1893
 1094 AAAGAGCTCTCAAGATCTTCAAAATCACTGAGGCTCCATAATGGAGAGTAAGAA 1153
 1894 AAAGAGCTCTCAAGATCTTCAAAATCACTGAGGCTCCATAATGGAGAGTAAGAA 1952
 1154 AAAGAGCTCTCAAGATCTTCAAAATCACTGAGGCTCCATAATGGAGAGTAAGAA 1213
 1953 AAAGAGCTCTCAAGATCTTCAAAATCACTGAGGCTCCATAATGGAGAGTAAGAA 2008

1214 ACACCTGTTGTTACCCAGCACCTTTGGGAGGACCAAGGAGGAGATACACTTACAGGTGAG 1273
 2009 GAGTTCGAGACAG--CCTGGCCACACATGTTAAAGCTGTGCC 2049
 1274 GAGTTCGAGACAGACCTGGGACCAACATGTTAAAGCTGTGACC 1316

RESULT 7
 US-09-009-893-5
 ; Sequence 5, Application US/09009893
 ; Publication NO. US20030087339A1
 ; GENERAL INFORMATION:
 ; APPLICANT: NI, JIAN
 ; APPLICANT: ROSEN, CRAIG A.
 ; APPLICANT: DIXIT, VISHVA M.
 ; APPLICANT: GENTZ, REINER L.
 ; APPLICANT: KENNETH, JOSEPH J.
 ; TITLE OF INVENTION: 1-FLICE, A NOVEL INHIBITOR OF TUMOR
 ; NUMBER OF SEQUENCES: 32
 ; TITLE OF INVENTION: NECROSIS FACTOR RECEPTOR-1 AND CD-95 INDUCED APOPTOSIS
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
 ; STREET: 1100 NEW YORK AVENUE, SUITE 600
 ; CITY: WASHINGTON
 ; STATE: DC
 ; COUNTRY: US
 ; ZIP: 20005
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/009,893
 ; FILING DATE: HEREWITH
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/034,205
 ; FILING DATE: 21-JAN-1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/054,800
 ; FILING DATE: 05-AUG-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: STEFFE, ERIC K.
 ; REGISTRATION NUMBER: 36,688
 ; REFERENCE/DOCKET NUMBER: 1488.0970002
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 371-2600
 ; TELEFAX: (202) 371-2540
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2597 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 304..1347
 ; US-09-009-893-5

Query Match 40.1%; Score 899.6; DB 11; Length 2597;
 Best Local Similarity 94.3%; Pred. No. 6.3e-275;
 Matches 966; Conservative 0; Mismatches 4; Indels 54; Gaps 1;
 762 GAGTCTGATGGCAGAGATTGGTGGAGATTGGTAAATCTGATGTCTCTCAATTT 821
 296 GAGTCTGATGGCAGAGATTGGTGGAGATTGGTAAATCTGATGTCTCTCAATTT 355
 822 TCCTCATGAGGATTACATGGGCGGAGGAGATAGCAGAGAGAGTTCTTGACC 881
 356 TCCTCATGAGGATTACATGGGCGGAGGAGATAGCAGAGAGAGTTCTTGACC 415

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QY 882 TTGTGGTTGAGTTGGAGAACTAAATTTGGTTGCCCCAGATCAACTGGATTATTAGAAA 941
Db 416 TTGTGGTTGAGTTGGAGAACTAAATTTGGTTGCCCCAGATCAACTGGATTATTAGAAA 475
QY 942 AATGCCTAAAGAAATCACAAGATAGACCTTGAAGACAAAATCCAGAAGTACAGCAGT 1001
Db 476 AATGCCTAAAGAAATCACAAGATAGACCTTGAAGACAAAATCCAGAAGTACAGCAGT 535
QY 1002 CTGTTCAAGGAGCGGACAAAGTTACAGGAATGTCTCCAAGCAGCAATCCAAAAGATC 1061
Db 536 CTGTTCAAGGAGCGGACAAAGTTACAGGAATGTCTCCAAGCAGCAATCCAAAAGATC 595
QY 1062 TCAAGGATCCCTCAAAATCACTTCAAGGCTCCATATAGGAGAGTAAAGAACAGACTTA 1121
Db 596 TCAAGGATCCCTCAAAATCACTTCAAGGCTCCATATAGGAGAGTAAAGAACAGACTTA 622
QY 1122 AGGAACAGCTTTGGGCTCAACAAGAACCAAGTGAAGAAATCCATTCAGGAATCAGAAGCTT 1181
Db 623 -----AGNAACCAAGTGAAGAAATCCATTCAGGAATCAGAAGCTT 661
QY 1182 TTTTGGCTCAGAGCATACCTGAAGAGAGATACAAGATGAAGCAAGCCCTAGGAATCT 1241
Db 662 TTTTGGCTCAGAGCATACCTGAAGAGAGATACAAGATGAAGCAAGCCCTAGGAATCT 721
QY 1242 GCCTGATTAATCGATTGGCAATGAGACAGAGCTTCTCGAGACACCTTCACCTCCC 1301
Db 722 GCCTGATTAATCGATTGGCAATGAGACAGAGCTTCTCGAGACACCTTCACCTCCC 781
QY 1302 TGGGCTATGAAGTCCAGAAATCTTGCATCTCAGTATGCATGGTATATCCAGAGTCTTG 1361
Db 782 TGGGCTATGAAGTCCAGAAATCTTGCATCTCAGTATGCATGGTATATCCAGAGTCTTG 841
QY 1362 GCCAATTTGCTGTATGCCGAGCACCGAGACTACGACAGCTTTGTGTCTCTGGTGA 1421
Db 842 GCCAATTTGCTGTATGCCGAGCACCGAGACTACGACAGCTTTGTGTCTCTGGTGA 901
QY 1422 GCCGAGGAGCTCCAGAGTCTGTATGGTGTGGATCAGACTCAGTCCAGGGCTCCCGCTGC 1481
Db 902 GCCGAGGAGCTCCAGAGTCTGTATGGTGTGGATCAGACTCAGTCCAGGGCTCCCGCTGC 961
QY 1482 ATCATATCAGGAGGATGTTATGGGAGATTCATGCCCTTATCTAGCAGGGAAGCCAAAGA 1541
Db 962 ATCATATCAGGAGGATGTTATGGGAGATTCATGCCCTTATCTAGCAGGGAAGCCAAAGA 1021
QY 1542 TGTATTTTATTCAGAACTATGTGTGTCTAGAGGCCAGCTGGAGAACAGCAGCTCTTTGG 1601
Db 1022 TGTATTTTATTCAGAACTATGTGTGTCTAGAGGCCAGCTGGAGAACAGCAGCTCTTTGG 1081
QY 1602 AGGTGGATGGCCAGCGATGAAGATGTGGAATTCAGGGCTCAGNAGCGAGGGCTGTGCA 1661
Db 1082 AGGTGGATGGCCAGCGATGAAGATGTGGAATTCAGGGCTCAGNAGCGAGGGCTGTGCA 1141
QY 1662 CAGTTACCGGAGAGCTGACTTCTTCTGGAGCCTGTGTACTGCGGACATGTCCCTGCTGG 1721
Db 1142 CAGTTACCGGAGAGCTGACTTCTTCTGGAGCCTGTGTACTGCGGACATGTCCCTGCTGG 1201
QY 1722 AGCAGTCTCAGAGCTCAGCGTCCCTGTACCTGTGAGTGCCTCTCCAGAAATCGAGACAAG 1781
Db 1202 AGCAGTCTCAGAGCTCAGCGTCCCTGTACCTGTGAGTGCCTCTCCAGAAATCGAGACAAG 1261
QY 1782 AAAG 1785
Db 1262 AAAG 1265
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RESULT 8
US-09-410-194-18
; Sequence 18, Application US/09410194
; Patent No. US20020095030A1
; GENERAL INFORMATION:
; APPLICANT: Tschopp, Jurg
; APPLICANT: Thome, Margot
; APPLICANT: Burns, Kimberly

```
; APPLICANT: Irmeler, Marten
; APPLICANT: Hahne, Michael
; APPLICANT: Schroter, Michael
; APPLICANT: Schneider, Pascal
; APPLICANT: Bodmer, Jean-Luc
; APPLICANT: Steiner, Veronique
; APPLICANT: Rimoldi, Donata
; APPLICANT: Hofmann, Kay
; APPLICANT: French, E. Lars
; TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
; FILE REFERENCE: 11141-002001
; CURRENT APPLICATION NUMBER: US/09/410,194
; CURRENT FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: PCT/EP98/01857
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 2452
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (172)...(1614)
; US-09-410-194-18

Query Match 37.9%; Score 849.6; DB 9; Length 2452;
Best Local Similarity 71.2%; Pred. No. 5e-259;
Matches 1173; Conservative 0; Mismatches 454; Indels 21; Gaps 3;

QY 313 AGCGCAGCAGAGTCCGGCCGACAGGACGCAACTCCCCACTGGAAGAGGATTCGAAAG 372
Db 9 AGCCTCTCAAGCGGCCACTTAGGGCCGACAGAGTCTCTATTTCGAAGAATCTCGAGAG 68
QY 373 AAATGAAGTCAGCCCTCAGAAATGAAGTTGACTGCCTGCTGG-----CTTTCCCTGT 423
Db 69 AAATGAAGAGAGTCTCAGCAATGATGTGGCTTCTCGTTCGCTCCAGAGCCCTGCTTAA 128
QY 424 TGACTTGGCCCGAGCTGACTGCAAGACCCCTGTGTCAGCTTCCCTAGTCTAAGAGTAGGAT 483
Db 129 TGGATGGAGACTGGACGAGAACCTGGCTGCTGTGTTCTTGAACATATGGCCAGGCCCTGT 188
QY 484 GTCTGCTCAAGTTCATCCACTCAGAGTGAAGAGCACTTGTATACAGATGAGAGAGATGCT 543
Db 189 GTCTCCCGAGGTCATTCACCAGGTGGAAGAGTGTCTTGTATGAAGACGAGAGAGATGAT 248
QY 544 GCTCTTTTGTGCCGGGATGTGCTATAGATGTGTTCCACCCTAATGTGTCAGGAGCCTTCT 603
Db 249 GCTCTTCTGTGTAGAGATGTGACTGAGAACCTGGCTGCACCTAACCTACGTCAGGAGCCTCT 308
QY 604 GGATATTTTACGGGAAAGAGGTGAAGCTGTCTGTCGGGACCTTGGCTGAACCTCTCTACAG 663
Db 309 GGATAGCTTATGTAGAGAGGCCAGCTCTCTTTTCTACCTTGGCTGAATTTCTCTACAG 368
QY 664 AGTGAGCGATTTGACCTGCTCAACAGTATCTTGAAGATGGACAGAAAAGCTGTGGAGAC 723
Db 369 AGTGAGCGGTTTGACCTTCTCAAGAGGATCTTGAAGACAGACAAAGAACCGTGGAGGA 428
QY 724 CCACCTGCTCAGGAAACCTCACCCTGTGTTCCGAGCTATAGAGTGTGCTGATGGCAGAGATGG 783
Db 429 CCACCTGCGCAGAAAACCTCACCCTGTGTTCTGATTTATAGGGTCTGCTGATGGAGATGG 488
QY 784 TGAGGATTTGGATAAATCTGATGTCTCATTAATTTTCCATGAAGAGATTACATGGG 843
Db 489 TGAGAGCTTATATCAGACGATGATATCTCTCTAGTTTCTTACAGGGATTACACAGG 548
QY 844 CCGAGGCAAGATAAGCAAGAGAGAGTTCCTTTGGACCTTCTTGGTGTAGTTGTTGGAAACT 903
Db 549 CAGAGGCAAGATAGCAAGACAGAGTTCCTTGATCTGCTGATTTGAATTTGGAGAACT 608
QY 904 AAATTTGGTTGCCCGCAGATCAACTGGATTATTATAGAAAAATGCCTTAAAGAACATCCACAG 963
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	609	DB	GAATCTAATTGCTTCAGACCAATTAATTTGGTAGAAAAATGCCTGAAGAACAATCCACAG	668
	964	QY	AATAGACCTTGAGACAAAATAATCCAGAACTFACAAGCAGTCTGTCCAAGGACGAGGACAAG	1023
	669	DB	AATAGACTTTGAACACAAAGATCCAGAACTFACACCAGTCCAGGCCAAGAGGACGAATCAA	728
	1024	QY	TTACAGGAATGTTCTCCAACAGCAGCAATCCAAAAGAGTCTCAAGGATCTTTCAAAATAACTT	1083
	729	DB	TATGAATACTCTCCAGGCTTCGCTCCCAAAATTGAGTATCAAG-----TATAACTC	779
	1084	QY	CAGGCTCCATATATGGGAGAAGTAAAGACAAGAAGCTTAAGNACAGCTTGGCGCTCAACA	1143
	780	DB	AAGGCTCCAGAAATGGCGGAAGTAAAGAGCCCAAGATTTGTGGAATACCGGTGACAGTCAAAG	839
	1144	QY	AGAACAGTGAAGAAATCCATTACAGGAATCAGAAGCTTTTTTGCCTCAGAGCATCACTGA	1203
	840	DB	AACACTGGTGAAGACATCCATCCAGGAATCAGGAGCTTTTAACTCCGCACATCCGTGA	899
	1204	QY	AGAGATACAAGATGAAGAGCAAGCCCCTAGGAATCTGCCCTGATTAATCGATTGCAATGG	1263
	900	DB	AGAGACTTACAGATGCAGAGCAAGCCCCCTAGGAATCTGCTTGATTCATTAATGTTATGG	959
	1264	QY	CAATGACAGAGCTTCTTCGAGACACCTTCACTTCCCTGGGCTATGAAGTCCAGAAAT	1323
	960	DB	CAAGCACAAAATATCTTCAAGAGAGCTTCACTTCCCTGGGCTATCATATCCAGCTTT	1019
	1324	QY	CTTGCACTCAGTATGATGGGTATATCCAGATTTCTTGGCCAAATTTGCTGTATGCCGA	1383
	1020	DB	CTTGTTTTCCCAAGTACATGACATAACCCAGATGTTTCGCCGATATGCAAGTATGCCCA	1079
	1384	QY	GCACCGAGACTAGCAACAGCTTTGTGTGTCTCTGTGTGAGCCGAGGAGGCTCCACAGTGT	1443
	1080	DB	ACATCAAGACTATGACAGCTTTTCATGTGTGTGTGTGAGCCTAGGAGGCTCCCAAAGCAT	1139
	1444	QY	GTAFTGTGTGATCAGACTCACTCAGGGCTCCGCCCTGCATCAGATCAGAGGATGTTTCAT	1503
	1140	DB	GATGGCAGAGATCAAGTCTCACTCAGGGTTCCTTTGGATCATGTCAAGAAGATGTTTCA	1199
	1504	QY	GGGAGATTATGCCCTTATCTAGCAGGGAAGCCAAAGATGTTTTTTATTCAAGAACTATGT	1563
	1200	DB	GGGGACACGTGCCCTTCTCTCAGAGGGAAGCCAAAGCTCTTTTATTTCAGAACTATGA	1259
	1564	QY	GGTCTCAGAGGGCCAGCTGGAGAACAGCACCTCTTTGGAGGTGGATGGGCCAGCGATGA	1623
	1260	DB	GTCGTTAGTAGCCAGTTGGAAGATAGCAGCC---TGGAGGTAGATGGGCCATCAATAAA	1316
	1624	QY	GAATCTGGAATTCAGGCTCAGAGCGAGGGCTGTGCACAGTTTCACCGAAGCTGACATT	1683
	1317	DB	AAATGTGGACHTTANGCCCTGCAACCCACACTGCACAACCTCACCCAGAACTGATAT	1376
	1684	QY	CTTCTGGAGCCTGTGTACTGGGACATGTCCCTGCTGGAGAGTCTCACAGTCAACGCTC	1743
	1377	DB	CTTTTGGAGCCTGTGCACAGCAGACGTATCTCACTTGGGAAGCCCTCCAGCTCATCCTC	1436
	1744	QY	CCTGTACTGTCAGTGCCTCTCCCAAGAACTGAGACAAGAAGAAAGCCCACTCCGTGA	1803
	1437	DB	TGTGTATCTGCAGAAAGCTCTCCAGCAGCTGAAGCAAGCGAGNGAGCCCACTCGTGA	1496
	1804	QY	TCCTTCAATTTGAATTCATGCTCATATGATTTGGAACAGCAGAGATTTCTGCCAAGGA	1863
	1497	DB	CCTCCACGTTGAATCATGTGACAAAGTGTATGCGTGGAAACAGTGGTGTTCGCTCAAGGA	1556
	1864	QY	GAATATTTATGCTGGCTGCAGCACACTCTGAGAAGAAATTTATCTCTCTCCATACATA	1923
	1557	DB	GAATATACAGCCTTCAGCCTTGCAGCACACTCTCAGGAAGAAACTCATCTTGGTCTACGTG	1616
	1924	QY	AGAAACCAAAAGGCTGGCGCTAGTGGCT	1951
	1617	DB	AGAACCCAGACCGTTGGTGTCTTGGT	1644

US-10-005-921-1
; Sequence 1, Application US/10005921
; Publication No. US20020174450A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Keith D.
; APPLICANT: Leviten, Michael W.
; TITLE OF INVENTION: TRANSGENIC MICE CONTAINING CASH GENE
; TITLE OF INVENTION: DISRUPTIONS
; FILE REFERENCE: R-714
; CURRENT APPLICATION NUMBER: US/10/005,921
; CURRENT FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: US 60/254,902
; PRIOR FILING DATE: 2000-12-11
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1:
; LENGTH: 2770
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-005-921-1

Query Match 36.3%; Score 813.6; DB 13; Length 2770;
Best Local Similarity 73.2%; Pred. No. 1.6e+247;
Matches 1092; Conservative 0; Mismatches 379; Indels 21; Gaps 3;

QY 469 GTCTAAAGATGAGTGGTCCTCCTGAAGTCATCCATCAGGTGTAAGAAGCACTTGTAACACA 528
Db | |||||
QY 77 GGCCACAGAGCCCTGTGTCTCGGAGGTCAATTACCAGGTGGAGAGTGTCTTTGATGAAGA 136
Db | |||||
QY 529 TGCAAGAGAGATGCTGCTCTTTTTGTGCCGGGATGTTCCTATAGATGTGGTTCCACCTAA 588
Db | |||||
QY 137 CGAAGAGAGATGATGCTCTCTCTGTACAGATGTACTGAGAACCCTGGCTGCACCTAA 196
Db | |||||
QY 589 TGTCAAGGACCTTCTGGATATTTTACGGGAAAAGGTGAAGTCTCTGTGCGGAGCTTTGGC 648
Db | |||||
QY 197 CGTCAGGACCTCTCTGGATAGCTTAAGTGAGAGAGCGCACCTCTCTTTGCTACCTTGGC 256
Db | |||||
QY 649 TGAACCTCTACAGATGAGGCGATTTGACCTTGCTCAAACGATCTCTTGAAGATGGACAG 708
Db | |||||
QY 257 TGAATGTCTACAGATGAGGCGGTTTGACCTTCTCAGAGGATCTTGNAGACACAGAA 316
Db | |||||
QY 709 AAAAGCTGTGAGACCCACCTGTCTCAGGAACCCCTCACCTTTGTTCCGAGCTATAGATGTCT 768
Db | |||||
QY 317 AGCAACCGTGCAGGACCACTCTGCAGAAACCCCTCACCTGTTTCTGATATATAGGTCCT 376
QY 769 GATGCCAGAGATTGGTGAGGATTTGGATAAATCTGATGTCTCTCATTAATTTTCC---- 824
Db | |||||
QY 377 GGTGATGAGATGGTGAGAGCTTAGATCAGAAGATGATPCTCTTAGTTTCTCTTAC 436
Db | |||||
QY 825 -----TCATGAGGATTCATATGGGCCGAGCAAGATAAGCAAGAGAGAGTTCCTTTGGA 879
Db | |||||
QY 437 AAGGATTACAAGGATTACACAGCAGAGGCAAGATAGCCAAGACAGAGTTCCTTTGGA 496
Db | |||||
QY 880 CCTTGTTGGTTGAGTGGAGAACCTAAATTTGGTTGGCCCCAGATCAACTGGATTTATAGA 939
Db | |||||
QY 497 TCTGTTGATGAATTTGGAGAACTGAATCTAATTTGCTTCAGACCAATTTGAATTTGTTAGA 556
Db | |||||
QY 940 AAATGCTCTAAAGACATCCACAGATAGACCTGAAGACAAAAATCCAGAGTACAGCA 999
Db | |||||
QY 557 AAATGCTTGAAGACATCCACAGATAGACTTGAACACAAAGATCCAGAAGTACACCCA 616
Db | |||||
QY 1000 GTCTGTTCAAGGAGGAGCAAGTTACAGGAATTTCTTCCACAGCAATCCAAAAGAG 1059
Db | |||||
QY 617 GTCCAGCCAAAGGAGCAAGATCAATATGAAATACTCTCCAGGCTTCGCTCCCAAAATTTGAG 676
Db | |||||
QY 1060 TCTCAGGATCTCTCAAAATAACTTCCAGGCTCCAAATGCGGAGAAAGTAAAGAACAACT 1119
Db | |||||-----TATACTCAAGCTCCAGATGGCGAAGTAAAGACCAAGATT 727
QY 1120 TAAGGAACAGCTTGGCGCTCAACAAGAACAGCTGAAGAAATCCATTCAGGAATCAGAGC 1179
Db | |||||
QY 728 TGTGGAAATACCGTGACGTCAAGAACACACTGGTGAAGACATCCATCCAGGAATCAGGAGC 787
Db | |||||

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QY 1180 TTTTGGCTCAGACATACCTGAAGAGAGATACAAAGATGAAGAGCAAGCCCTAGGAAT 1239
Db 788 TTTTACCTCGGCACATCCGTGAAGAGACTTACAGGATGAGAGCAAGCCCTAGGAAT 847
QY 1240 CTGCTGTATATGATTCGATTCGCAATGAGAGAGCTTCTTCGAGACACCTTCACATTC 1299
Db 848 CTGCTGTATATGATTCGCAATGAGAGAGCTTCTTCGAGACACCTTCACATTC 907
QY 1300 CTGCTGTATATGATTCGCAATGAGAGAGCTTCTTCGAGACACCTTCACATTC 1359
Db 908 CTGCTGTATATGATTCGCAATGAGAGAGCTTCTTCGAGACACCTTCACATTC 967
QY 1360 TGGCCAAATTTGCTGTATGCGGACACCGAGACTACACAGCTTTGTGTGCTCTGCT 1419
Db 968 TGGCCAAATTTGCTGTATGCGGACACCGAGACTACACAGCTTTGTGTGCTCTGCT 1027
QY 1420 GAGCCGAGAGGCTCCAGAGATGTATGATGATGATGATGATGATGATGATGATGAT 1479
Db 1028 GAGCCGAGAGGCTCCAGAGATGTATGATGATGATGATGATGATGATGATGATGAT 1087
QY 1480 GCATCAGATCAGAGAGATGTTTATGAGGAGATTCATGCTTATGAGGAGGAGGAGG 1539
Db 1088 GCATCAGATCAGAGAGATGTTTATGAGGAGATTCATGCTTATGAGGAGGAGGAGG 1147
QY 1540 GATGTTTTTATCAGAACTATGTTGTCAGAGGCGGAGCTGAGAGACAGAGCTTCT 1599
Db 1148 GATGTTTTTATCAGAACTATGTTGTCAGAGGCGGAGCTGAGAGAGATGAGAGCT 1204
QY 1600 GGAGTGGATGGGCGGAGGATGAGAAATGAGAAATGAGAAATGAGAAATGAGAAAT 1659
Db 1205 GGAGTGGATGGGCGGAGGATGAGAAATGAGAAATGAGAAATGAGAAATGAGAAAT 1264
QY 1660 CACATTTACAGAGAGAGTGTATCTTGTGAGGCTGTGTATGAGGAGGAGGAGG 1719
Db 1265 CACATTTACAGAGAGAGTGTATCTTGTGAGGCTGTGTATGAGGAGGAGGAGG 1324
QY 1720 GGAGAGGCTCACAGCTCACCTGCTGCTGAGGCTGCTGAGGCTGCTGAGGCTG 1779
Db 1325 GGAGAGGCTCACAGCTCACCTGCTGCTGAGGCTGCTGAGGCTGCTGAGGCTG 1384
QY 1780 AGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1839
Db 1385 AGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1444
QY 1840 GAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1899
Db 1445 GAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1504
QY 1900 GAACTTATCTCTCTCTACACATAGAAACCAACCAAGGCTGGGCTAGTGGCT 1951
Db 1505 GAACTTATCTCTCTCTACACATAGAAACCAACCAAGGCTGGGCTAGTGGCT 1556
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RESULT 10

US-09-410-194-14

; Sequence 14, Application US/09410194

; Patent No. US20020095030A1

; GENERAL INFORMATION:

; APPLICANT: Tschopp, Jurg

; APPLICANT: Thome, Margot

; APPLICANT: Burns, Kimberly

; APPLICANT: Immler, Marten

; APPLICANT: Hahne, Michael

; APPLICANT: Schroter, Michael

; APPLICANT: Schneider, Pascal

; APPLICANT: Bodmer, Jean-Luc

; APPLICANT: Steiner, Veronique

; APPLICANT: Rimoldi, Donata

; APPLICANT: Hofmann, Kay

; APPLICANT: French, E. Lars

; TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS

; FILE REFERENCE: 11141-002001

; CURRENT APPLICATION NUMBER: US/09/410,194

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; CURRENT FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: PCT/EP98/01857
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 1190
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (394)...(1056)
US-09-410-194-14
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Query Match 32.6%; Score 731.8; DB 9; Length 1190;
Best Local Similarity 99.6%; Pred. No. 9.8e-222;
Matches 744; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
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QY 343 GAACCTCCCCCACTGGAAAGGATTTCTGAAAGAAATGAAGTCAAGCCCTCAGAAATGAAGTTG 402
Db 256 GAACCTCCCCCACTGGAAAGGATTTCTGAAAGAAATGAAGTCAAGCCCTCAGAAATGAAGTTG 315
QY 403 ACTGCTCTGCTGCTTCTGTTGACTGCGCGGAGCTGTACTGCAAGACCCCTGTGTGAGCT 462
Db 316 ACTGCTCTGCTGCTTCTGTTGACTGCGCGGAGCTGTACTGCAAGACCCCTGTGTGAGCT 374
QY 463 TCCCTAGTCTAAGAGTAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 522
Db 375 TCCCTAGTCTAAGAGTAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 434
QY 523 TACAGATGAGAGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 582
Db 435 TACAGATGAGAGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 494
QY 583 ACCTAATGTCAGGGAGCTTCTGGATATTTTACGGGAAAGAGAGTAAAGCTGTCTGTGCGGGA 642
Db 495 ACCTAATGTCAGGGAGCTTCTGGATATTTTACGGGAAAGAGAGTAAAGCTGTCTGTGCGGGA 554
QY 643 CTGCTGCTGAACCTGCTCAGAGAGTGGGAGTTCACCTGCTGCTGCTGCTGCTGCTGCTGCT 702
Db 555 CTGCTGCTGAACCTGCTCAGAGAGTGGGAGTTCACCTGCTGCTGCTGCTGCTGCTGCTGCT 614
QY 703 GGACAGAAAGCTGTGGAGACCCACCTGCTCAGGAACCCCTCACCCTGTTTTCGGACTATAG 762
Db 615 GGACAGAAAGCTGTGGAGACCCACCTGCTCAGGAACCCCTCACCCTGTTTTCGGACTATAG 674
QY 763 AGTGTGTATGTCAGAGATTTGGTGTGAGATTTGGATTAATCTGTATGTCTCTCAATTAATTT 822
Db 675 AGTGTGTATGTCAGAGATTTGGTGTGAGATTTGGATTAATCTGTATGTCTCTCAATTAATTT 734
QY 823 CCTCATGAAGGATTACATGGGCGGAGGCAAGATAGCAAGGAGAGAGATTTCTTGGACCT 882
Db 735 CCTCATGAAGGATTACATGGGCGGAGGCAAGATAGCAAGGAGAGAGATTTCTTGGACCT 794
QY 883 TGTGTTGAGTTGGAGAAACTAAATTTGTTGCCCGCAGATCAACTGAGATTTATTTAGAAAA 942
Db 795 TGTGTTGAGTTGGAGAAACTAAATTTGTTGCCCGCAGATCAACTGAGATTTATTTAGAAAA 854
QY 943 ATGCCTAAAGAACATCCACAGAAATAGACCTGAGAGCAAAAAATCCAGAGATGACAGCAGTC 1002
Db 855 ATGCCTAAAGAACATCCACAGAAATAGACCTGAGAGCAAAAAATCCAGAGATGACAGCAGTC 914
QY 1003 TGTTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1062
Db 915 TGTTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 974
QY 1063 CAAGGATCTCTCAATAAATCTTCAGGCT 1089
Db 975 CAAGGATCTCTCAATAAATCTTCAGGAT 1001
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RESULT 11
US-09-918-995-26998
; Sequence 26998, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26998
; LENGTH: 495
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; LOCATION: (1)...(495)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-26998

Query Match      19.28; Score 431.4; DB 11; Length 495;
Best Local Similarity 99.38; Pred. No. 2.3e-126;
Matches 443; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 176 CCACGGAGGAGGTGTAGGAGAGAGCGCGCGAAGCAGCGATGCCCGACCAAGTCCG 235
Db 50 CCACGGAGGAGGTGTAGGAGAGAGCGCGCGAAGCAGCGATGCCCGACCAAGTCCG 109

QY 236 CTTCCAGGCTTTCGGTTTCTTTGCTCCATCTTGGGTGGGCTTCCCGGGTCTAGGGGA 295
Db 110 CTTCCAGGCTTTCGGTTTCTTTGCTCCATCTTGGGTGGGCTTCCCGGGTCTAGGGGA 169

QY 296 GCGAAGGCTGAGGTGGCAGCGGCGAGGAGTCCGCGCGCAGAGCAACTCCCCCACT 355
Db 170 GCGAAGGCTGAGGTGGCAGCGGCGAGGAGTCCGCGCGCAGAGCAACTCCCCCACT 229

QY 356 GGAAGAGATTCGAAAGAAATGAAGTACGCCCTCAGAAATCAAGTTCAGCTGCTGGC 415
Db 230 GGAAGAGATTCGAAAGAAATGAAGTACGCCCTCAGAAATCAAGTTCAGCTGCTGGC 289

QY 416 TTTCCTGTTGACTGCGCGGAGCTGTACTGCAAGACCCCTTGAGCTTCCCTAGTCTAAG 475
Db 290 TTT-CTGTTGACTGCGCGGAGCTGTACTGCAAGACCCCTTGAGCTTCCCTAGTCTAAG 348

QY 476 AGTAGATGTCGTGAAGTATCCATCAGTTGAGAGCACTTGATACAGATGAGAAG 535
Db 349 AGTAGATGTCGTGAAGTATCCATCAGTTGAGAGCACTTGATACAGATGAGAAG 408

QY 536 GAGATGCTCTCTTTTGTGCGGGATGTGCTATAGATGTGTTCCACCTTAATGTCAGG 595
Db 409 GAGATGCTCTCTTTTGTGCGGGATGTGCTATAGATGTGTTCCACCTTAATGTCAGG 468

QY 596 GACCTTCTGGAATATTTACGGGAAAG 621
Db 469 GACCTTCTGGAATATTTACGGGAAAG 494

RESULT 12
US-09-918-995-37866
; Sequence 37866, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; PRIOR FILING DATE: 2001-07-30

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; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 37866
; LENGTH: 479
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; LOCATION: (1)...(479)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-37866

Query Match      18.98; Score 423.2; DB 11; Length 479;
Best Local Similarity 97.68; Pred. No. 9.3e-124;
Matches 439; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

QY 889 TGAGTTGGAGAACTAAATTTGGTTGCCCGCAGATCACTGGATTATTAGAAAATGCCT 948
Db 31 TAAGANCAGCAACTAAATCTGGNTGCCCGCAGATCACTGGATTATTAGAAAATGCCT 90

QY 949 AAGAACATCCACAGATAGACCTGAAGACAAAAATCCAGAGTACAAAGCAGTCTGTTC 1008
Db 91 AAGAACATCCACAGATAGACCTGAAGACAAAAATCCAGAGTACAAAGCAGTCTGTTC 150

QY 1009 AGGAGCAGGACAAAGTTACAGGAATGTTCTCCAGCAGCAATCCAAAAGAGTCTCAAG 1068
Db 151 AGGAGCAGGACAAAGTTACAGGAATGTTCTCCAGCAGCAATCCAAAAGAGTCTCAAG 210

QY 1069 TCTTTCAATTAATCTCAGCTCCATAATGGGAGAGTAAAGAACAAAGACTTAAGGAACA 1128
Db 211 TCTTTCAATTAATCTCAGCTCCATAATGGGAGAGTAAAGAACAAAGACTTAAGGAACA 270

QY 1129 GCTTGGCGCTCAACAGAACACCAAGTGAAGAAATCCATTGAGGAATCAGAACTTTTGGC 1188
Db 271 GCTTGGCGCTCAACAGAACACCAAGTGAAGAAATCCATTGAGGAATCAGAACTTTTGGC 329

QY 1189 TCAGACATACCTGAAGAGAGATACAGATGAAGCAGAGCCCTAGGAATCTGCTGAT 1248
Db 330 TCAGACATACCTGAAGAGAGATACAGATGAAGCAGAGCCCTAGGAATCTGCTGAT 389

QY 1249 AATCGATTGCTTGGCAATGAGACAGAGCTTCTTCGAGACACTTCCTCCCTGGGCTA 1308
Db 390 AATCGATTGCTTGGCAATGAGACAGAGCTTCTTCGAGACACTTCCTCCCTGGGCTA 449

QY 1309 TGAAGTCCAGAAATTTCTGCATCTCAGTAT 1338
Db 450 TGAAGTCCAGAAATTTCTGCATCTCAGTAT 479

RESULT 13
US-09-918-995-24847
; Sequence 24847, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24847
; LENGTH: 479
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; LOCATION: (1)...(479)

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; OTHER INFORMATION: n - A,T,C or G
 US-09-918-995-24847

Query Match 18.7%; Score 419.4; DB 11; Length 479;
Best Local Similarity 95.9%; Pred. No. 1.5e-122;
Matches 440: Conservative 0; Mismatches 18; Indels 1;

Qy	1118	CTTTAAGAACACAGCTTGGCGCTCAACAAAGAACACAGTGAAGAAATCCATTCAGGAATCAGAA	1177
Db	22	CATTACGAGCAGCTTGGCGCTC-ACAAGAACCAAGTGAAGAAATCCATTCAGGAATCACAA	80
Qy	1178	GCCTTTTGTGGCTCAGAGCATACCTGGAAGAGAGATACAAGATGAAGACAGGCCCTTAGGA	1237
Db	81	GCCTTTTGTGGCTCACAGCATACCTGAAGAGAGATACAAGATGAAGACAGGCCCTTAGGA	140
Qy	1238	ATCTGCCTGATAATCGATTGCAATGGCAATGACAGAGGCTCTTCGAGACACCTTCACT	1297
Db	141	ATCTGCCTGATAATCGATTGCAATGGCAATGACAGAGGCTCTTCGAGACACCTTCACT	200
Qy	1298	TCCTCGGGCTPATCAAGTCCAGAAATCTTTCGATCTCAGATATGCATGCTATATCCAGATT	1357
Db	201	TTCTCGGGCTPATGAAGTGCAGAAATCTTTCGATCTCAGATATGCATGCTATATCCAGATT	260
Qy	1358	CTTGGCCAAATTTGCCCTGTATGCCCGAGCACCGAGACTACGACAGCTTTGTGTGTCTCG	1417
Db	261	CTTGGCCAAATTTGCCCTGTATGCCCGAGCACCGAGACTACGACAGCTTTGTGTGTCTCG	320
Qy	1418	GTGAGCGGAGGAGGCTCCCAAGTGTGTATGTTGTGGATCAGACTCACTCAGGGCTCCCC	1477
Db	321	GCAGCGGAGGAGGCTCCCAAGCCGGTATGTTGTGGATCAGACTCACTCAGGGCTCCCC	380
Qy	1478	CTGCATCACATCAGGAGGATGTTTCATGGGAGATTTCATGCCCTTATCTAGCAGGAGGCCA	1537
Db	381	CTGCATCACATCAAGAGGATGTTTCATGGGAGATTTCATGCCCTTATCTAGCAGGAGGCCA	440
Qy	1538	AAGATGTTTTTTTATTCAGAACTATGTTGTTCCAGAGGC	1576
Db	441	AAGATGTTTTTTTATTCAGAACTATGTTGTTCCAGAGGC	479

RESULT 14

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US-09-918-995-35401
; Sequence 35401, Application US/09918995
; Publication No. US20030073623a1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCING
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918, 995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 35401
; LENGTH: 441
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(441)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-35401

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Query Match	17.08;	Score 382.4;	DB 11;	Length 441;
Best Local Similarity	98.3%;	Pred. No. 8.5e-11;		
Matches 397;	Conservative	0;	Mismatches 6;	Indels 1; Gaps 1;
QY	268	TGGGTGCGCCTTCCCGCGCTCTAGGGGAGCGAAGGCTGAGTGGCGACGCCGAGGAGATC	327	
Db	39	TGCGGTGGAAATCCCGCGCTCTAGGGGAGCGAAGGCTGAGTGGCGACGCCGAGGAGATC	98	

Qy	328	CGGCCGGACAGCAGAACTCCCCACATGGAAAGATTCTTGAAGAAATGAAGTCAGCCC	387
Db	99	CGGCCGGACAGCAGAACTCCCCACATGGAAAGATTCTGAAAGAAATGAAGTCAGCCC	158
Qy	388	TCAGAAATGAAGTTGACTGCTGCTGGCTTTCTCTTTGACTGGCCCGGAGCTGTACTGCA	447
Db	159	TCAGAAATGAAGTTGACTGCTGCTGGCTTT-CTGTTGACTGGCCCGGAGCTGTACTGCA	217
Qy	448	AGACCCCTTGTCAGCTTCCTAGTCTAAACAGTAGGATGCTGCTGAAGTCATCCATCAGT	507
Db	218	AGACCCCTTGTCAGCTTCCTAGTCTAAACAGTAGGATGCTGCTGAAGTCATCCATCAGT	277
Qy	508	TGAAGAAGCACTTGATACAGATGAGAAGGAGATGCTCTTTTGTGCCGGATGTTGC	567
Db	278	TGAAGAAGCACTTGATACAGATGAGAAGGAGATGCTCTTTTGTGCCGGATGTTGC	337
Qy	568	TATAGATGTGGTTCACCTAATGTCCAGGACCTTCTGGATATTTTACGGGAAGAGGTAA	627
Db	338	TATAGATGTGGTTCACCTAATGTCCAGGACCTTCTGGATATTTTACGGGAAGAGGTAA	397
Qy	628	GCTGTCTCGGGGACTTGGCTGAACTGCTTACAGAGTGAGGC	671
Db	398	GCTGTCTCGGGGACTTGGCTGAACTGCTTACAGAGTGAGGC	441

RESULT 15

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RES001 13
US-09-918-995-35271
: Sequence 35271, Application US/09918995
: Publication No. US20030073623A1
:
: GENERAL INFORMATION:
:
: APPLICANT: Hyseq, Inc.
:
: TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQ
:
: TITLE OF INVENTION: FROM VARIOUS CDNA LI
:
: FILE REFERENCE: 20411-756
:
: CURRENT APPLICATION NUMBER: US/09/918,995
:
: CURRENT FILING DATE: 2001-07-30
:
: PRIOR APPLICATION NUMBER: US/09/235,076
:
: PRIOR FILING DATE: 1999-01-20
:
: NUMBER OF SEQ ID NOS: 38054
:
: SOFTWARE: FastSeq for Windows Version 3.0
:
: SEQ ID NO 35271
:
: LENGTH: 443
:
: TYPE: DNA
:
: ORGANISM: Homo sapiens
:
: FEATURE:
:
: NAME/KEY: misc_feature
:
: LOCATION: (1)...(443)
:
: OTHER INFORMATION: n = A,T,C or G
US-09-918-995-35271

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[illegible]

Mon Aug 25 09:11:02 2003

Oy	566	GCTATAGATGTGGTTCACCCCTAATGTCAGGACCTTCTGGATATTTACGGGAACAGGT	625
Db	331	GCTATATATGTGGATCCACCTAACGTTGAAGGACCTTCTGGATATTTCTCTGGAAGAGGA	390
Oy	626	AAGCTGTCTGTGCGGGACTTGGCTGAACCTCTACAGAGTGAGGCGATTGA	678
Db	391	AAACTGTCTGTGCGGAGACTTGAAGTCTCTACAAAGTGAGGCGATTGA	443

Search completed: August 22, 2003, 17:24:07
Job time : 519.885 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 22, 2003, 05:37:21; Search time 5123.69 Seconds
(without alignments)
10962.592 Million cell updates/sec

Title: US-09-380-546A-3

Perfect score: 1373

Sequence: 1 ggagctcagcattacaat.....aaaaaaaaaaaaaaaaaaaaa 1373

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

GenEmbl:

- 1: gb_ba.*
- 2: gb_hgt.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pi.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_srs.*
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- 14: gb_vt.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
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- 28: em_un.*
- 29: em_vt.*
- 30: em_hgt_hum.*
- 31: em_hgt_inv.*
- 32: em_hgt_other.*
- 33: em_hgt_mus.*
- 34: em_hgt_pln.*
- 35: em_hgt_rod.*
- 36: em_hgt_nam.*
- 37: em_hgt_vrt.*
- 38: em_sy.*
- 39: em_higo_hum.*
- 40: em_higo_mus.*
- 41: em_higo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1373	100.0	1373	6	A86558	A86558 Sequence 3
2	1373	100.0	1373	6	BD105909	BD105909 CASH(Casp
3	1373	100.0	1373	9	HSY14040	Y14040 Homo sapien
4	1087.4	79.2	2243	6	A86556	A86556 Sequence 1
5	1087.4	79.2	2243	6	BD105908	BD105908 CASH(Casp
6	1087.4	79.2	2243	6	HSY14039	Y14039 Homo sapien
7	1033.4	75.3	2040	6	AR194324	AR194324 Sequence
8	1033.4	75.3	2040	6	AF005774	AF005774 Homo sapi
9	1025.2	74.7	2045	6	AR156902	AR156902 Sequence
10	1008.6	73.5	1750	6	AR140520	AR140520 Sequence
11	1008.6	73.5	1750	6	BD093439	BD093439 FADD-like
12	1008.6	73.5	2056	9	AF009616	AF009616 Homo sapi
13	1003.8	73.1	2039	9	AF010127	AF010127 Homo sapi
14	975.8	71.1	2143	6	A84918	A84918 Sequence 9
15	975.8	71.1	2143	6	BD107658	BD107658 FLIP gene
16	975.8	71.1	2143	9	U97074	U97074 Homo sapien
17	860.8	62.7	2034	6	BD056976	BD056976 I-FLICE,
18	858.2	62.5	1190	6	A84916	A84916 Sequence 7
19	858.2	62.5	1190	6	BD107657	BD107657 FLIP gene
20	858.2	62.5	1190	6	BC001602	BC001602 Homo sapi
21	851.2	62.0	2025	9	AF005775	AF005775 Homo sapi
22	823	59.9	834	9	AF015450	AF015450 Homo sapi
23	743	54.1	2084	9	AF015458	AF015458 Homo sapi
24	619.8	45.1	1458	9	AF041458	AF041458 Homo sapi
25	607.6	44.3	1057	9	AF009617	AF009617 Homo sapi
26	604.8	44.0	879	9	AF015452	AF015452 Homo sapi
27	604.8	44.0	932	9	AF00619	AF00619 Homo sapi
28	604.8	44.0	1350	9	AF041460	AF041460 Homo sapi
29	604.8	44.0	1389	9	AF015451	AF015451 Homo sapi
30	604.8	44.0	1443	6	A84924	A84924 Sequence 3
31	604.8	44.0	1443	6	BD084807	BD084807 Protein f
32	604.8	44.0	1443	9	AF009618	AF009618 Homo sapi
33	604.8	44.0	1443	9	BT006751	BT006751 Homo sapi
34	604.8	44.0	1443	9	HSU85059	U85059 Human prote
35	604.8	44.0	1443	12	BT007958	BT007958 Synthetic
36	516.8	37.6	1361	9	AF041461	AF041461 Homo sapi
37	406.4	29.7	127361	9	AC007283	AC007283 Homo sapi
38	406.4	29.6	6193	9	AB038965S3	AB038967 Homo sapi
39	378.6	27.6	1501	10	AF244366	AF244366 Rattus no
40	373.8	27.2	2413	10	U97076	U97076 Mus musculu
41	373.8	27.2	2452	6	A84921	A84921 Sequence 12
42	373.8	27.2	2452	6	BD107659	BD107659 FLIP gene
43	369.4	26.9	3168	10	BC029223	BC029223 Mus muscu
44	369.4	26.9	214130	2	AC107701	AC107701 Mus muscu
45	337.8	24.6	1611	10	MMY14042	Y14042 Mus musculu

ALIGNMENTS

RESULT 1

A86558	A86558	Sequence 3 from Patent W09839435.	1373 bp	DNA	linear	PAT 21-JAN-2000
LOCUS	A86558	Sequence 3 from Patent W09839435.				
DEFINITION	A86558					
ACCESSION	A86558					
VERSION	A86558.1	GI:6735155				
KEYWORDS						
SOURCE	unidentified					
ORGANISM	unclassified					
REFERENCE	1 (bases 1 to 1373)					
AUTHORS	Wallach,D. and Goltsev,Y.					
TITLE	CASH (CASPASE HOMOLOGUE) WITH DEATH EFFECTOR DOMAIN, MODULATORS OF THE FUNCTION OF FAS RECEPTORS					
JOURNAL	Patent: WO 9839435-A 3 11-SEP-1998;					

FEATURES		WALLACH DAVID (IL); GOLTSEV YURA (IL)	
source	Location/Qualifiers	1..1373	
	/organism="unidentified"	/mol_type="genomic DNA"	
BASE COUNT		417 a	283 c 335 g 338 t
ORIGIN		100.0%; Score 1373; DB 6; Length 1373;	
Query Match		100.0%; Pred. No. 1.9e-263;	
Best Local Similarity		Matches 1373; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1	GGAGTCCAGGCAATACAAATCGCAAAACCAAGCCATAGCATGAACAGCAGCGCTTGCGC 60	
DB	1	GGAGTCCAGGCAATACAAATCGCAAAACCAAGCCATAGCATGAACAGCAGCGCTTGCGC 60	
QY	61	CTCAGCGAGAGTCTCAACTAAAGGGACTCCCGAGGAGTAGGGTGGGGACTCGGCCCTCA 120	
DB	61	CTCAGCGAGAGTCTCAACTAAAGGGACTCCCGAGGAGTAGGGTGGGGACTCGGCCCTCA 120	
QY	121	CACAGTGAATCGCGCTATTCGACTTTTGTCCAGTGAAGCTGAGACAACAGGACACG 180	
DB	121	CACAGTGAATCGCGCTATTCGACTTTTGTCCAGTGAAGCTGAGACAACAGGACACG 180	
QY	181	GGAGGAGGTGTAGGAGAAAGCGCGCAACAGCGATGCGCCAGCAACCAAGTCCGCTTC 240	
DB	181	GGAGGAGGTGTAGGAGAAAGCGCGCAACAGCGATGCGCCAGCAACCAAGTCCGCTTC 240	
QY	241	AGGCTTTGGTTCTTTGCCCTCCATCTTGGTGGCGCTTCCCGGCTCTAGGGGAGCA 300	
DB	241	AGGCTTTGGTTCTTTGCCCTCCATCTTGGTGGCGCTTCCCGGCTCTAGGGGAGCA 300	
QY	301	GGCTGAGTGGCAGCGGAGGAGTCCGGCGCGCACAGGACGAACTCCCGCACTGGAAA 360	
DB	301	GGCTGAGTGGCAGCGGAGGAGTCCGGCGCGCACAGGACGAACTCCCGCACTGGAAA 360	
QY	361	GGATTCTGAAGAAATGAAGTCAGCCCTCAGAAATGAAGTGAAGTCTCCTAGTGAAGTAG 480	
DB	361	GGATTCTGAAGAAATGAAGTCAGCCCTCAGAAATGAAGTGAAGTCTCCTAGTGAAGTAG 480	
QY	421	TGTTGACTGGCCGAGCTGTACTCAAGACCTTGTGAGCTTCCCTAGTGAAGTAG 480	
DB	421	TGTTGACTGGCCGAGCTGTACTCAAGACCTTGTGAGCTTCCCTAGTGAAGTAG 480	
QY	481	GATGCTGCTGAAGTCAATCAATCAGGTTGAAGAGCACTTGATACAGATGAAGAGAT 540	
DB	481	GATGCTGCTGAAGTCAATCAATCAGGTTGAAGAGCACTTGATACAGATGAAGAGAT 540	
QY	541	GCTGCTCTTTTGTCCGGGATGTGCTATAGATGTTCCACCTAATGTGAGGACCT 600	
DB	541	GCTGCTCTTTTGTCCGGGATGTGCTATAGATGTTCCACCTAATGTGAGGACCT 600	
QY	601	TCGTGATATTTACGGGAAGAGTGAAGTGTCTCGGGGACTTGGCTGAAGTCTCTA 660	
DB	601	TCGTGATATTTACGGGAAGAGTGAAGTGTCTCGGGGACTTGGCTGAAGTCTCTA 660	
QY	661	CAGAGTGAAGGATTTGACTGCTCAACAGTATCTTGAAGTGAAGAGCAAAAGCTGTGA 720	
DB	661	CAGAGTGAAGGATTTGACTGCTCAACAGTATCTTGAAGTGAAGAGCAAAAGCTGTGA 720	
QY	721	GACCCACCTGCTCAGGAACCTTCACTTGTTCGGACTATAGAGTGTGATGGCAGAT 780	
DB	721	GACCCACCTGCTCAGGAACCTTCACTTGTTCGGACTATAGAGTGTGATGGCAGAT 780	
QY	781	TGTTGAGGATTTGGATAAATCTGATGTGCTCTCAATTAATTTTCTCATGAAGATTACAT 840	
DB	781	TGTTGAGGATTTGGATAAATCTGATGTGCTCTCAATTAATTTTCTCATGAAGATTACAT 840	
QY	841	GGCCCCAGCAAGATGAAGCAAGAGAGATTTCTTGGACCTTGGTTGAGTTGGAGAA 900	
DB	841	GGCCCCAGCAAGATGAAGCAAGAGAGATTTCTTGGACCTTGGTTGAGTTGGAGAA 900	
QY	901	ACTAAATTTGGTTGCCCCAGATCAACTGGATTATTAGAAAAATGCCTAAGAAATCCA 960	
DB	901	ACTAAATTTGGTTGCCCCAGATCAACTGGATTATTAGAAAAATGCCTAAGAAATCCA 960	
QY	961	CAGAATAGACCTGAGACAAAAATCCAGAGTACAAGCAGTCTGTTCAAGGAGCAGGAC 1020	
DB	961	CAGAATAGACCTGAGACAAAAATCCAGAGTACAAGCAGTCTGTTCAAGGAGCAGGAC 1020	
QY	1021	AACTTACAGGAATGTTCTCAAGCAGCAATCCAAAAAGAGTCTCAAGGATCCTTCAATAA 1080	
DB	1021	AACTTACAGGAATGTTCTCAAGCAGCAATCCAAAAAGAGTCTCAAGGATCCTTCAATAA 1080	
QY	1081	CTTCAGGATGATAACACCCCTATGCCCATTTGCTGATCTGAAAAATTTCTTGGAAATTTGTT 1140	
DB	1081	CTTCAGGATGATAACACCCCTATGCCCATTTGCTGATCTGAAAAATTTCTTGGAAATTTGTT 1140	
QY	1141	CATGTGATTAACATGAAGTGCCTTACTTAATCAATTCGAATGATTAATCGTTTCAT 1200	
DB	1141	CATGTGATTAACATGAAGTGCCTTACTTAATCAATTCGAATGATTAATCGTTTCAT 1200	
QY	1201	TTCTAAATGTTTATATGTTTAGCCCTTTCTTGTGCTGCTGATCTTTAGATGCTTTCC 1260	
DB	1201	TTCTAAATGTTTATATGTTTAGCCCTTTCTTGTGCTGCTGATCTTTAGATGCTTTCC 1260	
QY	1261	AATCTTTTGTACTACTAATAATGCTATAAAATATATCCCTGTTACTTCTTAAAAAA 1320	
DB	1261	AATCTTTTGTACTACTAATAATGCTATAAAATATATCCCTGTTACTTCTTAAAAAA 1320	
QY	1321	AAAAAATTTTGTACTACTAATAATGCTATAAAATATATCCCTGTTACTTCTTAAAAAA 1373	
DB	1321	AAAAAATTTTGTACTACTAATAATGCTATAAAATATATCCCTGTTACTTCTTAAAAAA 1373	
RESULT 2		1373 bp DNA linear PAT 18-SEP-2002	
BD105909		CASH(Caspase Homologue) with death effector domain, modulators of	
LOCUS		the function of FAS receptors.	
DEFINITION		BD105909	
ACCESSION		BD105909.1 GI:23200727	
VERSION		JP 2002500508-A/2	
KEYWORDS		synthetic construct	
SOURCE		artificial sequences.	
ORGANISM		1 (bases 1 to 1373)	
REFERENCE		Wallach,D., Goltsev,Y., Kovalenko,A., Varfolomeev,E. and	
AUTHORS		Brodianski,V.	
TITLE		CASH(Caspase Homologue) with death effector domain, modulators of	
JOURNAL		the function of FAS receptors	
COMMENT		Patent: JP 2002500508-A 2 08-JAN-2002;	
		YEDA RESEARCH AND DEV CO LTD	
		PN JP 2002500508-A/2	
		PD 08-JAN-2002	
		PF 26-FEB-1998 JP 1998538331	
		PR 03-MAR-1997 IL 120367, 01-MAY-1997 IL 120759 PI	
		DAVID WALLACH, YURA GOLTSEV, ANDREI KOVALENKO, EUGENE VARFOLOMEEV,	
		PI VADIM BRODIANSKI	
		PC C12N15/12, C12N15/11, C12N9/64, A61K38/48, G01N33/68, C12N9/00 CC	
		Strandedness: Single;	
		CC Topology: Linear;	
		FH Key Location/Qualifiers.	
FEATURES		1..1373	
source		/organism="synthetic construct"	
		/mol_type="genomic DNA"	
		/db_xref="taxon:32630"	
BASE COUNT		417 a	283 c 335 g 338 t
ORIGIN		100.0%; Score 1373; DB 6; Length 1373;	
Query Match		100.0%; Pred. No. 1.9e-263;	
Best Local Similarity		Matches 1373; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	

Db	1081	CTTCAGGATGATACACCCTATGCCCATTTGTCTGATCTGAATAATTCTTGGAATTTGTC	1140
Qy	1141	CATGTGNTAACATGAACCTGCCTCTACTTAATCATCTCAATGATTAATCGTTTTCAAT	1200
Db	1141	CATGTGNTAACATGAACCTGCCTCTACTTAATCATCTCAATGATTAATCGTTTTCAAT	1200
Qy	1201	TTCCTAAATGTTTATATATGTTTAGCCCTTTCTGTTGCTGTATCTTTAGATGCTTTCC	1260
Db	1201	TTCCTAAATGTTTATATATGTTTAGCCCTTTCTGTTGCTGTATCTTTAGATGCTTTCC	1260
Qy	1261	AATCTTTTGTACTACTAATAATGCTATATAAATAATATCCTTGTACTTCTTAAAAAAA	1320
Db	1261	AATCTTTTGTACTACTAATAATGCTATATAAATAATATCCTTGTACTTCTTAAAAAAA	1320
Qy	1321	AA	1373
Db	1321	AA	1373
RESULT 3			
HSY14040			
LOCUS	HSY14040	1373 bp	mRNA linear PRI 30-NOV-1997
DEFINITION	Homo sapiens mRNA for CASH beta protein.		
ACCESSION	Y14040		
VERSION	Y14040.1 GI:2653417		
KEYWORDS	CASH beta protein.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE	1 Goltsev Y.V., Kovalenko A.V., Arnold E., Varfolomeev E.E., Brodianskii V.M. and Wallach D. CASH, a novel caspase homologue with death effector domains J. Biol. Chem. 272 (32), 19641-19644 (1997) 97426025		
TITLE	CASH, a novel caspase homologue with death effector domains		
JOURNAL	J. Biol. Chem. 272 (32), 19641-19644 (1997)		
MEDLINE			
PUBMED	9289491		
REFERENCE	2 (bases 1 to 1373)		
AUTHORS	Wallach D.		
TITLE	Direct Submission		
JOURNAL	Submitted (23-JUN-1997) D. Wallach, The Weizmann Institute,		
FEATURES	Department Of Membrane Research & Biophysics, Rehovot 76100, ISRAEL Location/Qualifiers		
source	1..1373		
	/organism="Homo sapiens"		
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DEFINITION Sequence 1 from Patent WO9839435.
ACCESSION A86556
VERSION A86556.1 GI:6735154
KEYWORDS
SOURCE unidentified
ORGANISM unclassified
REFERENCE 1 (bases 1 to 2243)
AUTHORS Wallach,D. and Goltsev,Y.
TITLE CASH (CASPASE HOMOLOGUE) WITH DEATH EFFECTOR DOMAIN, MODULATORS OF
JOURNAL THE FUNCTION OF FAS RECEPTORS
PATENT: WO 9839435-A 1 11-SEP-1998;
WALLACH DAVID (IL); GOLTSEV YURA (IL)
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Query Match 79.28; Score 1087.4; DB 6; Length 2243;
Best Local Similarity 99.9%; Pred. No. 1.6e-206;
Matches 1088; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy	601	TCGTGGATATTTACGGGAAGAGCTAAGCTGTCTGTGCGGGAGCTTGGCTGAACCTGCTCTA	660		
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Qy	841	GGGCCGAGGCAAGATAAGCAAGAGAGAGTTCTTTGGACCTTGTGGTTGAGTTGGAGAA	900		
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LOCUS	CASH(Caspase Homologue) with death effector domain, modulators of the function of FAS receptors.				
DEFINITION	BD105908				
ACCESSION	BD105908				
VERSION	BD105908.1	GI:23200726			
KEYWORDS	JP 2002500508-A/1.				
SOURCE	synthetic construct				
ORGANISM	artificial sequences.				
REFERENCE	1 (bases 1 to 2243)				
AUTHORS	Wallach,D., Goltsev,Y., Kovalenko,A., Varfolomeev,E. and Brodianski,V.				
TITLE	CASH(Caspase Homologue) with death effector domain, modulators of the function of FAS receptors				
JOURNAL	Patent: JP 2002500508-A 1 08-JAN-2002;				
COMMENT	YEDA RESEARCH AND DEV CO LTD				
	PN	JP 2002500508-A/1			
	PD	08-JAN-2002			
	PF	26-FEB-1998	JP 1998538331		
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	DAVID WALLACH, YURA GOLTSEV, ANDREI KOVALENKO, EUGENE VARFOLOMEEV,				
	PI	VADIM BRODIANSKI			
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Best Local Similarity			99.9%;	Pred. No. 1.6e-206;
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QY	61	CTCAGCGAGAGTCTCAACTAAAGGGACTCCGGAGACTAGGGTGGGACTCGGCTCA	120	
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QY	121	CACAGTGAGTCCGGCTATTGGACTTTTGTCCAGTCACAGCTGAGACAACAGGACGAC	180	
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DEFINITION Homo sapiens mRNA for CASH alpha protein.
ACCESSION Y14039
VERSION Y14039.1 GI:2653415
KEYWORDS CASH alpha protein.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Goltsev, Y.V., Kovalenko, A.V., Arnold, E., Varfolomeev, E.E.,
Brodianskii, V.M. and Wallach, D.
CASH, a novel caspase homologue with death effector domains
J. Biol. Chem. 272 (32), 19641-19644 (1997)
MEDLINE 97426025
PUBMED 9289491
REFERENCE 2 (bases 1 to 2243)
AUTHORS Wallach, D.
Direct Submission
TITLE Submitted (23-JUN-1997) D. Wallach, The Weizmann Institute,
Department of Membrane Research & Biophysics, Rehovot 76100, ISRAEL
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BASE COUNT 620 a 511 c 603 g 509 t
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Query Match 79.2%; Score 1087.4; DB 9; Length 2243;
Best Local Similarity 99.9%; Pred. No. 1.6e-206;
Matches 1088; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 7

ARI94324
LOCUS ARI94324 2040 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 33 from patent US 6348573.
ACCESSION ARI94324
VERSION ARI94324.1 GI:20240916
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2040)
AUTHORS Nunez,G., Inohara,N. and Koseki,T.
TITLE Compositions and methods for identifying apoptosis signaling
pathway inhibitors and activators
JOURNAL Patent: US 6348573-A 33 19-FEB-2002;
FEATURES Location/Qualifiers
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BASE COUNT 574 a 467 c 543 g 456 t
ORIGIN
Query Match 75.3%; Score 1033.4; DB 6; Length 2040;
Best Local Similarity 99.4%; Pred. No. 9.2e-196;
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QY 647 GCTGAACCTCTACAGAGTGTAGGCGATTGACCTGCTCAACAGTATCTTGAAGATGAC 706
Db 601 GCTGAACCTCTACAGAGTGTAGGCGATTGACCTGCTCAACAGTATCTTGAAGATGAC 660
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QY 767 CTGATGGCAGAGATTGGTGAGGATTGGGATAAATCTGATGTGCTCTCATTAATTTTCTC 826

Db 721 CTGATGGCAGAGATTGGTGCAGGATTGGATAAATCTGATGTCTCATTAATTTCTCTC 780
QY 827 ATGAAGGATTACATGGCGGAGGCAAGATAAGCAAGGAGAGAGTTTCTTGGACCTTGTG 886
Db 781 ATGAAGGATTACATGGCGGAGGCAAGATAAGCAAGGAGAGAGTTTCTTGGACCTTGTG 840
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AF005774
LOCUS
DEFINITION 2040 bp mRNA linear PRI 05-MAY-1998
Homo sapiens caspase-like apoptosis regulatory protein (clarp)
mRNA, alternatively spliced, complete cds.
ACCESSION AF005774
VERSION AF005774.1 GI:2286144
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 2040)
AUTHORS Inohara,N., Koseki,T., Hu,Y., Chen,S. and Nunez,G.
TITLE CLARP, a death effector domain-containing protein interacts with
caspase-8 and regulates apoptosis
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 94 (20), 10717-10722 (1997)
MEDLINE 98021435
PUBMED 9380701
REFERENCE 2 (bases 1 to 2040)
AUTHORS Inohara,N., Koseki,T., Hu,Y., Chen,S. and Nunez,G.
TITLE Direct Submission
JOURNAL Submitted (28-MAY-1997) Department of Pathology, University of
Michigan Medical School, 1150 W. Medical Center Dr., C558 MSRBII,
Ann Arbor, MI 48109, USA
FEATURES Location/Qualifiers
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QY	1007	CAAGGAGCAGGACAAGTTACAGGAATGTTCTTCAAGACGCAATCCAAAGAGTCTCAAG	1006
Db	961	CAAGGAGCAGGACAAGTTACAGGAATGTTCTTCAAGACGCAATCCAAAGAGTCTCAAG	1020
QY	1067	GATCCTTCAAATAAATCTCAGGAT	1089
Db	1021	GATCCTTCAAATAAATCTCAGGCT	1043
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LOCUS	AR156902	2045 bp	DNA
DEFINITION	Sequence 1 from patent US 6242569.		
ACCESSION	AR156902		
VERSION	AR156902.1	GI:15125606	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 2045)		
AUTHORS	Shu,H.-B. and Goeddel,D.V.		
TITLE	Regulators of apoptosis		
JOURNAL	Patent: US 6242569-A	1 05-JUN-2001;	
FEATURES	Location/Qualifiers		
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ORIGIN	/organism="unknown"		459 t
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Best Local Similarity 99.6%; Pred. No. 3.9e-194;			
Matches 1038; Conservative 0; Mismatches 3; Indels 1; Gaps 1;			
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QY	108	GGACTCGGCTCACAGTGTAGTCCGCTATTGGACTTTTGTCCAGTGACAGCTGAGAC	167
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QY	288	CTAGGGAGGAGGAGGTGAGCTGGCAGCGGACGAGAGTCCGGCGCGGACAGGACGAACT	347
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QY	348	CCCCACTGGAAAGGATCTGAAAGAAATGAAAGTCAGCCCTCAGAAATGAAGTTGACTGC	407
Db	378	CCCCACTGGAAAGGATCTGAAAGAAATGAAAGTCAGCCCTCAGAAATGAAGTTGACTGC	437
QY	408	CTGCTGCTTCTGTTGACTGGCCCGGAGCTGTACTGCAAGACCCCTTGTGAGCTTCCCT	467
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QY	468	AGTCTAAGAGTAGGATGCTCTGCTGAAAGTCAATCATCAGGTTGAAGAGCACTTGATACAG	527
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QY	528	ATGAGAAGGAGATGCTGCTCTTTTGTGCGGGATGTTGCTATAGATGTGTTCCACTTA	587
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QY	588	ATGTCAGGACCTTCGATATTTTACGGGAAAGAGTGAAGTGTCTGTGCGGACCTTGG	647
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BASE COUNT 546 a 469 c 562 g 479 t
ORIGIN

Query Match 73.5%; Score 1008.6; DB 9; Length 2056;
Best Local Similarity 99.5%; Pred. No. 8e-191;
Matches 1022; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

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RESULT 13
AF010127
LOCUS
DEFINITION Homo sapiens Casper mRNA, complete cds.
ACCESSION AF010127
VERSION AF010127.1 GI:2281475
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2039)
AUTHORS Shu,H.B., Halpin,D.R. and Goeddel,D.V.
TITLE Casper is a FADD- and caspase-related inducer of apoptosis
JOURNAL Immunity 6 (6), 751-763 (1997)
MEDLINE 97352452
PUBMED 9208847
REFERENCE 2 (bases 1 to 2039)
AUTHORS Shu,H.B., Halpin,D.R. and Goeddel,D.V.
TITLE Direct Submission
JOURNAL Submitted (23-JUN-1997) Biology, Tularik, Inc., Two Corporate Dr.,
South San Francisco, CA 94080, USA
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BASE COUNT 592 a 456 c 536 g 455 t
ORIGIN

Query Match 73.1%; Score 1003.8; DB 9; Length 2039;
Best Local Similarity 99.7%; Pred. No. 7.3e-190;
Matches 1016; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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DB 1 AGTCTCAACTAAAGGAGCTCCCGGAGCTAGGGGTGGGACTCGGCTCACACAGTGA 60
QY 131 GCCGGCTATTGGACTTTTGTCCAGTGACAGCTGAGACAAAGGAGCAGGAGGAGG 190
DB 61 GCCGGCTATTGGACTTTTGTCCAGTGACAGCTGAGACAAAGGAGCAGGAGGAGG 120
QY 191 TAGGAGAGAGCGCGCGGAGACGAGATGCCCGACCAAGTCCCGCTTCCAGGCTTTCGG 250
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TITLE	FEATURES	BASE COUNT	ORIGIN	Query Match	Best Local Similarity	Mismatches	Indels	Gaps	Length
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Patent: WO 9841104-A 9 08-OCT-1998;	Location/Qualifiers								
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	159 AGCTGAGACAAACAGGACCACGGGAGGAGGTGTAGAGAGAACGCGCGGACACGCGATC 218								
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	339 GGAGGAATCCCCACTGGGAAGGATTCGAAGAAATGAAGTCAGCCCTCAGAATGAA 398								
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	399 GTTGACTCGCTGCTGGCTTCTCTGTTGACTGGCCCGGAGCTGTACTGCAAGACCCCTGTG 458								
	301 GTTGACTCGCTGCTGGCTTCTCTGTTGACTGGCCCGGAGCTGTACTGCAAGACCCCTGTG 359								
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720	TTTTTCTCATGAAGGATTACATGGCCCGCAGCAGATAAGCAAGGACAAGAGTTCTTGG	779
Db		
879	ACCTTGTGGTTGAGTTGGAGAAACTAAATTTGGTTGCCCGCAGTCACTGGATTTATTAG	938
QY		
780	ACCTTGTGGTTGAGTTGGAGAAACTAAATCTGGTTGCCCGCAGTCACTGGATTTATTAG	839
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Db 900 AGTCGTGTTCAAGGACGAGGACAAAGTTACAGAAATGTTCTCCAGCAGCAATCCAAAGA 959

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RESULT 15

BD107658

LOCUS BD107658 2143 bp DNA linear PAT 18-SEP-2002

DEFINITION FLIP gene and FLIP protein.

ACCESSION BD107658

VERSION BD107658.1 GI:23202476

KEYWORDS JP 2002501371-A/2.

SOURCE unidentified

ORGANISM unidentified

REFERENCE 1 (bases 1 to 2143)

AUTHORS Tschoep, J., Thome, M., Burns, K., Imler, M., Hahne, M., Schroter, M., Schneider, P., Bodmer, J.L., Steiner, V., Rimoldi, D., Hofmann, K. and French, L.E.

TITLE FLIP gene and FLIP protein

JOURNAL Patent: JP 2002501371-A 2 15-JAN-2002;

COMMENT APOTEC SA

OS Homo sapiens, long version of FLIP-DNA

PN JP 2002501371-A/2

PD 15-JAN-2002

PF 31-MAR-1998 JP 1998541154

PR 01-APR-1997 DE 197 13 393.2

PI JURG TSCHOPP, MARGOT THOME, KIMBERLY BURNS, MARTIN IRLMER, MICHAEL HAHNE.

PI MICHAEL SCHROTER, PASCAL SCHNEIDER, JEAN LUC BODMER, VERONIQUE STEINER,

PI DONATA RIMOLDI, KAY HOFMANN, LARS E FRENCH

PC C12N15/12, C07K14/47, C12N5/10, G01N33/68

CC Strandedness: Single;

CC Topology: Linear;

CC FLIP gene and FLIP protein

FH Key Location/Qualifiers

FT source 1. .2143

FT /organism='Homo sapiens, long version of FT

FEATURES

Source Location/Qualifiers

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BASE COUNT 590 a 482 c 576 g 495 t

ORIGIN

Query Match 71.1%; Score 975.8; DB 6; Length 2143;

Best Local Similarity 99.7%; Pred. No. 2.8e-184;

Matches 988; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 99 TAGGGTGGGACTCGGCTCACACAGTACAGTACGTCGGCTATTGGACTTTTGTCCAGTGAC 158

Db 1 TAGGGTGGGACTCGGCTCACACAGTACAGTACGTCGGCTATTGGACTTTTGTCCAGTGAC 60

QY 159 AGCTGAGACAAAGACCCAGGAGGAGTGTAGGAGAGAGCGCGGACAGCGATC 218

Db 61 AGCTGAGACAAAGACCCAGGAGGAGTGTAGGAGAGAGCGCGGACAGCGATC 120

QY 219 GCCAGACCAAGTCCGCTTCCAGGCTTTTCGGTTTTCGCTTCCATCTTGGTGGCGCT 278

Db 121 GCCAGACCAAGTCCGCTTCCAGGCTTTTCGGTTTTCGCTTCCATCTTGGTGGCGCT 180

QY 279 TCCGGGCTCTAGGGAGGAGGAGTGTAGGTGGCAGGCGGACGAGTCCGGCGCGGACA 338

Db 181 TCCCGGCGTCTAGGGGAGCGAAGGCTGAGGTGGCAGCGCAGAGAGTCCGCCCGCGACA 240

QY 339 GGACGAATCCCGCCACTGGAAAGGATTCCTGAAGAAATGAAGTCAGCCCTCAGAATGAA 398

Db 241 GGACGAATCCCGCCACTGGAAAGGATTCCTGAAGAAATGAAGTCAGCCCTCAGAATGAA 300

QY 399 GTTGAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 458

Db 301 GTTGAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 359

QY 459 AGCTTCCCTAGTCTAAGAGTAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 518

Db 360 AGCTTCCCTAGTCTAAGAGTAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 419

QY 519 TTGATACAGATGAGAAGGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 578

Db 420 TTGATACAGATGAGAAGGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 479

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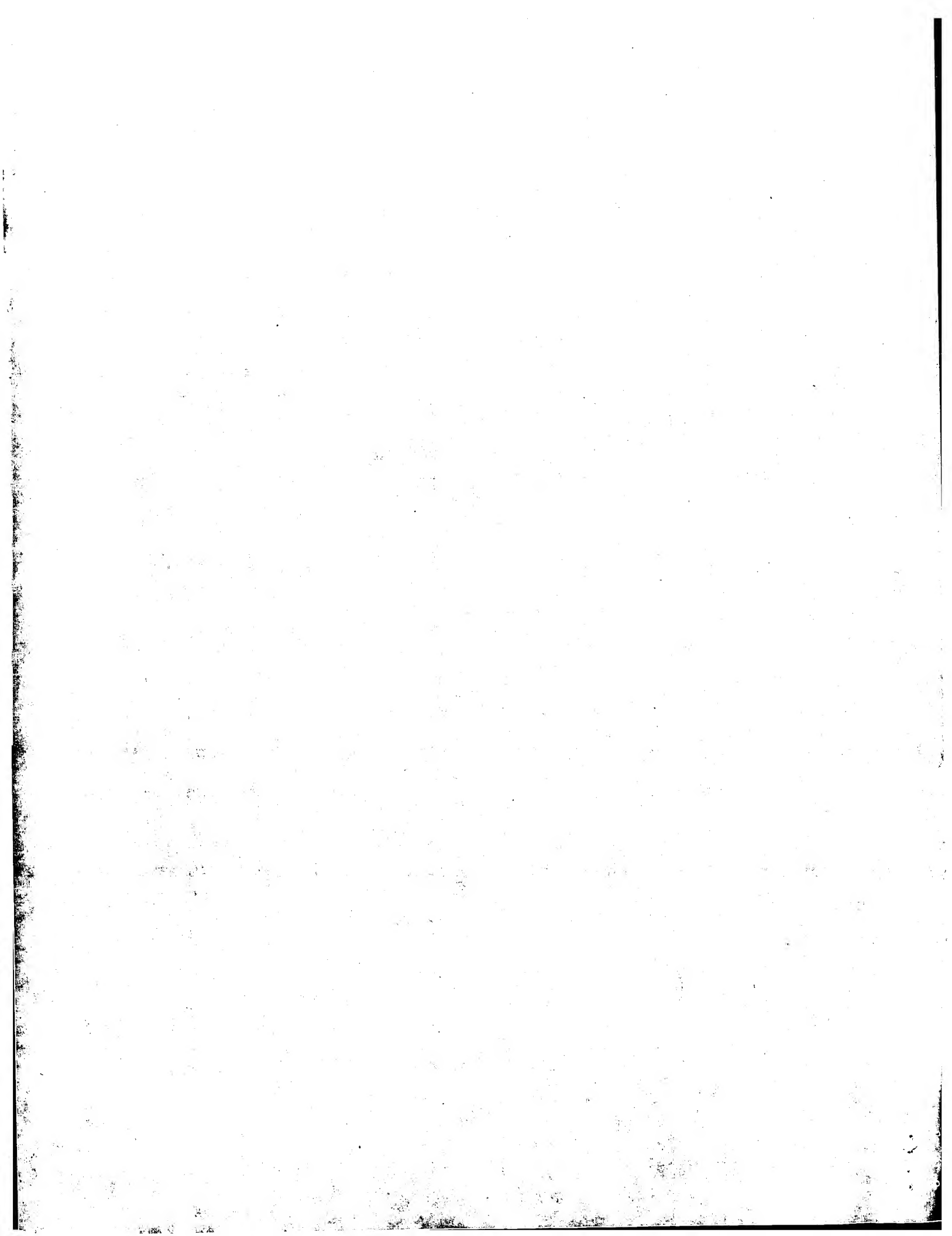
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1059 GTCTCAAGGATCCTTCAATAACTTCAGGAT 1089

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GenCore version 5.1.6
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Run on: August 22, 2003, 05:36:22 ; Search time 378.562 Seconds
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Title: US-09-380-546A-3

Perfect score: 1373

Sequence: 1 ggaagtcgagcattacaat.....aaaaaaaaaaaaaaaaaaaa 1373

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2532756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- N_Geneseq_19Jun03.*
- 1: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.*
 - 2: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.*
 - 3: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.*
 - 4: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.*
 - 5: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.*
 - 6: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1985.DAT.*
 - 7: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1986.DAT.*
 - 8: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1987.DAT.*
 - 9: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1988.DAT.*
 - 10: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1989.DAT.*
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 - 12: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1991.DAT.*
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 - 14: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1993.DAT.*
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 - 19: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1998.DAT.*
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 - 21: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.*
 - 22: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
 - 23: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
 - 24: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*
 - 25: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1373	100.0	1373	19	AAV52969 Human G1 protein i
2	1276.6	93.0	1308	20	AAV25510 Human MACH related
3	1087.4	79.2	2243	19	AAV52968 Human G1 protein i
4	1044.4	76.1	2352	21	AAZ47926 Human apoptosis as
5	1033.4	75.3	2040	21	AAZ48769 Human CLARP coding
6	1026.8	74.8	1996	20	AAV25508 Human MACH related
7	1025.2	74.7	2045	19	AAV50436 Human Casper gene.
8	1014.8	73.9	2188	19	AAV31375 Human FIN-1 encodi

9	1008.6	73.5	1750	20	AAV74136
10	1008.6	73.5	1750	24	AAV43202
11	975.8	71.1	2143	19	AAV61937
12	975.8	71.1	2143	20	AAZ39040
13	975.8	71.1	2143	24	ABL52333
14	860.8	62.7	2034	19	AAV44806
15	858.2	62.5	1062	20	AAZ39041
16	858.2	62.5	1062	24	ABL52332
17	855.4	62.3	1190	19	AAV61936
18	823	59.9	834	24	ABK83474
19	739.8	53.9	2084	21	AAZ56987
20	604.8	44.0	879	21	AAZ56989
21	604.8	44.0	1389	21	AAZ56988
22	604.8	44.0	1517	21	AAV54301
23	408	29.7	38358	22	AAK73535
24	373.8	27.2	2413	24	ABL52342
25	373.8	27.2	2452	19	AAV61938
26	337.8	24.6	1611	24	ABL52343
27	337.8	24.6	2770	24	ABL52325
28	337.8	24.6	2770	25	ABV72474
29	324.8	23.7	2420	20	AAZ25509
30	324.4	23.6	1319	22	AAV16535
31	324.4	23.6	1319	22	AAV34790
32	324.4	23.6	1319	24	ABV64125
33	324.4	23.6	2597	19	AAV44807
34	311.4	22.7	313	19	AAV46493
35	276	20.1	437	22	ABA44441
36	276	20.1	437	22	ABA54888
37	276	20.1	437	22	ABA24654
38	276	20.1	437	22	AAK03164
39	276	20.1	437	22	AAK28614
40	276	20.1	437	22	AAI13188
41	276	20.1	437	22	AAI34540
42	276	20.1	437	22	AAI03093
43	276	20.1	437	23	ABS28210
44	276	20.1	437	24	ABS03125
45	196.2	14.3	203	16	AAV21949

ALIGNMENTS

RESULT 1

AAV52969

ID AAV52969 standard; cDNA; 1373 BP.

XX AAV52969;

AC AAV52969;

XX 11-JAN-1999 (first entry)

XX Human G1 protein isoform beta (CASH-beta) cDNA.

XX DE Human G1 protein isoform beta (CASH-beta) cDNA.
XX KW G1 protein; CASH-beta; human; caspase homologue; Fas receptor;
KW modulator; apoptosis; cell death; inflammation; tumour; HIV;
KW therapy; ss.
XX OS Homo sapiens.
XX FH Key
XX FT CDS
XX FT Location/Qualifiers
XX FT 482..1137
XX FT /*tag= a

XX WO9839435-A1.

XX PD 11-SEP-1998.

XX PF 26-FEB-1998; 98WO-IL00098.

XX PR 01-MAY-1997; 97IL-0120759.

XX PR 03-MAR-1997; 97IL-0120367.

XX PA (YEDA) YEDA RES & DEV CO LTD.

XX

PI Brodianski V, Goltsev Y, Kovalenko A, Varfolomeev E, Wallach D;
XX WPI; 1998-495842/42.
DR P-PSDB; AAW78904.
XX New DNA encoding isoforms of G1 protein which bind MORT-1 - and
PT regulate the effects of FAS and tumour necrosis factor receptors,
PT useful for killing of cells e.g. HIV and cancer cells
XX
XX Claim 4; Fig 2; 132pp; English.
XX This cDNA sequence codes for the beta isoform (see AAW78904) of novel
CC human G1 protein. It was isolated from a human skin fibroblast
CC cDNA library using a cDNA probe corresponding to the G1 sequence.
CC G1-beta (also called CASH beta, CASH being caspase homologue)
CC and a longer isoform, G1-alpha (see AAW78903), represent 2 splice
CC variants of the G1 protein. These G1 proteins are capable of
CC binding to, or interacting directly or indirectly, with MORT-1
CC or with MORT-binding proteins such as Mch4 (CASP-10) and MACH
CC (CASP-8), and thereby of binding to the intracellular domain of
CC the FAS-R receptor, to which MORT-1 binds, or of binding to the
CC intracellular domain of the p55 tumour necrosis factor (TNF)
CC receptor, to which TRADD binds and to which TRADD protein MORT-
CC 1 binds. Hence, they are considered as mediators or modulators of
CC FAS-R having a role in e.g. the signalling process that is initiated
CC by the binding of FAS ligand to FAS-R, and also having a role in
CC the signalling process initiated by the binding of TNF to p55-R.
CC G1 DNA (I) and polypeptide (II), vectors and fragments are used to
CC regulate cell death or inflammatory processes. (II) is used to
CC inhibit cell death, and its inhibitors augment/enhance the
CC processes. (I) and (II) regulate the FAS-R ligand or TNF effect on
CC cells carrying an FAS-R or p55-R. Tumour, HIV-infected or other
CC diseased cells can be treated using a viral vector encoding a viral
CC surface protein, which binds a specific cell surface receptor and a
CC sequence encoding (II), which kills the cell. Antisense
CC oligonucleotides, introduced using the above vector, block the
CC expression of (II), and can also regulate the above effects. These
CC effects can also be regulated using a vector encoding a ribozyme
CC that interacts with a cellular mRNA encoding (II), and allows (II)
CC expression.
XX
SQ Sequence 1373 BP; 417 A; 283 C; 335 G; 338 T; 0 other;

Query Match	100.0%;	Score 1373;	DB 19;	Length 1373;	
Best Local Similarity	100.0%;	Pred. No. 1.4e-222;			
Matches 1373;	Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	GGAGCTCGAGCGATTACAAATCGGAAACCAAGCCATGACATGAACACAGCGAGCTTGCAGC	60		
DB	1	GGAGCTCGAGCGATTACAAATCGGAAACCAAGCCATGACATGAACACAGCGAGCTTGCAGC	60		
QY	61	CTCACCGCAGAGTCTCAACTAAAAGGGGACTCCCGGAGGTAGGGGTGGGGAATCGGCGCTCA	120		
DB	61	CTCACCGCAGAGTCTCAACTAAAAGGGGACTCCCGGAGGTAGGGGTGGGGAATCGGCGCTCA	120		
QY	121	CACAGTGAAGTCCCGGCTATTGGACATTTGTCCAGTCAGCTGAGACAGCAACAGGACCACG	180		
DB	121	CACAGTGAAGTCCCGGCTATTGGACATTTGTCCAGTCAGCTGAGACAGCAACAGGACCACG	180		
QY	181	GGAGGAGGTGTAGGAGAAAGCCGCGAAACAGCGATCGCCAGACCAACAGTCCGCTTCC	240		
DB	181	GGAGGAGGTGTAGGAGAAAGCCGCGAAACAGCGATCGCCAGACCAACAGTCCGCTTCC	240		
QY	241	AGGCTTTTCGGTTCCTTTCCTCCATCTTGGGTGCGCCTTCCCGGGCGTCTAGGGGAGCGAA	300		
DB	241	AGGCTTTTCGGTTCCTTTCCTCCATCTTGGGTGCGCCTTCCCGGGCGTCTAGGGGAGCGAA	300		
QY	301	GGCTGAGGTGGCAGCGGAGGAGTCCGGCCGCGACAGAGCAACTCCCCCAGTGGAA	360		
DB	301	GGCTGAGGTGGCAGCGGAGGAGTCCGGCCGCGACAGAGCAACTCCCCCAGTGGAA	360		
QY	361	GGATTCTGAAGAAATGAAGTCAGGCCCTCAGAAATGAAGTTGACTGCCTGCTGGGCTTCC	420		

XX 02-AUG-1999 (first entry)
XX Human MACH related inducer of toxicity MRIT beta 1 DNA.
XX
XX
XX MRIT beta 1; MACH related inducer of toxicity; human; apoptosis;
KW pro-apoptotic; cancer; autoimmune disease; infection; angiogenesis;
KW atherosclerosis; neurodegenerative disease; Alzheimer's disease;
KW Parkinson's disease; retinitis pigmentosa; stroke; AIDS;
KW aplastic anaemia; myocardial infarction; therapy; ss.
XX
XX Homo sapiens.
XX
XX
XX Key Location/Qualifiers
FH CDS 435..1100
FT /*tag= a
FT
XX
XX WO918230-A2.
XX
XX
XX 15-APR-1999.
XX
XX 07-OCT-1998; 98WO-US21132.
XX
XX 07-OCT-1997; 97US-0946226.
XX
XX (UNIW) UNIV WASHINGTON.
XX
XX Chaudhary PM;
XX
XX WPI: 1999-277275/23.
XX P-PSDB; AAY05789.
XX
XX Identifying regulators of MACH-related inducer of toxicity
XX
XX Example 1; Fig 1H; 78pp; English.
XX
XX The present sequence represents DNA coding for MACH-related inducer
CC of toxicity (MRIT) isoform MRIT beta 1 (see AAY05789), a CED-4
CC homologue that has pro-apoptotic activity. An EST sequence having
CC homology to the p20 domain of human ICE-like protease MACH1/FLICE
CC was isolated from an EST database. Several overlapping EST clones
CC were sequenced to deduce the sequence of the full-length MRIT alpha
CC 1 clone (see AAX25508) and 2 isoforms, alpha 2 (see AAX25509) and beta
CC 1. The MRIT gene was localised to the human chromosome 2q32-33
CC region. MRIT beta 1 lacks the N-terminal death effector domain
CC of MRIT alpha 1. Selective enhancers and inhibitors of MRIT
CC apoptotic activity can be identified and used to treat diseases
CC mediated by the dysfunction of programmed cell death or
CC proliferation. In addition, nucleic acid molecules encoding
CC pro-apoptotic isoforms of MRIT can also be used as inducers of
CC programmed cell death. A cell accumulation disorder such as
CC cancer, autoimmune disease, viral infection, angiogenesis and
CC atherosclerosis is treated by administering an agent that
CC selectively enhances MRIT apoptotic activity, thereby inducing
CC apoptosis in a subject. A disorder of cell loss, such as a
CC neurodegenerative disorder, including Alzheimer's disease,
CC Parkinson's disease, retinitis pigmentosa, stroke, aplastic
CC anaemia, myocardial infarction or AIDS can be treated by
CC administering an agent that selectively inhibits MRIT apoptotic
CC activity.
XX
XX Sequence 1308 BP; 367 A; 275 C; 330 G; 334 T; 2 other;
XX
XX Query Match 93.0%; Score 1276.6; DB 20; Length 1308;
XX Best Local Similarity 99.5%; Pred. No. 2.5e-206;
XX Matches 1290; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
XX
XX 47 ACCGAGCTTGCAGCCTCACCGAGAGTCTCAACTAAAGGGGACTCCCGAGCTAGGGGTG 106
XX
XX 1 ACCGAGCTTGCAGCCTCACCGAGAGTCTGAGNCTAAAGGGGACTCCCGAGCTAGGGGTG 60
XX
XX 107 GGGACTCGGCTCACACAGTGTAGTCCGGCTATTGGACTTTTGTCCAGTGTGAGTGTGAG 166
XX
XX
XX

Db 61 GGGACTCGGCTCACACAGTGTAGTCCCGCTATTGGACTTTTGTCCAGTGTGAGTGTGAGA 120
QY 167 CAACAAGGACCAACGAGGAGGTGTAGGAGAAAGCGCGGAGAGGATGCGCCAGCA 226
Db 121 CAACAAGGACCAACGAGGAGGTGTAGGAGAAAGCGCGGAGAGGATGCGCCAGCA 180
QY 227 CCAAGTCCGCTTCCAGGCTTTTCGGTTTCTTTCCTCCATCTTTCCTCCATCTTTCCTCCGCTTCCGCGG 286
Db 181 CCAAGTCCGCTTCCAGGCTTTTCGGTTTCTTTCCTCCATCTTTCCTCCGCTTCCGCGG 240
QY 287 TCTAGGGAGGCAAGCTGTAGGTGCGAGGCGGAGAGTGTCCGCGGCGGAGGAGGAC 346
Db 241 TCTAGGGAGGCAAGCTGTAGGTGCGAGGCGGAGAGTGTCCGCGGCGGAGGAGGAC 300
QY 347 TCCCCCACTGGAAAGGATTTCTGAAAGAAATGAAGTCAGCCCTCAGAAATGAAGTTGACTG 406
Db 301 TCCCCCACTGGAAAGGATTTCTGAAAGAAATGAAGTCAGCCCTCAGAAATGAAGTTGACTG 360
QY 407 CCTGCTGGCTTTCTTCTGTGACTGCGCGGAGGTGTACTGCAAGACCCCTTGTGAGCTTCC 466
Db 361 CCTGCTGGCTTT - CTGTTGACTGCGCGGAGGTGTACTGCAAGACCCCTTGTGAGCTTCC 419
QY 467 TAGTCTAAGAGTAGGATGCTGCTGAAGTCATCCATCAGTTTGAAGAACACTTGTATACA 526
Db 420 TAGTCTAAGAGTAGGATGCTGCTGAAGTCATCCATCAGTTTGAAGAACACTTGTATACA 479
QY 527 GATGAGAGGAGATGCTGCTCTTTTGTGCGGGGATTTGCTATAGATGTGCTCCACCT 586
Db 480 GATGAGAGGAGATGCTGCTCTTTTGTGCGGGGATTTGCTATAGATGTGCTCCACCT 539
QY 587 AATGTCAGGGACCTTCTTGATATTTTACGGGAAAGAGGTGAAGTGTCTCTCGGGGACTTG 646
Db 540 AATGTCAGGGACCTTCTTGATATTTTACGGGAAAGAGGTGAAGTGTCTCTCGGGGACTTG 599
QY 647 GCTGAAGTCTCTACAGAGTGTAGGCGATTTGACCTGCTCAACAGTATCTTGAAGATGAC 706
Db 600 GCTGAAGTCTCTACAGAGTGTAGGCGATTTGACCTGCTCAACAGTATCTTGAAGATGAC 659
QY 707 AGAAAGTGTGTGAGACCCACCTGCTCAGGAACCCCTCAGCTTTGTCGAGCTATAGAGTG 766
Db 660 AGAAAGTGTGTGAGACCCACCTGCTCAGGAACCCCTCAGCTTTGTCGAGCTATAGAGTG 719
QY 767 CTGATGGCAGAGTGTGTGAGGATTTGGATAAATCTGATGTCTCTCATTAATTTTCTC 826
Db 720 CTGATGGCAGAGTGTGTGAGGATTTGGATAAATCTGATGTCTCTCATTAATTTTCTC 779
QY 827 ATGAAGGATTACATGGCGGAGCAAGATAAGCAAGGAGAGGTTTCTTGGACCTTGTG 886
Db 780 ATGAAGGATTACATGGCGGAGCAAGATAAGCAAGGAGAGGTTTCTTGGACCTTGTG 839
QY 887 GTTGAGTTGGAGAAACTAAATTTGGTTGCCCCAGATCAACTGGATTTATTAGAAAATGC 946
Db 840 GTTGAGTTGGAGAAACTAAATCTGTTGCCCCAGATCAACTGGATTTATTAGAAAATGC 899
QY 947 CTAAAGACATCCAGAGATAGACCTGGAAGACAAATAATCCAGAGTACAGAGTGTGTT 1006
Db 900 CTAAAGACATCCAGAGATAGACCTGGAAGACAAATAATCCAGAGTACAGAGTGTGTT 959
QY 1007 CAAGGAGGAGGACAAAGTTACAGGATGTCTTCCAGGAGCAATCCAAAGAGTGTCTCAAG 1066
Db 960 CAAGGAGGAGGACAAAGTTACAGGATGTCTTCCAGGAGCAATCCAAAGAGTGTCTCAAG 1019
QY 1067 GATCTCTCAATAACTTTCAGGATGATTAACACCCCTATGCCATTTGCTGATCTGAAAAT 1126
Db 1020 GATCTCTCAATAACTTTCAGGATGATTAACACCCCTATGCCATTTGCTGATCTGAAAAT 1079
QY 1127 CTTGGAATTTGTTCCATGTATTAACTAGAACTGCCTCTACTTAATCATTTCTGAATGAT 1186
Db 1080 CTTGGAATTTGTTCCATGTATTAACTAGAACTGCCTCTACTTAATCATTTCTGAATGAT 1139
QY 1187 TAAATCGTTTCATTTCTAAATGTATTAAATGTGTTAGCCCTTTCTTGTGCTGTATG 1246
Db 1140 TAAATCGTTTCATTTCTAAATGTATTAAATGTGTTAGCCCTTTCTTGTGCTGTATG 1199

QY 1247 TTTAGATGCTTCCAAATCTTTTCTTACTATAATGCTATAATAAATAATTCCTTGA 1306
Db 1200 TTTAGATGCTTCCAAATCTTTTCTTACTATAATGCTATAATAAATAATTCCTTGA 1259
QY 1307 CTTCTTAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1342
Db 1260 CTTCTTAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1295

RESULT 3
AAV52968 standard; cDNA; 2243 BP.
XX AAV52968;
XX 11-JAN-1999 (first entry)
XX Human G1 protein isoform alpha (CASH-alpha) cDNA.
XX G1 protein; CASH-alpha; human; caspase homologue; Fas receptor;
KW modulator; apoptosis; cell death; inflammation; tumour; HIV;
KW therapy; ss.
XX Homo sapiens.
OS
FH Key Location/Qualifiers
FT CDS 482..1294
FT /*tag= a
XX WO9839435-A1.
XX 11-SEP-1998. 98WO-IL00098.
XX 26-FEB-1998;
XX 01-MAY-1997; 97IL-0120759.
XX 03-MAR-1997; 97IL-0120367.
XX (YEDA) YEDA RES & DEV CO LTD.
XX Brodianski V, Goltsev Y, Kovalenko A, Varfolomeev E;
XX Wallach D;
XX WPI: 1998-495842/42.
XX P-PSDB; AAW78903.
XX New DNA encoding isoforms of G1 protein which bind MORT-1 - and
XX regulate the effects of Fas and tumour necrosis factor receptors,
XX useful for killing of cells e.g. HIV and cancer cells
XX Claim 3; Fig 1A; 132pp; English.

XX This cDNA sequence codes for the alpha isoform (see AAW78903) of novel
XX human G1 protein. It was isolated from a skin fibroblast cDNA
XX library using a cDNA probe corresponding to the G1 sequence.
XX G1-alpha (also called CASH alpha, CASH being caspase homologue)
XX and a shorter isoform, G1-beta (see AAW78904), represent 2 splice
XX variants of the G1 protein. These G1 proteins are capable of
XX binding to, or interacting directly or indirectly, with MORT-1
XX or with MORT-binding proteins such as Mch4 (CASP-10) and MACH
XX (CASP-8), and thereby of binding to the intracellular domain of
XX the Fas-R receptor, to which MORT-1 binds, or of binding to the
XX intracellular domain of the p55 tumour necrosis factor (TNF)
XX receptor, to which TRADD binds and to which TRADD protein MORT-
XX 1 binds. Hence, they are considered as mediators or modulators of
XX Fas-R having a role in e.g. the signalling process that is initiated
XX by the binding of Fas ligand to Fas-R, and also having a role in
XX the signalling process initiated by the binding of TNF to p55-R.
XX G1 DNA (I) and polypeptide (II), vectors and fragments are used to
XX regulate cell death or inflammatory processes. (II) is used to
XX inhibit cell death, and its inhibitors augment/enhance the
XX processes. (I) and (II) regulate the Fas-R ligand or TNF effect on

CC cells carrying an FAS-R or p55-R. Tumour, HIV-infected or other
CC diseased cells can be treated using a viral vector encoding a viral
CC surface protein, which binds a specific cell surface receptor and a
CC sequence encoding (II), which kills the cell. Antisense
CC oligonucleotides, introduced using the above vector, block the
CC expression of (II) and can also regulate the above effects. These
CC effects can also be regulated using a vector encoding a ribozyme
CC that interacts with a cellular mRNA encoding (II), and allows (II)
CC expression.
XX
SQ Sequence 2243 BP; 620 A; 511 C; 603 G; 509 T; 0 other;
Query Match 79.2%; Score 1087.4; DB 19; Length 2243;
Best Local Similarity 99.9%; Pred. No. 1.9e-174;
Matches 1088; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGACGTCGAGGCTTACATCGGAACCAAGCCATAGCATGAAACAGAGCTTCGACG 60
Db 1 GGACGTCGAGGCTTACATCGGAACCAAGCCATAGCATGAAACAGAGCTTCGACG 60
QY 61 CTCACGACGAGTCTCACTAAAGGGACTCCCGGAGCTAGGGTGGGACTTCGGCTCA 120
Db 61 CTCACGACGAGTCTCACTAAAGGGACTCCCGGAGCTAGGGTGGGACTTCGGCTCA 120
QY 121 CACAGTGAGTGCCTGCTATTTGACTTTTGTCCAGTGACAGCTCAGACACAGGACG 180
Db 121 CACAGTGAGTGCCTGCTATTTGACTTTTGTCCAGTGACAGCTCAGACACAGGACG 180
QY 181 GGAGGAGGTGTAGGAGAGAGCGCCGCAACAGCAGATCCCGAGCAACCAAGTCCG 240
Db 181 GGAGGAGGTGTAGGAGAGAGCGCCGCAACAGCAGATCCCGAGCAACCAAGTCCG 240
QY 241 AGGCTTTCGGTTCCTTTTGGCTCCATCTTGGGTGGCTTCCCGGCTCTAGGGGCGAA 300
Db 241 AGGCTTTCGGTTCCTTTTGGCTCCATCTTGGGTGGCTTCCCGGCTCTAGGGGCGAA 300
QY 301 GGCTGAGGTGGCAGCGAGGAGTCCGGCCCGACAGAGCAAGTCCCGGCTCTAGGGG 360
Db 301 GGCTGAGGTGGCAGCGAGGAGTCCGGCCCGACAGAGCAAGTCCCGGCTCTAGGGG 360
QY 361 GGATTCCTGAAAGAAATGAAGTCAAGCTCAGCCCTCAGAAATGAAGTTCCTGCTG 420
Db 361 GGATTCCTGAAAGAAATGAAGTCAAGCTCAGCCCTCAGAAATGAAGTTCCTGCTG 420
QY 421 TGTGACTGCGCGGAGCTGCTGCTGCAAGACCTTGTGAGCTTCCCTAGTCTAAGAGTAG 480
Db 421 TGTGACTGCGCGGAGCTGCTGCTGCAAGACCTTGTGAGCTTCCCTAGTCTAAGAGTAG 480
QY 481 GATGCTGCTGAAGTATCCATCAGTGTGAAGAGCATTGTGATACAGATGAGAAGGAGAT 540
Db 481 GATGCTGCTGAAGTATCCATCAGTGTGAAGAGCATTGTGATACAGATGAGAAGGAGAT 540
QY 541 GCTGCTCTTTTGTGCGGGATGTTGCTATAGATGTTGTTCCACCTAATCTCAGGGACCT 600
Db 541 GCTGCTCTTTTGTGCGGGATGTTGCTATAGATGTTGTTCCACCTAATCTCAGGGACCT 600
QY 601 TCTGATATTTTACGGGAAAGAGTAAGTGTCTGTCGGGAGCTTGGCTGAAGTCTCTA 660
Db 601 TCTGATATTTTACGGGAAAGAGTAAGTGTCTGTCGGGAGCTTGGCTGAAGTCTCTA 660
QY 661 CAGAGTGAGGGGATTTGACCTGCTCAACGATCTTCAAGATGACAGAGAAAGCTGTGA 720
Db 661 CAGAGTGAGGGGATTTGACCTGCTCAACGATCTTCAAGATGACAGAGAAAGCTGTGA 720
QY 721 GACCCCTGCTCAGGAAACCTCACCCTGTTTTCGAGCTATAGAGTGTGATGGCAGAGAT 780
Db 721 GACCCCTGCTCAGGAAACCTCACCCTGTTTTCGAGCTATAGAGTGTGATGGCAGAGAT 780
QY 781 TGGTGAGGATTTGGATAAATCTGATGTCTCTCATTAATTTTCTCATGAGGAGTACAT 840
Db 781 TGGTGAGGATTTGGATAAATCTGATGTCTCTCATTAATTTTCTCATGAGGAGTACAT 840
QY 841 GGGCCCGCAAGATAAGCAAGGAGAGAGTCTTCTTGGACCTTGTGTTGAGTTGGAGAA 900

Db 841 GGGCCGAGCAAGTAAGCAAGAGAGTTTCTTGGACCTGTGGTTGAGTTGGAGAA 900
QY 901 ACTAAATTTGGTTGGCCAGATCAACTGGATTATTAGAAAAATGCTAAAGAACATCCA 960
Db 901 ACTAAATTTGGTTGGCCAGATCAACTGGATTATTAGAAAAATGCTAAAGAACATCCA 960
QY 961 CAGATAGACCTGAGACAAAAATCCAGAAAGTACAGAGTCTGTTCAAGGAGCAGGAC 1020
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QY 1021 AAGTTACAGGAATGTTCTCAAGCAGCAATCCAAAGAGTCTCAAGGATCCTCAATAA 1080
Db 1021 AAGTTACAGGAATGTTCTCAAGCAGCAATCCAAAGAGTCTCAAGGATCCTCAATAA 1080
QY 1081 CTTCAGGAT 1089
Db 1081 CTTCAGGCT 1089
RESULT 4
AAZ47926
ID AAZ47926 standard; cDNA; 2352 BP.
XX
AC AAZ47926;
XX
DT 10-MAR-2000 (first entry)
DE Human apoptosis associated protein HAPOP-1 encoding cDNA.
XX
KW Human; apoptosis associated protein; HAPOP; diagnosis; cytostatic;
KW antiarteriosclerotic; antiarthritic; hepatotropic; apoptosis regulator;
KW cell proliferative disorder; atherosclerosis; arteriosclerosis; cancer;
KW immune disorder; rheumatoid arthritis; systemic lupus erythematosus;
KW reproductive disorder; tumour; gastrointestinal disorder; cirrhosis;
KW colitis; hepatitis; pancreatitis; ss.
XX
OS Homo sapiens.
XX
PN WO9558692-A2.
XX
PD 18-NOV-1999.
PD
PF 11-MAY-1999; 99WO-US10386.
PF
PR 13-MAY-1998; 98US-0078402.
PR
XX (INCY-) INCYTE PHARM INC.
XX
PI Hillman JL, Corley NC, Guegler KJ, Patterson C, Baughn M;
PI
DR WPI; 2000-062303/05.
DR
DR P-PSDB; AAY57606.
XX
PT New protein for diagnosing, treating or preventing disorders associated
PT with increased or decreased apoptosis -
XX
PS Claim 7; Page 71-72; 81pp; English.
XX
CC The present sequence encodes a human apoptosis associated protein
CC designated HAPOP-1. HAPOP proteins are apoptosis regulators which have
CC antiarteriosclerotic, cytostatic, antiarthritic and hepatotropic
CC activity. A pharmaceutical composition comprising HAPOP in conjunction
CC with a carrier, a purified antagonist of HAPOP, vectors and agonists of
CC HAPOP, are administered for diagnosing, treating or preventing disorders
CC associated with increased or decreased apoptosis, e.g. cell proliferative
CC disorders such as atherosclerosis, arteriosclerosis and cancers; immune
CC disorders such as rheumatoid arthritis, systemic lupus erythematosus;
CC reproductive disorders such as prostate cancer, endometrial and ovarian
CC tumours; and gastrointestinal disorders such as cirrhosis, colitis,
CC hepatitis and pancreatitis. The polynucleotides encoding HAPOP proteins
CC may be useful to detect and quantitate expression of HAPOP genes which
CC are correlated with diseases and are also useful to detect differences

CC in the chromosomal location due to translocation, inversion etc., among
CC normal, carrier, or affected individuals. The combination of the
CC therapeutic agents may act synergistically to effect the treatment or
CC prevention of various disorders providing improved efficacy with lower
CC dosages of each agent and thus reducing the potential for adverse side
CC effects.
XX
SQ Sequence 2352 BP; 652 A; 546 C; 628 G; 526 T; 0 other;
Query Match 76.1%; Score 1044.4; DB 21; Length 2352;
Best Local Similarity 98.9%; Pred. No. 3 4e-167;
Matches 1062; Conservative 0; Mismatches 11; Indels 1; Gaps 1;
QY 16 ACAATCGGAAACCAAGCCATAGCATGAAACAGCAGCTTGACGCTCCACGACGAGTCT 75
Db 147 ATACTCAGTCACACAAAGCCATAGCAGGAAACAGCAGCTTGACGCTCCACGACGAGTCT 206
QY 76 CAACTAAAAGGAGACTCCCGAGCTAGGGTGGGACTCGGCTCACACAGTGAAGTCCGG 135
Db 207 CAACTAAAAGGAGACTCCCGAGCTAGGGTGGGACTCGGCTCACACAGTGAAGTCCGG 266
QY 136 CTATTGGACTTTTGTCCAGTGCAGCTGAGACAAAGAGCAGCAGGAGGAGGTAGGA 195
Db 267 CTATTGGACTTTTGTCCAGTGCAGCTGAGACAAAGAGCAGCAGGAGGAGGTAGGA 326
QY 196 GAGAAGCGCGGAACAGCAGATGCCAGCACCAAGTCCGCTTCCAGGCTTTCCGGTTCT 255
Db 327 GAGAAGCGCGGAACAGCAGATGCCAGCACCAAGTCCGCTTCCAGGCTTTCCGGTTCT 386
QY 256 TTGCTCCATCTGGGTGGCCCTTCCGGCTTAGGGAGCGAAGCTGAGGTGGCAGC 315
Db 387 TTGCTCCATCTGGGTGGCCCTTCCGGCTTAGGGAGCGAAGCTGAGGTGGCAGC 446
QY 316 GGCAGGAGAGTCCGGCGGACAGAGCAAGTCCGCCACTGGAAGAGATCTCAAGAGAA 375
Db 447 GGCAGGAGAGTCCGGCGGACAGAGCAAGTCCGCCACTGGAAGAGATCTCAAGAGAA 506
QY 376 TGAAGTCAGCCCTCAAGAAATGAAGTTGACTGCTGCTGGCTTCTGTTGACTGGCCCG 435
Db 507 TGAAGTCAGCCCTCAGAAATGAAGTTGACTGCTGCTGGCTTCTGTTGACTGGCCCG 565
QY 436 AGCTGTACTGCAAGACCCCTTGTGAGCTTCCCTAGTCTAAGTAGTAGTCTCTCTCTAG 495
Db 566 AGCTGTACTGCAAGACCCCTTGTGAGCTTCCCTAGTCTAAGTAGTAGTCTCTCTCTAG 625
QY 496 CATCCATCAGGTTGAAGAACACACTTCATACAGATGAGAGGAGATGCTGCTCTTTGTG 555
Db 626 CATCCATCAGGTTGAAGAACACACTTCATACAGATGAGAGGAGATGCTGCTCTTTGTG 685
QY 556 CCGGGATGTTGCTATAGATGTGGTCCACTAATGTACAGGACCTTCTGGATATTTTACG 615
Db 686 CCGGGATGTTGCTATAGATGTGGTCCACTAATGTACAGGACCTTCTGGATATTTTACG 745
QY 616 GGAAGCAGGTAGCTGCTGCGGACCTGGCTGAAGTCTCTACAGAGTGGAGGATTT 675
Db 746 GGAAGCAGGTAGCTGCTGCGGACCTGGCTGAAGTCTCTACAGAGTGGAGGATTT 805
QY 676 TGACCTGCTCAAAACGATATCTTGAAGATGGACAGAAAAGCTGTGGAGACCCACCTCAG 735
Db 806 TGACCTGCTCAAAACGATATCTTGAAGATGGACAGAAAAGCTGTGGAGACCCACCTCAG 865
QY 736 GAACCTCAGCTTGTTCGGACTATAGATGTGCTGATGGCAGAGATTTGGTGAAGATTGGA 795
Db 866 GAACCTCAGCTTGTTCGGACTATAGATGTGCTGATGGCAGAGATTTGGTGAAGATTGGA 925
QY 796 TAAATCTGATGTCTCTCAATTAATTTCTCATGAAGATTAACATGGCCGAGGCAAGAT 855
Db 926 TAAATCTGATGTCTCTCAATTAATTTCTCATGAAGATTAACATGGCCGAGGCAAGAT 985
QY 856 AAGCAAGGAGAGAGTCTTCTTGACCTTGTGGTGGAGTGGAGAACTAAATTTGGTTGC 915
Db 986 AAGCAAGGAGAGAGTCTTCTTGACCTTGTGGTGGAGTGGAGAACTAAATCTGGTTGC 1045

Db 901 CTAAGAACATCCACAGATAGACCTGAAGACACAAAAATCCAGAGTACAGAGCTCTGTT 960
QY 1007 CRAAGGACGGGACAAAGTTACAGGAATGTTCTCAAGCAGCAATCCAAAGAGCTCTCAAG 1066
Db 961 CRAAGGACGGGACAAAGTTACAGGAATGTTCTCAAGCAGCAATCCAAAGAGCTCTCAAG 1020
QY 1067 GATCCTTCAAAATACCTCAGGAT 1089
Db 1021 GATCCTTCAAAATACCTCAGGCT 1043

RESULT 6

AA25508
ID AAX25508 standard; DNA; 1996 BP.

XX AC AAX25508;

XX DT 02-AUG-1999 (first entry)

XX DE Human MACH related inducer of toxicity MRIT alpha 1 DNA.

XX KW MRIT alpha 1; MACH related inducer of toxicity; human; apoptosis;
KW pro-apoptotic; cancer; autoimmune disease; infection; angiogenesis;
KW atherosclerosis; neurodegenerative disease; Alzheimer's disease;
KW Parkinson's disease; retinitis pigmentosa; stroke; AIDS;
KW aplastic anaemia; myocardial infarction; therapy; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
XX CDS 435..1877
XX /tag= a

XX PN WO9918230-A2.

XX PD 15-APR-1999.

XX PF 07-OCT-1998; 98WO-US211132.

XX PR 07-OCT-1997; 97US-0946226.

XX PT (UNIW) UNIV WASHINGTON.

XX PA Chaudhary PM;

XX DR WPI; 1999-277275/23.

XX DR P-PSDB; AAY05787.

XX PT Identifying regulators of MACH-related inducer of toxicity

XX PS Example 1; Fig 1F; 78pp; English.

XX CC The present sequence represents DNA coding for MACH-related inducer
CC of toxicity (MRIT) isoform MRIT alpha 1 (see AAY05787), a CED-4
CC homologue that interacts simultaneously with caspases and Bcl-2
CC family polypeptides, and which has pro-apoptotic activity. An EST
CC sequence having homology to the p20 domain of human ICE-like
CC protease MACH1/FLICE was isolated from an EST database. Several
CC overlapping EST clones were sequenced to deduce the sequence of
CC the full-length MRIT alpha 1 clone and 2 isoforms, alpha 2 (see
CC AAX25509) and beta 1 (see AAX25510). The MRIT gene was localised to
CC the human chromosome 2q32-33 region. MRIT alpha 1 includes an
CC N-terminal death effector domain and a C-terminal caspase homology
CC domain, but is not a cysteine protease. Selective enhancers and
CC inhibitors of MRIT apoptotic activity can be identified and used
CC to treat diseases mediated by the dysfunction of programmed cell
CC death or proliferation. In addition, nucleic acid molecules
CC encoding pro-apoptotic isoforms of MRIT can also be used as
CC inducers of programmed cell death. A cell accumulation disorder
CC such as cancer, autoimmune disease, viral infection, angiogenesis
CC and atherosclerosis is treated by administering an agent that
CC selectively enhances MRIT apoptotic activity, thereby inducing
CC apoptosis in a subject. A disorder of cell loss, such as a

CC neurodegenerative disorder, including Alzheimer's disease,
CC Parkinson's disease, retinitis pigmentosa, stroke, aplastic
CC anaemia, myocardial infarction or AIDS can be treated by
CC administering an agent that selectively inhibits MRIT apoptotic
CC activity.
XX Sequence 1996 BP; 543 A; 461 C; 540 G; 451 T; 1 other;
SQ Query Match 74.8%; Score 1026.8; DB 20; Length 1996;
Best Local Similarity 99.6%; Pred. No. 3.le-164;
Matches 1039; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
QY 47 AGCGAGCTTGCAGCCTCACGACGAGTCTCAACATAAAGGAGTCCCGGAGCTAGGGGTG 106
Db 1 AGCGAGCTTGCAGCCTCACGACGAGTCTCAACATAAAGGAGTCCCGGAGCTAGGGGTG 60
QY 107 GGGACTCGGCCTCACACAGTGTAGTGGCGCTATTGGACTTTTCTCCAGTACACGCTGAGA 166
Db 61 GGGACTCGGCCTCACACAGTGTAGTGGCGCTATTGGACTTTTCTCCAGTACACGCTGAGA 120
QY 167 CAACAAGGACCCAGGAGGAGTGTAGGAGAGAGCGCCGCAACAGCGATCCGCCAGCA 226
Db 121 CAACAAGGACCCAGGAGGAGTGTAGGAGAGAGCGCCGCAACAGCGATCCGCCAGCA 180
QY 227 CCAAGTCCGCTTCCAGGCTTTCGGTTTCTTTCGCTCCATCTTGGGTGCGCTTCCCGGCG 286
Db 181 CCAAGTCCGCTTCCAGGCTTTCGGTTTCTTTCGCTCCATCTTGGGTGCGCTTCCCGGCG 240
QY 287 TCTAGGGAGCGAAGGCTGAGTGGCGGAGGAGAGTCCCGCGCGACAGCGAAGCAAC 346
Db 241 TCTAGGGAGCGAAGGCTGAGTGGCGGAGGAGAGTCCCGCGCGACAGCGAAGCAAC 300
QY 347 TCCCCCAGCTGGAAGAGTCTGAAAGAAATGAAGTACGCCCTCAGAAATGAAGTTGACTG 406
Db 301 TCCCCCAGCTGGAAGAGTCTGAAAGAAATGAAGTACGCCCTCAGAAATGAAGTTGACTG 360
QY 407 CTTGCTGGCTTTCCTGTGTACTGGCGGAGCTGTACTCAAGACCCCTTGTGAGCTTCCC 466
Db 361 CTTGCTGGCTTTCCTGTGTACTGGCGGAGCTGTACTCAAGACCCCTTGTGAGCTTCCC 419
QY 467 TAGTCTAAGAGTAGGATGCTGCTGAAGTCAATCAGGTTGAAGAGCAGTGTATACA 526
Db 420 TAGTCTAAGAGTAGGATGCTGCTGAAGTCAATCAGGTTGAAGAGCAGTGTATACA 479
QY 527 GATGAGAAGGAGATGCTGCTTCTTTTGTGCGGGATGTTGCTATAGATGTGGTTCCACCT 586
Db 480 GATGAGAAGGAGATGCTGCTTCTTTTGTGCGGGATGTTGCTATAGATGTGGTTCCACCT 539
QY 587 AATGTCAGGGACCTTCTGGATATTTTACGGGAAGAGGTAAGCTGTCTGCGGGAGCTTG 646
Db 540 AATGTCAGGGACCTTCTGGATATTTTACGGGAAGAGGTAAGCTGTCTGCGGGAGCTTG 599
QY 647 GCTGAAGTCTCTACAGAGTGGCGGATTTGACCTGCTCAACGTATCTTTGAGATGGAC 706
Db 600 GCTGAAGTCTCTACAGAGTGGCGGATTTGACCTGCTCAACGTATCTTTGAGATGGAC 659
QY 707 AGAAAAGCTGTGGAGACCCACCTGCTCAGGAACCCCTCACCTTGTTCGGAGTATAGAGTG 766
Db 660 AGAAAAGCTGTGGAGACCCACCTGCTCAGGAACCCCTCACCTTGTTCGGAGTATAGAGTG 719
QY 767 CTGATGGCAGAGATTTGGTGGAGTATTTGGATTAATCTGATGTGCTCATTAATTTTCCCTC 826
Db 720 CTGATGGCAGAGATTTGGTGGAGTATTTGGATTAATCTGATGTGCTCATTAATTTTCCCTC 779
QY 827 ATGAAGGATTTACATGGGCCGAGCAAGATAAGCAAGAGAGTGTCTTGGACCTTGTG 886
Db 780 ATGAAGGATTTACATGGGCCGAGCAAGATAAGCAAGAGAGTGTCTTGGACCTTGTG 839
QY 887 GTTGAGTTGGAGAACTAAATTTGGTTGCCCGAGATCACTGAGTATTTAGAAAATGC 946
Db 840 GTTGAGTTGGAGAACTAAATTTGGTTGCCCGAGATCACTGAGTATTTAGAAAATGC 899
QY 947 CTAAGAACAATCCACAGAAATAGACCTGAAGACAAAAATCCAGAGTACAGAGCTGTGTT 1006

Db 900 CTAAGACATCCAGAGTACAGCTGAAGACAAAATCCAGAAAGTACAGAGTCTGTT 959
QY 1007 CAAGGAGGAGGACAAAGTTACAGGAATCTCTCCAGCAGCAATCCAAAAGAGTCTCAAG 1066
Db 960 CAAGGAGGAGGACAAAGTTACAGGAATCTCTCCAGCAGCAATCCAAAAGAGTCTCAAG 1019
QY 1067 GATCCTTCAAAATACCTCAGGAT 1089
Db 1020 GATCCTTCAAAATACCTCAGGCT 1042

RESULT 7

AAV50436

ID AAV50436 standard; cDNA; 2045 BP.

XX

AC AAV50436;

XX

DT 24-NOV-1998 (first entry)

XX

DE Human Casper gene.

XX

KW Casper gene; caspase-eight-related protein; human; apoptosis; ds.

XX

OS Homo sapiens.

XX

PH Key Location/Qualifiers

FT CDS 511..1953

FT /*tag= a

XX

XX WO9833883-A1.

PN

PD 06-AUG-1998.

XX

XX 05-FEB-1998; 98WO-US02117.

PF

XX 05-FEB-1997; 97US-0795088.

XX

XX (TULA-) TULARIK INC.

PA

PI Goeddel DV, Shu H;

XX

XX WPI; 1998-437440/37.

DR

DR P-PSDB; AAW69715.

XX

XX New Casper protein involved in regulation of apoptosis - used, e.g.

PT

PT to identify specific modulators, identify or isolate similar

PT sequences and in gene therapy

XX

XX Claim 7; Page 21; 29pp; English.

PS

XX This cDNA clone includes a coding region for a novel human protein

CC (see AAW69715), designated Casper (for caspase-eight-related protein),

CC that is involved in regulation of apoptosis. The clone was

CC isolated from a human expressed sequence tag database in a

CC search for potential FADD-related genes. The isolated protein, or

CC cells that express the protein, can be used to screen for agents,

CC e.g. antibodies or T-cell receptors, that specifically modify the

CC binding of Casper to a target, and thus its function. Nucleic acid

CC sequences encoding Casper, or fragments of them, are used e.g. as

CC probes and primers for diagnostic detection of Casper genes and

CC their transcripts, for isolation of related sequences and for

CC identification of wild-type or mutant alleles, also in gene therapy

CC to modulate expression of active Casper protein (using antisense or

CC sense sequences). They are also used for recombinant production of

CC Casper and to generate transgenic animals for testing candidate

CC drugs for Casper-associated diseases.

XX

XX Sequence 2045 BP; 551 A; 475 C; 560 G; 459 T; 0 other;

SQ

Query Match 74.7%; Score 1025.2; DB 19; Length 2045;
Best Local Similarity 99.6%; Pred. No. 5.7e-164;
Matches 1038; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 48 GCGAGCTTCACGCTCACGACGAGTCTCACTAAAGGGAGTCCCGGAGCTCCGGAGCTAGGGTGG 107
Db 78 GAGAGCTTCGACGCTCACGACGAGTCTCACTAAAGGGAGTCCCGGAGCTAGGGTGG 137
QY 108 GGAAGCTCGGCTCACAGTGAAGTGGGCTATTTGGAGCTTTTTCAGTGAAGTGAAGTGAAGT 167
Db 138 GGAAGCTCGGCTCACAGTGAAGTGGGCTATTTGGAGCTTTTTCAGTGAAGTGAAGTGAAGT 197
QY 168 AACAAGGACGAGGAGGAGTGAAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 227
Db 198 AACAAGGACGAGGAGGAGGAGTGAAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 257
QY 228 CAAGTCCGCTTCAGGCTTTTCGCTTTTCGCTTTTCGCTTTTCGCTTTTCGCTTTTCGCTTTTC 287
Db 258 CAAGTCCGCTTCAGGCTTTTCGCTTTTCGCTTTTCGCTTTTCGCTTTTCGCTTTTCGCTTTTC 317
QY 288 CTAGGAGGAGGAGGAGTGAAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 347
Db 318 CTAGGAGGAGGAGGAGTGAAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 377
QY 348 CCCCAGTGGAGGAGGAGTCTGAAAGAGAAATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 407
Db 378 CCCCAGTGGAGGAGGAGTCTGAAAGAGAAATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 437
QY 408 CTGCTGGCTTTCTGTTGAGTGGGAGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 467
Db 438 CTGCTGGCTTTCTGTTGAGTGGGAGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 496
QY 468 AGTCTAGAGTGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 527
Db 497 AGTCTAGAGTGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 556
QY 528 ATGAGAAGGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 587
Db 557 ATGAGAAGGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 616
QY 588 ATGAGAAGGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 647
Db 617 ATGAGAAGGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 676
QY 648 CTGAAGTGTCTACAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 707
Db 677 CTGAAGTGTCTACAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 736
QY 708 GAAAGAGTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 767
Db 737 GAAAGAGTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 796
QY 768 TGATGGCAGAGATTTGGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 827
Db 797 TGATGGCAGAGATTTGGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 856
QY 828 TGAAGGATTAATGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 887
Db 857 TGAAGGATTAATGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 916
QY 888 TTGAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 947
Db 917 TTGAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 976
QY 948 TAAAGAGCATCCACAGATAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1007
Db 977 TAAAGAGCATCCACAGATAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1036
QY 1008 AAGGAG 1067
Db 1037 AAGGAG 1096
QY 1068 ATCCCTTCAAAATACCTTCAGGAT 1089
Db 1097 ATCCCTTCAAAATACCTTCAGGAT 1118

RESULT 8
AAV31375
ID AAV31375 standard; cDNA; 2188 BP.
XX
AC AAV31375;
XX
DT 07-SEP-1998 (first entry)
XX
DE Human FIN-1 encoding cDNA.
XX
KW Human; FIN-1; FLICE inhibitor-1; ICE-LAP7; death effector domain; DED;
KW apoptosis-related protein; caspase; viral infection; cancer; tumour;
KW diagnosis; ischaemic injury; neuro-degenerative disorder; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 422..1864
FT /tag= a
FT /product= "FIN-1"
XX
XX EP841399-A2.
XX
PD 13-MAY-1998.
XX
PF 10-NOV-1997; 97EP-0309003.
XX
PR 12-NOV-1996; 96US-0748086.
XX
PA (SMTK) SMITHKLINE BEECHAM CORP.
XX
PI Emery JG, Kikly K;
XX
DR WPI: 1998-252943/23.
DR P-PSDB; AAW58578.
XX
PT New nucleic acid encoding human apoptosis-related protein - used for
PT diagnosis and treatment of e.g. viral infections, tumour, ischaemic
PT injury and neuro-degenerative disorders
XX
PS Claim 4; Page 22-25; 48pp; English.
XX
CC The present sequence encodes human FIN-1 (FLICE inhibitor-1), which is
CC a caspase. FLICE (ICE-LAP7) is a protease of the interleukin-converting
CC enzyme family, a protein involved in the regulation of cell death. A
CC host cell, comprising a vector containing FIN-1 encoding DNA, can be
CC used to produce FIN-1. The vector containing the DNA can be used for
CC producing a cell which expresses a polypeptide by transforming or
CC transfecting the cell with it so that the cell expresses the polypeptide
CC encoded the human cDNA contained in the vector. The polypeptide or its
CC antagonist can be used in the treatment of patients needing FIN-1 by
CC in-vivo administration. Conditions which may be treated include viral
CC infection, tumours (especially solid tumours), ischaemic injury (e.g.
CC stroke or myocardial infarction), neurodegenerative disorders (e.g.
CC Alzheimer's or Parkinson's disease), osteoporosis, osteoarthritis,
CC polycystic kidney disease, chronic degenerative liver disease, acquired
CC immunodeficiency syndrome (AIDS) and aplastic anaemia. The
CC polynucleotides may also be used for chromosome identification.
XX
SQ Sequence 2188 BP; 606 A; 496 C; 586 G; 500 T; 0 other;

Query Match 73.9%; Score 1014.8; DB 19; Length 2188;
Best Local Similarity 99.7%; Pred. No. 3.3e-162;
Matches 1027; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
QY 60 CCTACCGACGAGTCTCAACTAAAGGGACTCCCGGAGCTAGGGTGGGGACTCGGCCTC 119
DB 1 CCTACCGACGAGTCTCAACTAAAGGGACTCCCGGAGCTAGGGTGGGGACTCGGCCTC 60
QY 120 ACACAGTGAGTCCCGGCTATTGGACTTTGTCCAGTGACAGCTGACACAAAGACAC 179
DB 61 ACACAGTGAGTCCCGGCTATTGGACTTTGTCCAGTGACAGCTGACACAAAGACAC 120

QY 180 GGGAGAGGTGTAGGAGAGAAAGCGCCGCGAAGCAGCGATCGCCAGCACCAAGTCGCTTC 239
DB 121 GGGAGAGGTGTAGGAGAGAAAGCGCCGCGAAGCAGCGATCGCCAGCACCAAGTCGCTTC 180
QY 240 CAGGCTTTCGGTTCCTTTGGCTCCATCTTTGGTGGCGCTTCCCGGCGTCTAGGGAGGGA 299
DB 181 CAGGCTTTCGGTTCCTTTGGCTCCATCTTTGGTGGCGCTTCCCGGCGTCTAGGGAGGGA 240
QY 300 AGGCTGAGTGGCAGCGCAGGAGAGTCCGGCCGCGACAGAGCAAGCAACCTCCCTCTGAA 359
DB 241 AGGCTGAGTGGCAGCGCAGGAGAGTCCGGCCGCGACAGAGCAAGCAACCTCCCTCTGAA 300
QY 360 AGGATTCTGAAGAAATGAAGTCAAGCTCAGCAATGAAGTTGACTGCTGCTGCTTC 419
DB 301 AGGATTCTGAAGAAATGAAGTCAAGCTCAGCAATGAAGTTGACTGCTGCTGCTTC 359
QY 420 CTGTTGACTGGCCCGGAGCTGTACTGCAAGACCTTTGAGCTTCCCTAGTCTAAGATGA 479
DB 360 CTGTTGACTGGCCCGGAGCTGTACTGCAAGACCTTTGAGCTTCCCTAGTCTAAGATGA 419
QY 480 GGATGCTGCTGAAGTCAATCAGCTTGAAGAAAGCACTTGTATACAGATGAGAAGGAGA 539
DB 420 GGATGCTGCTGAAGTCAATCAGCTTGAAGAAAGCACTTGTATACAGATGAGAAGGAGA 479
QY 540 TGCTGCTCTTTTGTGCGGGATGTGCTATAGATGTGTTCCACCTAATGTCAAGGAC 599
DB 480 TGCTGCTCTTTTGTGCGGGATGTGCTATAGATGTGTTCCACCTAATGTCAAGGAC 539
QY 600 TTCGTGATATTTACGGGAAGAGGTAGCTGCTGTCGGGACGTGGCTGAAGTGTCT 659
DB 540 TTCGTGATATTTACGGGAAGAGGTAGCTGCTGTCGGGACGTGGCTGAAGTGTCT 599
QY 660 ACAGAGTGAGGCGATTGACCTGCTCAACGCTATCTTGAAGATGACAGAAAGCTGTGG 719
DB 600 ACAGAGTGAGGCGATTGACCTGCTCAACGCTATCTTGAAGATGACAGAAAGCTGTGG 659
QY 720 AGACCCACCTGCTCAGGAACCCCTCACCTGTTTCGGGACTATAGAGTGTGATGGCAGAGA 779
DB 660 AGACCCACCTGCTCAGGAACCCCTCACCTGTTTCGGGACTATAGAGTGTGATGGCAGAGA 719
QY 780 TTGGTGAGATTTGGATTAATCTGATGTCTCTATTAATTTCTCATGAAGGATTA 839
DB 720 TTGGTGAGATTTGGATTAATCTGATGTCTCTCTATTAATTTCTCATGAAGGATTA 779
QY 840 TGGCCGAGGCGAAGATAGCAAGAGAGAGTTCTTGACCTCTGTTGAGTTGGAGA 899
DB 780 TGGCCGAGGCGAAGATAGCAAGAGAGAGTTCTTGACCTCTGTTGAGTTGGAGA 839
QY 900 AACTAAATTTGGTTGCCCGCAGATCAACTGGATTTATTAGAAAATGCCTTAAAGAACATCC 959
DB 840 AACTAAATTTGGTTGCCCGCAGATCAACTGGATTTATTAGAAAATGCCTTAAAGAACATCC 899
QY 960 ACAGAAATGACCTGAAGACAAAATCCAGAACTACAGCAGTCTGTTCAAGAGAGGAGA 1019
DB 900 ACAGAAATGACCTGAAGACAAAATCCAGAACTACAGCAGTCTGTTCAAGAGAGGAGA 959
QY 1020 CAAGTTACAGGAATGTTCTTCAAGCAGCAATCCAAAAGAGTCTCAAGGATCTTCAATA 1079
DB 960 CAAGTTACAGGAATGTTCTTCAAGCAGCAATCCAAAAGAGTCTCAAGGATCTTCAATA 1019
QY 1080 ACTTCAGGAT 1089
DB 1020 ACTTCAGGCT 1029

RESULT 9
AAV74136
ID AAV74136 standard; cDNA; 1750 BP.
XX
AC AAV74136;
XX
DT 12-APR-1999 (first entry)

```
XX DE Human FLAME-1 cDNA.
XX KW FLAME-1; FADD-like apoptotic/anti-apoptotic molecule; human;
XX KW apoptosis; HIV; infection; Alzheimer's disease; cancer; therapy;
XX KW ds.
XX OS Homo sapiens.
XX Key Location/Qualifiers
XX FT 413..1750
XX FT /*tag= a
XX PN WO9852963-Al.
XX PD 26-NOV-1998.
XX PF 20-MAY-1998; 98WO-US10200.
XX PR 20-MAY-1997; 97US-0859167.
XX PA (UYJE-) UNIV JEFFERSON THOMAS.
XX PI Alnemri ES;
XX WPI: 1999-045296/04.
XX P-PSDB; AAW90107.
XX New isolated FADD-like anti-apoptotic molecules - used to develop
XX PT apoptotic and anti-apoptotic agents for treating, e.g. HIV
XX PT Infection, Alzheimer's disease or neoplastic conditions
XX PS ClalM 12; Page 36-38; 68pp; English.
XX This cDNA sequence codes for human FLAME-1 (see AAW90107), or
XX CC FADD-like apoptotic/anti-apoptotic molecule 1. FLAME-1 is a novel
XX CC anti-apoptotic protein that interacts specifically with FADD, Mch4,
XX CC Mch5 and FLAME-2. It is recruited to the Fas receptor complex and
XX CC can abrogate Fas/TNF-induced apoptosis upon expression in
XX CC a Jurkat cDNA library using a partial FLAME-1 cDNA probe that had
XX CC chromosome 2q33-34. The full-length FLAME-1 gene was mapped to
XX CC a Jurkat cDNA library using the Jurkat library using primers (see
XX CC AAW84139-42) based on an isolated EST clone. Host cells, recombinant
XX CC vectors, and methods of using FLAME-1 to identify substrates,
XX CC activators or inhibitors of FLAME-1 are provided. FLAME-1,
XX CC FLAME-2 (see AAW90108) and agonists can be used to inhibit apoptosis,
XX CC e.g. for treating HIV infection or Alzheimer's disease. Inhibitors
XX CC of the polypeptides can be used as apoptotic agents. FLAME nucleic
XX CC acid molecules can be used for gene therapy, e.g. antisense
XX CC oligonucleotides can be used in vivo for antineoplastic purposes.
XX SQ Sequence 1750 BP; 465 A; 400 C; 476 G; 409 T; 0 other;

Query Match 73.5%; Score 1008.6; DB 20; Length 1750;
Best Local Similarity 99.5%; Pred. No. 3 6e-161;
Matches 1022; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 69 CGAGTCTCACTAAAGGAGACTCCCGAGCTAGGGTGGGACTCACAGTGA 128
DB 1 CGAGTCTCACTAAAGGAGACTCCCGAGCTAGGGTGGGACTCACAGTGA 60
QY 129 GTCCGGCTATTGGACTTTTGTCCAGTGACGTGAGACCAAGACCAAGGAGGAGG 188
DB 61 GTCCGGCTATTGGACTTTTGTCCAGTGACGTGAGACCAAGGAGGAGGAGG 120
QY 189 TGTAGAGAGAGAGCGCGGAGAGGATGCGCCAGCACCAAGTCCGCTTCAGGCTTTC 248
DB 121 TGTAGAGAGAGAGCGCGGAGAGGATGCGCCAGCACCAAGTCCGCTTCAGGCTTTC 180
QY 249 GGTTCCTTTCCTCATCTTTGGTGGCTTCCCGCGCTCTAGGGGAGCGAGGCTGAGG 308
DB 181 GGTTCCTTTCCTCATCTTTGGTGGCTTCCCGCGCTCTAGGGGAGCGAGGCTGAGG 240

309 TGGCAGCGCAGGAGAGTCCGCGCGACAGGACGAACTCCCCACTGGAAGGATTCTG 368
DB 241 TGGCAGCGCAGGAGAGTCCGCGCGACAGGACGAACTCCCCACTGGAAGGATTCTG 300
QY 369 AAGAAATGAAGTCAGCCCTCAGAAATGAAGTGTGACTGCTGCTGGCTTCTGTTGACT 428
DB 301 AAGAAATGAAGTCAGCCCTCAGAAATGAAGTGTGACTGCTGCTGGCTTCTGTTGACT 359
QY 429 GCGCGGAGCTGACTGCAAGACCTTGTGAGCTTCCCTAGTCTAAGAGTAGGATGCTG 488
DB 360 GCGCGGAGCTGACTGCAAGACCTTGTGAGCTTCCCTAGTCTAAGAGTAGGATGCTG 419
QY 489 CTGAAGTCATCCATCAGGTTGAAGACCTTGTGATACAGATGAGAGGAGATGCTGCT 548
DB 420 CTGAAGTCATCCATCAGGTTGAAGACCTTGTGATACAGATGAGAGGAGATGCTGCT 479
QY 549 TTTTGTGCGGGATGTTGCTATAGATGTTGTTCCACCTTAATGTCAGGACCTTCTGGATA 608
DB 480 TTTTGTGCGGGATGTTGCTATAGATGTTGTTCCACCTTAATGTCAGGACCTTCTGGATA 539
QY 609 TTTTACGGGAAGAGGTAAGCTGCTGTCGCGGACTTGGCTGAATGCTTACAGAGTGA 668
DB 540 TTTTACGGGAAGAGGTAAGCTGCTGTCGCGGACTTGGCTGAATGCTTACAGAGTGA 599
QY 669 GCGCATTTGACCTGCTCAACGTAICTTGAAGATGACACAGAAAGCTGTGGAGACCCACC 728
DB 600 GCGCATTTGACCTGCTCAACGTAICTTGAAGATGACACAGAAAGCTGTGGAGACCCACC 659
QY 729 TGCTCAGGAACCTCACCCTTGTTCGAGCTATAGAGTGTGATGGCAGAGATTGGTGAGG 788
DB 660 TGCTCAGGAACCTCACCCTTGTTCGAGCTATAGAGTGTGATGGCAGAGATTGGTGAGG 719
QY 789 ATTTGGATAAATCTGATGCTCTCATTAATTTTCTCATGAGGATTACATGGCCGAG 848
DB 720 ATTTGGATAAATCTGATGCTCTCATTAATTTTCTCATGAGGATTACATGGCCGAG 779
QY 849 GCAAGATAAGCAAGGAGAGAGTTCCTTGACCTTGTGTTGAGTTGGAGAACTAAAT 908
DB 780 GCAAGATAAGCAAGGAGAGAGTTCCTTGACCTTGTGTTGAGTTGGAGAACTAAATC 839
QY 909 TGGTTGCCCCAGATCAACTGGATTATTAGAAAAATGCCCTAAGACATCCACAGATAG 968
DB 840 TGGTTGCCCCAGATCAACTGGATTATTAGAAAAATGCCCTAAGACATCCACAGATAG 899
QY 969 ACCTGGAAGACAAAAATCCAGAGTACAGCAGTCTGTTCAGGAGCAGGAGCAAGTTACA 1028
DB 900 ACCTGGAAGACAAAAATCCAGAGTACAGCAGTCTGTTCAGGAGCAGGAGCAAGTTACA 959
QY 1029 GGAATGTTCTCCAGCAGCAATCCAAAGAGTCTCAAGGATCCTTCAATACTTCAGGA 1088
DB 960 GGAATGTTCTCCAGCAGCAATCCAAAGAGTCTCAAGGATCCTTCAATACTTCAGGA 1019
QY 1089 TGATAAC 1095
DB 1020 GCATACC 1026

RESULT 10
AAAD43202 standard; cDNA; 1750 BP.
ID AAD43202
XX AC AAD43202;
XX DT 14-NOV-2002 (first entry)
XX DE Human FLAME-1 cDNA.
XX KW Human; FADD-like apoptotic/anti-apoptotic protein; Alzheimer's disease;
XX KW gene therapy; human immunodeficiency virus; HIV infection; apoptosis;
XX KW FLAME-1; gene; ss.
XX OS Homo sapiens.
```

XX	Key	Location/Qualifiers
FT	CDS	413..1750
FT		/*tag= a
FT		/product= "Human FLAME-1 protein"
XX		US2002086983-A1.
XX		04-JUL-2002.
XX		22-AUG-2001; 2001US-0935223.
XX		28-OCT-1997; 97US-0959167.
PR		26-MAR-1999; 99US-0276993.
PR		28-NOV-2000; 2000US-0723450.
XX		(UYJE-) UNIV JEFFERSON THOMAS.
XX		Alnemr1 ES;
DR		WPI; 2002-642259/69.
DR		P-PSDB; AAE26086.
XX		Novel FADD-like apoptotic/anti-apoptotic proteins useful for inhibiting
PT		apoptosis, treating diseases characterized by apoptosis e.g. HIV
PT		infection and Alzheimer's disease, and for identifying modulators of
PT		the protein
XX		Claim 7; Page 12-14; 35pp; English.
XX		The invention relates to FADD-like apoptotic/anti-apoptotic proteins
CC		(FLAME 1 or 2) and nucleic acid molecules encoding such proteins.
CC		FLAME sequences are useful for inhibiting apoptosis and for gene
CC		therapy of diseases characterized by apoptosis including HIV
CC		infection and Alzheimer's disease. FLAME inhibitors are useful as
CC		apoptotic agents and activators are useful as anti-apoptotic agents.
CC		FLAME-1 is useful as a substrate for caspase in assays to identify
CC		caspase inhibitors. The present sequence is human FLAME-1 cDNA.
XX		Sequence 1750 BP; 465 A; 400 C; 476 G; 409 T; 0 other;
XX		Query Match 73.5%; Score 1008.6; DB 24; Length 1750;
XX		Best Local Similarity 99.5%; Pred. No. 3.6e-161;
XX		Matches 1022; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
QY	69	CGAGTCTCAACTAAAGGAGCTCCGGAGCTAGGGTGGGACTCGGCCTCACAGTGA 128
Db	1	CGAGTCTCAACTAAAGGAGCTCCGGAGCTAGGGTGGGACTCGGCCTCACAGTGA 60
QY	129	GTGCGCGCTATTGGACTTTTGTCCAGTGACAGCTGAGACAAAGGACCACGGGAGG 188
Db	61	GTGCGCGCTATTGGACTTTTGTCCAGTGACAGCTGAGACAAAGGACCACGGGAGG 120
QY	189	TGTAGGAGAGAGCCGCGACAGGATCGCCAGCAGCAAGTCCGCTTCAGGCTTTC 248
Db	121	TGTAGGAGAGAGCCGCGACAGGATCGCCAGCAGCAAGTCCGCTTCAGGCTTTC 180
QY	249	GGTTTCTTTGCCCTCCACTTTGGGTGCGCCTTCCCGCGCTCTAGGGGAGGAGGCTGAGG 308
Db	181	GGTTTCTTTGCCCTCCACTTTGGGTGCGCCTTCCCGCGCTCTAGGGGAGGAGGCTGAGG 240
QY	309	TGGCAGCGCAGGAGATCCGGCCGCGCAGCAGCAACTCCCCACTGGAAAGGATCTCG 368
Db	241	TGGCAGCGCAGGAGATCCGGCCGCGCAGCAGCAACTCCCCACTGGAAAGGATCTCG 300
QY	369	AAAGAAGTCACTAGCCCTCAGAAATGAAGTTGACTGCCTGCTGCTTCTGCTGACT 428
Db	301	AAAGAAGTGAATCAGCCCTCAGAAATGAAGTTGACTGCCTGCTGCTTCTGCTGACT 359
QY	429	GGCCCGGAGCTGACTGCAAGACCCTTGTGAGCTTCCCTAGTCTAAGAGTAGGATGCTCG 488
Db	360	GGCCCGGAGCTGACTGCAAGACCCTTGTGAGCTTCCCTAGTCTAAGAGTAGGATGCTCG 419

QY	489	CTGAAGTCTATCCATCAGGTTGAAGAGCACTTGTATACAGATGAGAAGGAGATGCTCTCT 548
Db	420	CTGAAGTCTATCCATCAGGTTGAAGAGCACTTGTATACAGATGAGAAGGAGATGCTCTCT 479
QY	549	TTTTGTGCGCGGATGTTGCTATAGATGTGTGTTCCACCTAATGTCTCAGGGACCTTCTGATA 608
Db	480	TTTTGTGCGCGGATGTTGCTATAGATGTGTGTTCCACCTAATGTCTCAGGGACCTTCTGATA 539
QY	609	TTTACGGGAAAGAGGTAAGCTGCTGTCGGGAGCTTGGCTGAACCTGCTCTACAGAGTGA 668
Db	540	TTTACGGGAAAGAGGTAAGCTGCTGTCGGGAGCTTGGCTGAACCTGCTCTACAGAGTGA 599
QY	669	GGCGATTTGACCTGCTCAAAACGTATCTTGAAGATGGACAGAAAGCTGTGGAGACCCACC 728
Db	600	GGCGATTTGACCTGCTCAAAACGTATCTTGAAGATGGACAGAAAGCTGTGGAGACCCACC 659
QY	729	TGCTCAGGAACCTCACCTTGTTCGGACTATAGAGTGTGATGGCAGAGATTGGTGAGG 788
Db	660	TGCTCAGGAACCTCACCTTGTTCGGACTATAGAGTGTGATGGCAGAGATTGGTGAGG 719
QY	789	ATTGGATAAATCTGATGTGCTCTAATTAATTTCTCATGAAGGATTACATGGGCGGAG 848
Db	720	ATTGGATAAATCTGATGTGCTCTAATTAATTTCTCATGAAGGATTACATGGGCGGAG 779
QY	849	GCAAGATAAGCAAGAGAGAGTTTCTTGGACCTTGTGTTGAGTTGGAGAACTAAAT 908
Db	780	GCAAGATAAGCAAGAGAGAGTTTCTTGGACCTTGTGTTGAGTTGGAGAACTAAATC 839
QY	909	TGTTTGGCCCGAGATCAACTGGATTATTAGAAAATGCTTAAAGACATCCACAGATAG 968
Db	840	TGTTTGGCCCGAGATCAACTGGATTATTAGAAAATGCTTAAAGACATCCACAGATAG 899
QY	969	ACCTGAAGACAAAAATCCAGAGTCAAGCAGTCTTCTCAAGGAGCAGGACAAAGTTACA 1028
Db	900	ACCTGAAGACAAAAATCCAGAGTCAAGCAGTCTTCTCAAGGAGCAGGACAAAGTTACA 959
QY	1029	GGAATGTTCTCAAGCAGCAATCCAAAAGAGTCTCAAGGATCCTTCAATAACTTTCAGGA 1088
Db	960	GGAATGTTCTCAAGCAGCAATCCAAAAGAGTCTCAAGGATCCTTCAATAACTTTCAGGA 1019
QY	1089	TGATAAC 1095
Db	1020	GCATACC 1026
XX	RESULT 11	
XX	AAV61937	
ID	AAV61937	standard; DNA; 2143 BP.
XX	AC	AAV61937;
XX	XX	
DT	12-JUL-1999	(first entry)
XX	Human CFLIP-L DNA.	
DE	Death effector domain; human; murine; anti-apoptotic; treatment;	
KW	HIV infection; autoimmune disease; FLIP protein; ss.	
XX	Homo sapiens.	
OS		
XX	Key	Location/Qualifiers
FT	CDS	383..1825
FT		/*tag= a
FT		/product= "CFLIP-L"
XX		DE19713393-A1.
PN		08-OCT-1998.
XX		01-APR-1997; 97DE-1013393.
XX		01-APR-1997; 97DE-1013393.
XX		

RESULT 13
ABL52333
ID ABL52333 standard; cDNA: 2143 BP.
XX AC ABL52333;
AC ABL52333;
DT DT 15-JUL-2002 (first entry)
XX XX Human FLIP-C encoding cDNA SEQ ID NO:11.
DE DE Human; FLIP-C; caspase 8 dominant negative regulator; antiinflammatory; KW anti-tumour; FLIP-C inhibitor; apoptosis; antisense gene therapy; KW phosphorothioate; antisense modulation; infection; inflammation; KW tumour; gene; ss. XX OS Homo sapiens.
OS PH Key Location/Qualifiers FH CDS 383..1825 FT FT /*tag= a FT FT /product= "FLIP-C" XX WO300224717-Al.
PN PD 28-MAR-2002.
PD PF 14-SEP-2001; 2001WO-US28732.
PF PR 20-SEP-2000; 2000US-O666269.
PR PA (ISIS-) ISIS PHARM INC.
PA PI Ackermann EJ, Bennett CF, Zhang H, Watt AT, Ricketts W, Dean NM; PI P-PSDB; ABB09294.
DR DR Novel antisense compound that hybridizes and inhibits nucleic acid PT encoding a natural dominant negative regulator of caspase 8, FLIP-C, PT useful for preventing or delaying infection, inflammation or tumor PT formation . XX Example 13; Page 118-120; 154pp; English.
PS CC The present invention describes a compound (I) 8-50 nucleobases in length CC targeted to a nucleic acid molecule (II) encoding a natural dominant CC negative regulator of caspase 8, FLIP-C, where (I) specifically CC hybridises with and inhibits expression of the protein, or specifically CC hybridises with at least an 8-nucleobase portion of an active site on CC (II). (I) has anti-inflammatory and anti-tumour activities. (I) is an CC inhibitor of FLIP-C expression, a modulator of apoptosis and can be used CC in antisense gene therapy. (I) is useful for inhibiting the expression of CC FLIP-C in cells or tissues, and for treating an animal having a disease CC or condition associated with FLIP-C. (I) is also useful for modulating CC apoptosis in a cell, where a caspase such as caspase 8, caspase 3 or CC caspase 7 is activated, and the FLIP-C is the long form of FLIP-C. (I) is CC also useful for diagnostics, therapeutics, prophylaxis, as research CC reagents and kits, for distinguishing functions of various members of a CC biological pathway, e.g., in antisense gene therapy. (I) is also useful CC prophylactically, e.g., to prevent or delay infection, inflammation or CC tumour formation. The present sequence encodes human FLIP-C as given in CC an example from the present invention.
XX SQ Sequence 2143 BP; 590 A; 482 G; 576 G; 495 T; 0 other;
Query Match 71.1%; Score 975.8; DB 24; Length 2143; Best Local Similarity 99.7%; Pred. No. 1.2e-155; Matches 988; Conservative 0; Mismatches 2; Indels 1; Gaps 1
Oy 99 TAGGGGTGGGACTCGGCCTCACAGATGAGTCGCCGATTGGACTTTTGTCCAGTGAC 158 Db 1 TAGGGGTGGGACTCGGCCTCACAGATGAGTCGCCGATTGGACTTTTGTCCAGTGAC 60

QY	883	TGTGGTTGAGTTGGAGAACTAAATTTGGTTGCCCCAGATCAACTGGATTATTAGAAA	942
Db	695	TGTGGTTGAGTTGGAGAACTAAATCTGGTTGCCCCAGATCAACTGGATTATTAGAAA	754
QY	943	ATGCTAAAGAACATCCACAGATAGACCTGAAGACAAAATCCAGAAGTACAAAGCAGTC	1002
Db	755	ATGCTAAAGAACATCCACAGATAGACCTGAAGACAAAATCCAGAAGTACAAAGCAGTC	814
QY	1003	TGTTCAAGGAGCAGGGACAAGTTACAGGAATGTTCTCCAAAGCAGCAATCCAAAAGAGTCT	1062
Db	815	TGTTCAAGGAGCAGGGACAAGTTACAGGAATGTTCTCCAAAGCAGCAATCCAAAAGAGTCT	874
QY	1063	CAAGGATCCTTCAATAACTTCAGGATCAACACACCTATGCCCATTTGCTGATCTGAA	1122
Db	875	CAAGGATCCTTCAATAACTTCAGGATCAACACACCTATGCCCATTTGCTGATCTGAA	934
QY	1123	AATTCCTTGGAAATTTCCATGTGATTAAACATGGAAGTGGCTCTACTTAATCATCTGAA	1182
Db	935	AATTCCTTGGAAATTTCCATGTGATTAAACATGGAAGTGGCTCTACTTAATCATCTGAA	994
QY	1183	TGATTAAATCGTTTCATTTCTTAATGTGTTATA	1217
Db	995	TGATTAAATCGTTTCATTTCTTAATGTGTTATA	1029

Search completed: August 22, 2003, 07:51:31
Job time : 383.562 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 22, 2003, 07:06:39 ; Search time 3003.82 Seconds
(without alignments)
11109.213 Million cell updates/sec

Title: US-09-380-546A-3
Perfect score: 1373
Sequence: 1 ggaagtcgagcattacaat.....aaaaaaaaaaaaaaaaaaaa 1373

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues
Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- EST:*
- 1: em_estba:*
 - 2: em_esthum:*
 - 3: em_estin:*
 - 4: em_estmu:*
 - 5: em_estov:*
 - 6: em_estpl:*
 - 7: em_estro:*
 - 8: em_htc:*
 - 9: gb_est1:*
 - 10: gb_est2:*
 - 11: gb_hic:*
 - 12: gb_est3:*
 - 13: gb_est4:*
 - 14: gb_est5:*
 - 15: em_estfun:*
 - 16: em_estom:*
 - 17: em_gss_hum:*
 - 18: em_gss_inv:*
 - 19: em_gss_pln:*
 - 20: em_gss_vrt:*
 - 21: em_gss_fun:*
 - 22: em_gss_mam:*
 - 23: em_gss_mus:*
 - 24: em_gss_pro:*
 - 25: em_gss_rod:*
 - 26: em_gss_phg:*
 - 27: em_gss_vrl:*
 - 28: gb_gss1:*
 - 29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	973.2	70.9	1071	9	AL526318
2	912	66.4	1054	12	BM928334
3	864.6	63.0	896	13	BM928334
4	863	62.9	929	13	BM928334

5	857.2	62.4	1004	12	BM555216
6	836	60.9	927	13	BM912545
7	829.8	60.4	915	13	BM912545
8	828.6	60.3	982	13	BM912545
9	789.2	57.5	898	13	BM912545
10	781.6	56.9	1201	9	AL552025
11	774.2	56.4	839	13	BM912545
12	772.8	56.3	826	9	AL552025
13	759	55.3	902	13	BM912545
14	734.4	53.5	795	9	AL552025
15	719.6	52.4	900	14	BM912545
16	714	52.0	725	12	BM912545
17	712.4	51.9	716	12	BM912545
18	707.4	51.5	757	12	BM912545
19	688.6	50.2	898	13	BM912545
20	672.4	49.0	700	12	BM912545
21	672	48.9	948	13	BM912545
22	669.4	48.8	671	13	BM912545
23	669.4	48.8	671	13	BM912545
24	668.2	48.7	690	14	BM912545
25	663.4	48.3	699	10	BM912545
26	651.2	47.4	668	12	BM912545
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28	645.2	47.0	1107	12	BM912545
29	637.2	46.4	788	14	BM912545
30	632.8	46.1	667	10	BM912545
31	632.8	46.1	667	10	BM912545
32	628.4	45.8	655	10	BM912545
33	627.6	45.7	885	10	BM912545
34	619	45.1	774	10	BM912545
35	617.4	45.0	774	10	BM912545
36	605.8	44.1	1020	12	BM912545
37	602.4	43.9	727	10	BM912545
38	599	43.6	611	14	BM912545
39	595.2	43.4	639	9	BM912545
40	587.6	42.8	647	10	BM912545
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42	579.2	42.2	595	9	BM912545
43	578.6	42.1	585	12	BM912545
44	573.4	41.8	622	9	BM912545
45	573	41.7	799	13	BM912545

ALIGNMENTS

RESULT 1
AL526318
LOCUS
DEFINITION
AL526318 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
CDNA clone CS0DC016Y006 5-PRIME, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1071 bp mRNA linear EST 23-MAY-2003
CDNA clone CS0DC016Y006 5-PRIME, mRNA sequence.
AL526318.2 GI:31064178
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1071)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
On Feb 13, 2001 this sequence version replaced gi:12789811.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 1297.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DC016BH03QPl&cluster=1297.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :

Db 432 CTTGAAATGGACAGAAAACCTGTGGAGACCCACCTGCTCAGGAACCTCACCTTGTTC 491
QY 754 GGACTATAGAGTGTGTGACAGAGATTGGTAGGATTGGGATAAATCTGATGTCTTC 813
Db 492 GGACTATAGAGTGTGTGACAGAGATTGGTAGGATTGGGATAAATCTGATGTCTTC 551
QY 814 ATTAATTTCTCTATGAAGATTACATGGGCCGAGCAAGATAGCAAGGAGAGAGTTT 873
Db 552 ATTAATTTCTCTATGAAGATTACATGGGCCGAGCAAGATAGCAAGGAGAGAGTTT 611
QY 874 CTTGAGCTGTGTGTGAGTTGGAGAACTAAATTTGTTGCCGCCAGATCAACTGGATT 933
Db 612 CTTGAGCTGTGTGTGAGTTGGAGAACTAAATTTGTTGCCGCCAGATCAACTGGATT 671
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Db 792 AAGAGTCTCAAGGATCCTCAAAATCTCAGGATGATACACCCCTATGCCCATTTGCC 851
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Db 852 TGATCTGAATTTCTTGAATTTGTTCCATGTGATTAACATGGAA 896

RESULT 4
B0706783
LOCUS
DEFINITION B0706783 929 bp mRNA linear EST 16-JUL-2002
5', mRNA sequence.
B0706783
VERSION B0706783.1 GI:21845682
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 929)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapuser@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Prepared by: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L1CM2382 row: 0 column: 08
High quality sequence stop: 669.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon.9606"
/clone="IMAGE:6214879"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_113"
/note="Organ: spleen; Vector: pOTB7; Site: 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and

Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
BASE COUNT 251 a 196 c 261 g 220 t 1 others
ORIGIN
Query Match 62.9%; Score 863; DB 13; Length 929;
Best Local Similarity 98.5%; Pred. No. 9,7e-67;
Matches 902; Conservative 0; Mismatches 11; Indels 3; Gaps 3;
QY 179 CGGAGGAGGTGTAGAGAGAGCGCGCAACAGCGATCGCCACAGCAAGTCCGCTT 238
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Db 61 CCAGGCTTTTCGTTTCTTTGCTCCATCTTGGGTGGGCTTCCCGGCTGTAGGGAGCG 120
QY 299 AAGGCTGAGTGGCAGCGCAGAGAGTCCCGCGGACAGCAAGTCCCGCACTGGA 358
Db 121 AAGGCTGAGTGGCAGCGCAGAGAGTCCCGCGGACAGCAAGTCCCGCACTGGA 180
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Db 181 AAGGATTTCTGAAGAAATGAAGTCAAGCTCAGCCCTCAGAAATGAAGTTGACTGCTGCTT 240
QY 419 CTTGTTGACTGGCCCGGAGCTGTACTGCAAGACCTTGTGAGCTTCCCTAGTCTAAGACT 478
Db 241 -CTGTTGACTGGCCCGGAGCTGTACTGCAAGACCTTGTGAGCTTCCCTAGTCTAAGACT 299
QY 479 AAGATGCTCTGCAAGTCAATCATCAGTTGAAGAACACTTGTATACAGATGAGAAGAG 538
Db 300 AAGATGCTCTGCAAGTCAATCATCAGTTGAAGAACACTTGTATACAGATGAGAAGAG 359
QY 539 ATGCTGCTCTTTTGGCGGGATGTGCTATAGATGTGGTCCACCTATGTCAGGGAC 598
Db 360 ATGCTGCTCTTTTGGCGGGATGTGCTATAGATGTGGTCCACCTATGTCAGGGAC 419
QY 599 CTTCTGGATATTTTACGGGAAAGAGTGAAGTCTCTCTGGGGACCTTGGCTCAACTGCTC 658
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QY 659 TACAGAGTGGCGGATTTGACCTGCTCAAAAGTATCTTGAAGATGGACAGAAAGCTGTG 718
Db 480 TACAGAGTGGCGGATTTGACCTGCTCAAAAGTATCTTGAAGATGGACAGAAAGCTGTG 539
QY 719 GAGACCCACCTGCTCAGGAACCTCACTTGTTCGGACTATAGAGTGTGATGGCAGAG 778
Db 540 GAGACCCACCTGCTCAGGAACCTCACTTGTTCGGACTATAGAGTGTGATGGCAGAG 599
QY 779 ATTGCTGAGGATTTGGATAAATCTGATGTCTCTCATTAATTTTCCTCATGAAGGATTAC 838
Db 600 ATTGCTGAGGATTTGGATAAATCTGATGTCTCTCATTAATTTTCCTCATGAAGGATTAC 659
QY 839 ATGGGCGGAGCAGATTAAGCAAGGAGAGTCTTGGACCTTGGTGGTGGTGGTGGAG 898
Db 660 ATGGGCGGAGCAGATTAAGCAAGGAGAGTCTTGGACCTTGGTGGTGGTGGTGGAG 719
QY 899 AAACATAAATTTGTTGCCAGATCAACTGGATTATTAGAAAATGCCCTAAAGAACATC 958
Db 720 AAACATAAATTTGTTGCCAGATCAACTGGATTATTAGAAAATGCCCTAAAGAACATC 779
QY 959 CACAGATAGACCTGAAGACAAAATCCAGAGTGTCTTCAAGGAGCAGCG 1018
Db 780 CACAGATAGACCTGAAGACAAAATCCAGAGTGTCTTCAAGGAGCAGCG 839
QY 1019 ACAAGTTACAGGAATGTTCTCCAAAGCAGCAATCCAAAAGAGTCTCAAGGATCCCTTCAAAT 1078
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QY 1079 AACTTCAGGATGATAA 1094
Db 898 AACTTCAGGATCCCTTA 913

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RESULT 5
BM555216
LOCUS
DEFINITION
AGENCOURT_6541158 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:5550264
5', mRNA sequence.
ACCESSION
BM555216
VERSION
BM555216.1 GI:18795496
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1004)
NIH-MGC http://mgi.nci.nih.gov/.
NATIONAL INSTITUTES OF HEALTH, MAMMALIAN GENE COLLECTION (MGC)
JOURNAL
Unpublished
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12262 row: c column: 01
High quality sequence stop: 713.
FEATURES
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1..1004
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5550264"
/tissue_type="duodenal adenocarcinoma, cell line"
/lab_host="PH10B (phage-resistant)"
/clone_lib="NIH_MGC_88"
Note=Organ: small intestine; Vector: pCMV-SPO66;
Site:1: Not; Site:2: SalI; Cloned unidirectionally;
oligo-dt primed. Average insert size 1.767 kb. Library
enriched for full-length clones and constructed by Life
Technologies. Note: this is a NIH-MGC Library."
BASE COUNT 261 a 220 c 291 g 228 t 4 others
ORIGIN
Query Match 62.4%; Score 857.2; DB 12; Length 1004;
Best Local Similarity 97.6%; Pred. No. 3e-66;
Matches 932; Conservative 0; Mismatches 16; Indels 7; Gaps 6;
QY 42 GAAACAGCAGGTTGCGAGCTCACCAGCAGGTCTCAACTAAAGGAGCTCCCGAGCTAG 101
DB 1 GAAACAGCAGGTTGCGAGCTCACCAGCAGGTCTCAACTAAAGGAGCTCCCGAGCTAG 60
QY 102 GGGTGGGAGCTGGCTTCACAGTACAGTGGCGGCTATTGGACTTTGTCCAGTGACAGC 161
DB 61 GGGTGGGAGCTGGCTTCACAGTACAGTGGCGGCTATTGGACTTTGTCCAGTGACAGC 120
QY 162 TGAGACAACAGGACACCGAGGAGGCTGTAGAGAGAGCGCGGAGACGAGTCGCC 221
DB 121 TGAGACAACAGGACACCGAGGAGGCTGTAGAGAGAGCGCGGAGACGAGTCGCC 180
QY 222 GAGCACAAGTCGCTTCCAGGCTTTCGGTTTCTTTGCTCCATCTTGGGTGGCGCTTCC 281
DB 181 GAGCACAAGTCGCTTCCAGGCTTTCGGTTTCTTTGCTCCATCTTGGGTGGCGCTTCC 240
QY 282 CGGCGCTAGGGAGGAGGCTGAGTGGCGAGCGGAGAGTCCGCGCGAGCAGGA 341
DB 241 CGGCGCTAGGGAGGAGGCTGAGTGGCGAGCGGAGAGTCCGCGCGAGCAGGA 300
QY 342 CGAATCCCCCCTGGAAGGATTCCTGAAGAAATGAAGTCAAGCTCAGACCTCAGAATGAAGTT 401
DB 301 CGAATCCCCCCTGGAAGGATTCCTGAAGAAATGAAGTCAAGCTCAGACCTCAGAATGAAGTT 360
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QY 359 AAGGATTCGAGAAATGAAGTCAAGCTCAGCCCTCAGAAATGAAGTTGACTGCTGCTGCTTT 418
Db 181 AAGGATTCGAGAAATGAAGTCAAGCTCAGCCCTCAGAAATGAAGTTGACTGCTGCTGCTTT 240
QY 419 CCGTGTGACTGCGCCGGAGCTGACTGCAAGACCCTGTGTAGCTTCCCTAGTCTAAGAGT 478
Db 241 -CTGTTGACTGCGCCGGAGCTGACTGCAAGACCCTGTGTAGCTTCCCTAGTCTAAGAGT 299
QY 479 AGGATGCTGCTGGAAGTCAATCATCAGTGTGAAGAGCACTTGTATACAGATGAGAAGGAG 538
Db 300 AGGATGCTGCTGGAAGTCAATCATCAGTGTGAAGAGCACTTGTATACAGATGAGAAGGAG 359
QY 539 ATGCTGCTCTTTTGTGCGGGAGTGTGCTATAGATGGTTCACCTTAATGTCAAGGAC 598
Db 360 ATGCTGCTCTTTTGTGCGGGAGTGTGCTATAGATGGTTCACCTTAATGTCAAGGAC 419
QY 599 CTTCTGGATATTTTACGGGAAGAGTGAAGTGTCTGTGCGGGAGCTTGGCTCAACTGCTC 658
Db 420 CTTCTGGATATTTTACGGGAAGAGTGAAGTGTCTGTGCGGGAGCTTGGCTCAACTGCTC 479
QY 659 TACAGAGTGAGCGGATTTGACCTGCTCAACGATCTTTGAAGATGGACAGAAAAGCTGTG 718
Db 480 TACAGAGTGAGCGGATTTGACCTGCTCAACGATCTTTGAAGATGGACAGAAAAGCTGTG 539
QY 719 GAGACCCACCTGCTCAGGAACCTCACCCTGTTTGGACTATAGAGTGTGATGGCAGAG 778
Db 540 GAGACCCACCTGCTCAGGAACCTCACCCTGTTTGGACTATAGAGTGTGATGGCAGAG 599
QY 779 ATTGTGAGGATTTGGATAAACTGTATGTCTCATTAATTTTCTCATGAAGGATTAC 838
Db 600 ATTGTGAGGATTTGGATAAACTGTATGTCTCATTAATTTTCTCATGAAGGATTAC 659
QY 839 ATGGGCGGAGCAAGATAGCAAGGAGAGAGTCTTGGACCTTGTGTTGAGTTGGAG 898
Db 660 ATGGGCGGAGCAAGATAGCAAGGAGAGAGTCTTGGACCTTGTGTTGAGTTGGAG 719
QY 899 AAACATAATTTGGTGGCCCATCATCACTGGATTTATAGAAAATGCCATAAGACATC 958
Db 720 AAACATAATTTGGTGGCCCATCATCACTGGATTTATAGAAAATGCCATAAGACATC 779
QY 959 CACAGATAGACTGAAGCAAAAATCCAGAGTACAAGCAGTCTGTCTCAAGGAGCA -GS 1017
Db 780 CACAGATAGACTGAAGCAAAAATCCAGAGTACAAGCAGTCTGTCTCAAGGAGCA -GS 839
QY 1018 GACAAAGTTACAGG--AATGTTCTCCAAGCAGCAATCCAAA 1056
Db 840 GACAAAGTTACAGGAAATGTTCTCCAAGCAGCAATCCAAA 880

RESULT 8
BQ644010
LOCUS
DEFINITION BQ644010 NIH_MGC_100 Homo sapiens cDNA clone IMAGE:6284871
5', mRNA sequence.
ACCESSION BQ644010
VERSION BQ644010.1 GI:21768182
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 982)
NIH-MGC http://imgc.ncl.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: CGAP (Stanford)
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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http://image.llnl.gov
Plate: LLCM2483 row: c column: 16
High quality sequence stop: 627.
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/db_xref="taxon:9606"
/clone="IMAGE:6284871"
/tissue_type="hepatocellular carcinoma, cell line"
/lab_host="PH108 (phage-resistant)"
/clone_lib="NIH_MGC_100"
/note="Organ: liver; Vector: pOTB7; Site_1: xhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally cloned
into ECORI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."
BASE COUNT 270 a 199 c 262 g 250 t 1 others
ORIGIN
Query Match 60.3%; Score 828.6; DB 13; Length 982;
Best Local Similarity 96.7%; Pred. No. 9.2e-64;
Matches 899; Conservative 0; Mismatches 25; Indels 6; Gaps 5;
QY 294 GAGCGAAGGCTCAGGTGGCGGCGGAGGAGTCCGGCGGCGGAGGAGCAACTCCCCCA 353
Db 6 GAGGGAAGGCTCAGGTGGCGGCGGAGGAGTCCGGCGGCGGAGGAGCAACTCCCCCA 65
QY 354 CTGGAAGGATCTCAAAGAAATGAAGTCAGCCCTCAGAAATGAAGTTGACTGCCCTGCTG 413
Db 66 CTGGAAGGATCTCAAAGAAATGAAGTCAGCCCTCAGAAATGAAGTTGACTGCCCTGCTG 125
QY 414 GCTTTCTCTTGTGCTGCGGCGGAGCTGTACTGCAAGACCCCTGTGTAGCTTCCCTAGTCTA 473
Db 126 GCTTT-CTGTTGACTGCGCGGAGCTGTACTGCAAGACCCCTGTGTAGCTTCCCTAGTCTA 184
QY 474 ACAGTAGGATGCTGCTGAAGTCATCCATCAGGTTCGAAGACCTTGAAGAGCACTTGATACAGATGAGA 533
Db 185 ACAGTAGGATGCTGCTGAAGTCATCCATCAGGTTCGAAGACCTTGAAGAGCACTTGATACAGATGAGA 244
QY 534 AGGAGATGCTGCTTTTGTGCGGGGATGTGCTATAGATGTGTGTTCCACCTTAATGTCA 593
Db 245 AGGAGATGCTGCTTTTGTGCGGGGATGTGCTATAGATGTGTGTTCCACCTTAATGTCA 304
QY 594 GGGACCTCTGGATATTTTACGGGAAGAGGTAAGCTGTCTGCGGGGACTTGGCTGAAC 653
Db 305 GGGACCTCTGGATATTTTACGGGAAGAGGTAAGCTGTCTGCGGGGACTTGGCTGAAC 364
QY 654 TGTCTACAGAGTGAGCGGATTTGACCTGCTCAAAGCTATCTTTGAAGATGGACAGAAAAG 713
Db 365 TGTCTACAGAGTGAGCGGATTTGACCTGCTCAAAGCTATCTTTGAAGATGGACAGAAAAG 424
QY 714 CTGTGGAGACCCACCTGCTCAGGAACCCCTCACCTTCTTTCGGACTATAGAGTCTGATGG 773
Db 425 CTGTGGAGACCCACCTGCTCAGGAACCCCTCACCTTCTTTCGGACTATAGAGTCTGATGG 484
QY 774 CAGAGATTTGGTGGAGATTTGGATTAATCTGATGTGCTCCTCAATTAATTTTCCCTCATGAAGG 833
Db 485 CAGAGATTTGGTGGAGATTTGGATTAATCTGATGTGCTCCTCAATTAATTTTCCCTCATGAAGG 544
QY 834 ATTACATGGCGGAGGCAAGATTAAGCAAGAGAGTTTCTTGGACCTTGTGGTTGACT 893
Db 545 ATTACATGGCGGAGGCAAGATTAAGCAAGAGAGATTTCTTGGACCTTGTGGTTGACT 604
QY 894 TGGAGAAACTAAATTTGGTTGGCCCGAGATCAACTGGATTTATTAGAAAAATGCTTAAAGA 953
Db 605 TGGAGAAACTAAATCTGGTTGGCCCGAGATCAACTGGATTTATTAGAAAAATGCTTAAAGA 664
QY 954 ACATCCACAGATAGACCTGAAGACAAAATCCAGAAAGTACAGCAGTCTGTTCAGAGGAG 1013
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Db 665 ACATCCAGCAATAGAGCTGAAGACAAAATCAGAAAGTACAGAGTCTGTTCAGGAG 724
QY 1014 CAGGACAAAGTTACAGCAAGTGTCTCAAGCAGCAATCCAAAAGAGTCTCAAGAGTCTT 1073
Db 725 CAGGACAAAGTTACAGCAAGTGTCTCCAGCAGCAATCCAAAAGAGTCTCAAGAGTCTT 784
QY 1074 CAATAAATCTCAGGATGATAACACCCCTATG-CCGATGCTCTGATCTGAAATCTTGA 1132
Db 785 TCAATAAATCTCAGGATGATAACACCCCTATGCCCATGGTCTGATCTGAAATCTTGGG 844
QY 1133 AATT-GTTCATGCTTACATGGAAT-GCTTCTACTTAATCAATCTCTGAATG--ATTA 1188
Db 845 AATTGGTCCCATGATTTACATGGAATGCTGCTCTACTTANCAATCTCTGAATGATTA 904
QY 1189 AATCGTTTCAATTTCTAAATGTGTATAAT 1218
Db 905 ATCGGTTTCCITTTCTAAATGGGGCTATT 934

RESULT 9
BX353372/c 898 bp mRNA linear EST 05-MAY-2003
LOCUS BX353372 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
DEFINITION cDNA clone CS0DC005Y016 3-PRIME, mRNA sequence.
ACCESSION BX353372.1 GI:30381783
VERSION BX353372.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 898)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 1297.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DC005Y016&cluster=1297.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paradise Avenue Genoscope sequence ID : CS0DC005Y016NP1.
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/organism="Homo sapiens"
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/clone="CS0DC005Y016"
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/clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
216 a 213 c 172 g 193 t 104 others
BASE COUNT 216 a 213 c 172 g 193 t 104 others
ORIGIN
Query Match 57.5%; Score 789.2; DB 13; Length 898;
Best Local Similarity 85.2%; Pred. No. 2.6e-60;
Matches 762; Conservative 99; Mismatches 32; Indels 1; Gaps 1;
QY 349 CCCCACTGGAAGAGTCTGAAAGAAATGAAGTCAGCCCTCAGAAATGAAGTGAATGCC 408
Db 898 CCCGCTGGAAGAGTCTGAAAGAAATGAAGTCAGCCCTCAGAAATGAAGTGAATGCC 839
QY 409 TCGTGGCTTCTGTGTACTGGCCGGAGTGTACTGCAAGACCCCTGTGAGCTTCCTTA 468

838 TGTGCTGCTT-CTGTGACTGGCCGGGCTGTACTGCAAGACCCCTGTGAGCTTCCTA 780
QY 469 GTCTAAGAGTAGGATGTCTGCTGAAGTCAATCCATCAGCTTGAAGAAGCACTTGTATACAGA 528
Db 779 KTYTAAGAGTAGGATGTCTGCTGAGTCAATCCATCAGTTCGAARAAGCACTTGTATACAGA 720
QY 529 TGAGAAGAGAGATGTCTCTTTTTTTGTGCGGGATGTTGCTATAGATGTGTTCCACCTAA 588
Db 719 TGAGAAGAGAGATGTCTCTTTTTTTGTGCGGGATGTTGCTATAGATGTGTTCCACCTAA 660
QY 589 TGTGAGGACCTCTGAGATATTTACGGGAAGAGTAAAGCTGTCTGTCGGGGACTTGGC 648
Db 659 TGTGAGGACCTCTGAGATATTTACGGGAAGAGTAAAGCTGTCTGTCGGGGACTTGGC 600
QY 649 TGAATCTGCTCTACAGAGTGAAGCTGCTCAACGATGCTTGAAGATGGACAG 708
Db 599 TGAATCTGCTCTACAGAGTGAAGCTGCTCAACGATGCTTGAAGATGGACAG 540
QY 709 AAAAGCTGTGGAGACCCCTGCTCAGGAACCTCACCCTGTTTCGGGACTATAGAGTCT 768
Db 539 AAAAGCTGTGGAGACCCCTGCTCAGGAACCTCACCCTGTTTCGGGACTATAGAGTCT 480
QY 769 GATGGCAGAGATTTGAGATTTGATAAATCTGATGTCTCTCATTAATTTTCTCTCAT 828
Db 479 GRTGGCAGAGATTTGAGATTTGATAAATCTGATGTCTCTCATTAATTTTCTCTCAT 420
QY 829 GAAGGATACATGCGCGGAGGCAAGTAAGCAAGGAGAGAGTCTTGGACCTTGTGCT 888
Db 419 GRAGGRTTACATGCGCGGAGGCAAGTAAGCAAGGAGAGAGTCTTGGACCTTGTGCT 360
QY 889 TGAAGTGGAGAACTAAATTTGTTGCTCCAGATCAACTGGATTTATTAGAAAATGCT 948
Db 359 KGRKKGGGAGAACTAAATTTGTTGCTCCAGATCAACTGGATTTATTAGAAAATGCT 300
QY 949 AAAGAACATCCAGATACACCTGTAAGCAAAATCCAGAGTACAGCACTGCTGTCA 1008
Db 299 AAAGAACATCCAGATACACCTGTAAGCAAAATCCAGAGTACAGCACTGCTGTCA 240
QY 1009 AGGAGCAGGACAAAGTTTACAGAAATCTTCTCCAGCAGCAATCCAAAGAGTCTCAAGA 1068
Db 239 AGGGCAGGACAAAGTTTACAGAAATCTTCTCCAGCAGCAATCCAAAGAGTCTCAAGA 180
QY 1069 TCCCTCAAAATCACTTCAAGATGATACACCTATGCCATGCTGCTGATCTGAAATCT 1128
Db 179 TCCCTCAAAATCACTTCAAGATGATACACCTATGCCATGCTGCTGATCTGAAATCT 120
QY 1129 TGGAAATGTTTCCATGATTAACATGGAATGCTCTTACTTAATCATTTCTGAATGATTA 1188
Db 119 TGGAAATGTTTCCATGATTAACATGGAATGCTCTTACTTAATCATTTCTGAATGATTA 60
QY 1189 AATCGTTTCAATTTCTAAATGTGTATAATGTTTGAAGCCCTTCTTGTGCTG 1242
Db -59 AATKTTTWT 6

RESULT 10
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LOCUS AL552025 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CS0DI060Y011 5-PRIME, mRNA sequence.
ACCESSION AL552025
VERSION AL552025.2 GI:31273841
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
On Feb 15, 2001 this sequence version replaced gi:12890528.
Contact: Genoscope

Query Match	56.9%	Score 781.6	DB 9	Length 1201
Best Local Similarity	91.2%	Pred. No. 9.8e-60		
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QY	46	CACGCGAGCTGCAAGCTCACCGACGAGTCTCAACTAAA-AGGGACTCCCGGAGCTAGGGG	104	
DB	52	CCGGGATCTTGAGCCTCACCGACGAGTCTCACTAATAGGNGCTCCCGGAGCTAGGGG	111	
QY	105	TGGGGACTCG-GCCTCACACAGTGAGTGCCGGCTATTGGACTTTTGTTCAGTGCACAGCTG	163	
DB	112	TGGGGACTCGTCTCACACAGTGAGTGCCGGCTATTGGACTTTTGTTCAGTGCACAGCTG	171	
QY	164	AGACAACAAGGACACGGGAGGAGGTGTAGGAGAGAAGCCGCGGAACACGCGATCGCCCCA	223	
DB	172	AGACACACAGGACACGGGAGGAGGTGTAGGAGAGAAGCCGCGGAACACGCGATCGCCCCA	231	
QY	224	GCACCAAGTCGGTTCACAGCTTTTCAGCTTTTCGGTTCCTTTGGCTCCATCTTGGGTGCGCTTCCCG	283	
DB	232	GCACCAAGTCGGTTCACAGCTTTTCAGCTTTTCGGTTCCTTTGGCTCCATCTTGGGTGCGCTTCCCG	291	
QY	284	GCCTCTAGGGGAGCGAAGGCTGAGGTGGCAGCGCAGGAGAGTCCGCGCCGACAGGACG	343	
DB	292	GCCTCTAGGGGAGCGAAGGCTGAGGTGGCAGCGCAGGAGAGTTCGCGCCGCGACAGGACG	351	
QY	344	AACTCCCCCACTGGAAAGGATTCCTGAAGAAATGAAGTCAGCCCTCAGAAATGAAGTTGA	403	
DB	352	AACTCCCCCACTGGAAAGGATTCCTGAAGAAATGAAGTCAGCCCTCAGAAATGAAGTTGA	411	
QY	404	CTGCGCTGCTGGCTTCTCTGTGACTGCCCGGAGCTGTACTGCNAAGACCTTTGTGAGCTT	463	
DB	412	CTGCGCTGCTGGCTTCTCTGTGACTGCCCGGAGCTGTACTGCNAAGACCTTTGTGAGCTT	470	
QY	464	CCCTAGTCTAAGAGTAGGATGTCTGCTGAAAGTCAATCATCAGGTTGAAGAACACTTTGAT	523	
DB	471	CCCTAGTCTAAGAGTAGGATGTCTGCTGAAAGTCAATCATCAGGTTGAAGAACACTTTGAT	530	
QY	524	ACAGATGAGNAGAGATGCTGCTTTTGTGCGGGATGTTGCTATAGATGTGGTTCCA	583	
DB	531	ACAGATGAGNAGAGATGCTGCTTTTGTGCGGGATGTTGCTATAGATGTGGTTCCA	590	
QY	584	CTTAATGTCAAGGACCTTCTGGATATTTTACGGGAAGAGGTAAAGCTGTCTGTCCGGGAC	643	
DB	591	CTTAATGTCAAGGACCTTCTGGATATTTTACGGGAAGAGGTAAAGCTGTCTGTCCGGGAC	650	
QY	644	TTGGCTGAAGTGTCTACAGAGTGAGCGGATTTGACCTGTCTCAACAGTATCTTGAAGATG	703	
DB	651	TTGGCTGAAGTGTCTACAGAGTGAGCGGATTTGACCTGTCTCAACAGTATCTTGAAGATG	710	

Mon Aug 25 09:11:10 2003

BASE COUNT	NIH). Note: this is a NIH_MGC Library."	Length 839;	Score 774.2;	DB 13;	Indels 0;	Gaps 0;
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Best Local Similarity	96.1%;	Pred. No. 5.4e-59;				
Matches 791;	Conservative 0;	Mismatches 32;	Indels 0;	Gaps 0;		
QY	473 AAGAGTAGGATGCTGCTGAAGTCATCCATCAGCTTGAAGAGCAGCTTGATACAGATGAG	532				
Db	4 AAGAGTAGGATGCTGCTGAAGTCATCCATCAGCTTGAAGAGCAGCTTGATACAGATGAG	63				
QY	533 AAGAGATGCTGCTTTTGTGCGGGATGTTGCTATAGATGCTGCTCCACCTAATGTC	592				
Db	64 AAGAGATGCTGCTTTTGTGCGGGATGTTGCTATAGATGCTGCTCCACCTAATGTC	123				
QY	593 AGGACCTCTCGGATATTTACGGGAAGAGGTAAGCTGCTGCTCGGGGACTTTGGCTGAA	652				
Db	124 AGGACCTCTCGGATATTTACGGGAAGAGGTAAGCTGCTGCTCGGGGACTTTGGCTGAA	183				
QY	653 CTGCTCTACAGAGTAGGCGGATTTGACCTGCTCAAGCTATCTGTAAGATGGACAGAAA	712				
Db	184 CTGCTCTACAGAGTAGGCGGATTTGACCTGCTCAAGCTATCTGTAAGATGGACAGAAA	243				
QY	713 GCTGTGGAGCCACCTGCTCAGAACCCCTCACCTTCTGTTCCGACTATAGATGCTGATG	772				
Db	244 GCTGTGGAGCCACCTGCTCAGAACCCCTCACCTTCTGTTCCGACTATAGATGCTGATG	303				
QY	773 GCAGAGATGTTGAGGATTTGGATTAATCTGATGTCCTCATTAATTTTCCCTCATGAG	832				
Db	304 GCAGAGATGTTGAGGATTTGGATTAATCTGATGTCCTCATTAATTTTCCCTCATGAG	363				
QY	833 GATTACATGGCCGAGGCAAGTAAGCAAGGAGAGGATTTCTTGGACCTTGTGTTGAG	892				
Db	364 GATTACATGGCCGAGGCAAGTAAGCAAGGAGAGGATTTCTTGGACCTTGTGTTGAG	423				
QY	893 TTGGAGAACTAAATTTGTTGTTGCCCCAGATCAATCGGATTTATTAGAAAATGCTAAAG	952				
Db	424 TTGGAGAACTAAATTTGTTGTTGCCCCAGATCAATCGGATTTATTAGAAAATGCTAAAG	483				
QY	953 ACATCCAGATAGACCTGAGACCAAAATCCAGAGTACAGCAGCTGTTCAAGGA	1012				
Db	484 ACATCCAGATAGACCTGAGACCAAAATCCAGAGTACAGCAGCTGTTCAAGGA	543				
QY	1013 GCAGGAGCAAGTACAGGATGTTCTCCAAGCAGCAATCCAAAAGAGTCTCAAGATCCT	1072				
Db	544 GCAGGAGCAAGTACAGGATGTTCTCCAAGCAGCAATCCAAAAGAGTCTCAAGATCCT	603				
QY	1073 TCAATTAATCTCAGGATGATACACCCATGCCCCATGCTGATGCTGATGCTGATGCTGGA	1132				
Db	604 TCAATTAATCTCAGGATGATACACCCATGCCCCATGCTGATGCTGATGCTGATGCTGGA	663				
QY	1133 AATTGTTCCATGTTAATCAATGGAATGCTGCTTACTTAACTATCTGAATGATTAATC	1192				
Db	664 AATTGTTCCATGTTAATCAATGGAATGCTGCTTACTTAACTATCTGAATGATTAATC	723				
QY	1193 GTTTCATTTCTAAATGTTTATATGTTTATAGCCCTTCTGTTGCTGATGTTTGA	1252				
Db	724 GTTTCATTTCTAAATGTTTATATGTTTATAGCCCTTCTGTTGCTGATGTTTGA	783				
QY	1253 TGCTTTCCATCTTTTGTACTACTAATATGCTATAAATAA	1295				
Db	784 TGCTTTCCATCTTTTGTACTACTAATATGCTATAAATAA	826				
RESULT 12						
LOCUS	AI347041/c	826 bp	mRNA	linear	EST 02-FEB-1999	
DEFINITION	qp60a03.x1 NCI_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1927372 3'					
	Similar to TR:O15138 O15138 CASPASE-LIKE APOPTOSIS REGULATORY					
	PROTEIN 2. [1] ; mRNA sequence.					
ACCESSION	AI347041					
VERSION	AI347041.1 GI:4084259					

EST.	Homo sapiens (human)
KEYWORDS	Homo sapiens
SOURCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (Bases 1 to 826)
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL	Unpublished
COMMENT	Contact: Robbs-R@mail.nih.gov Email: cgapbs-r@mail.nih.gov Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emert-Buck, M.D., Ph.D. CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Insert Length: 1238 Std Error: 0.00 Seq primer: -40UP from Gibco High quality sequence stop: 458.
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	/mol_type="mRNA"
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	/clone="IMAGE:1927372"
	/tissue_type="adenocarcinoma"
	/lab_host="DH10B"
	/clone_lib="NCI-CGAP_Co8"
	/note="Organ: colon; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from colon adenocarcinoma, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo.
BASE COUNT	243 a 187 c 151 g 244 t
ORIGIN	1 others
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Matches 813; Conservative	0; Mismatches 13; Indels 3; Gaps 3;
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QY 902 CTAAATTTGGTGGCCCCAGATCAACTGGATTATTAGAAAAATGCTTAAAGAACATCCAC 961

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LOCUS BX457155 902 bp mRNA linear EST 22-MAY-2003

DEFINITION BX457155 Homo sapiens THYMUS Homo sapiens cDNA clone CS0CAP006YN07

ACCESSION BX457155

VERSION BX457155.1 GI:31026861

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Li.W.B., Gruber,C., Jessee,J. and Polayes,D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished

COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 1297.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0CAP006G04Q1&cluster=1297.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
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FEATURES

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Library was not normalized."
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BASE COUNT

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LOCUS AU122196

DEFINITION AU122196 MAMMAL Homo sapiens cDNA clone MAMMAL1001850 5', mRNA sequence.

ACCESSION AU122196

VERSION AU122196.1 GI:10937431

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

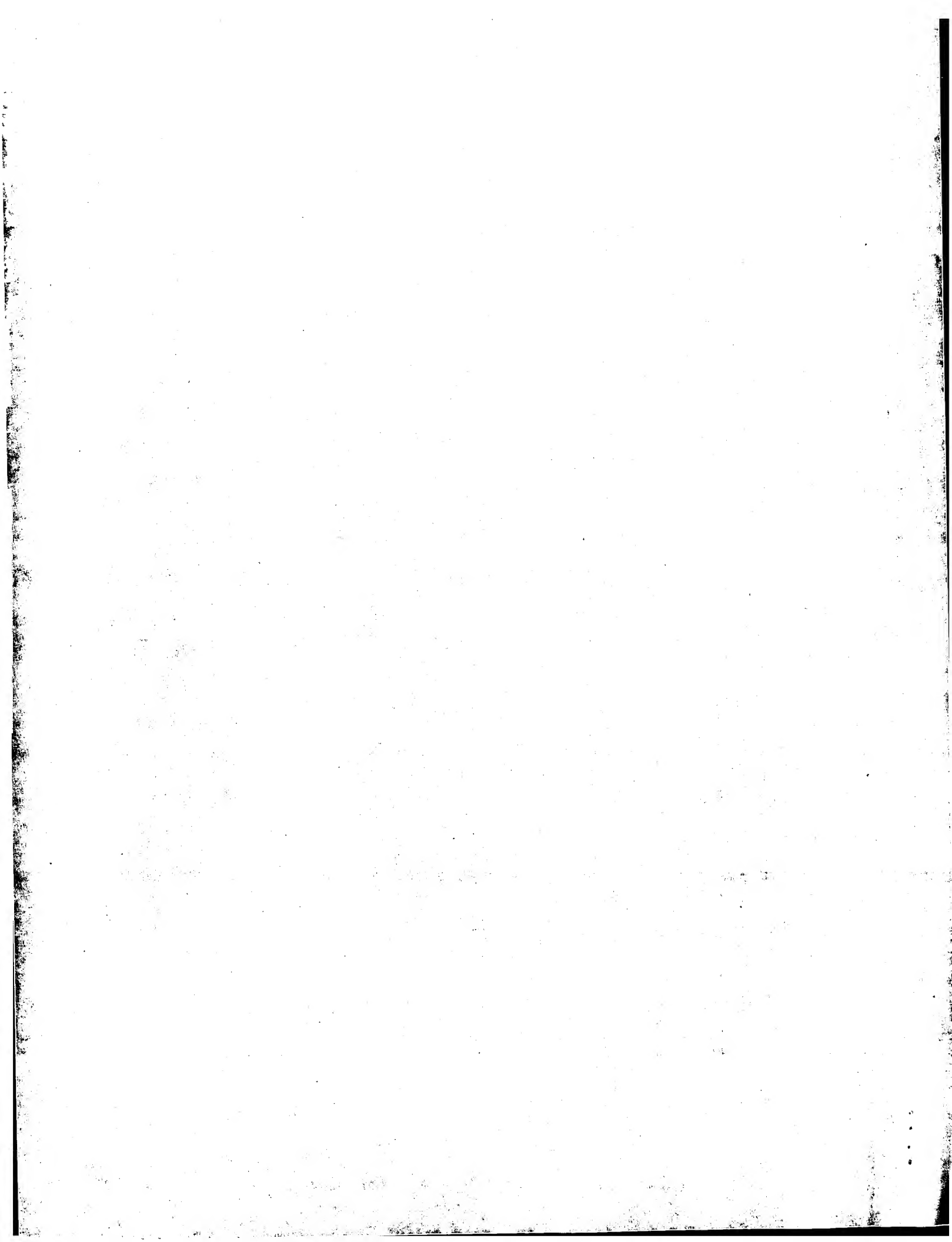
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1 (bases 1 to 795)
Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and Isogai, T.
HRI human cDNA project
Unpublished
Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.
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KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE 1. (bases 1 to 900)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapsof-email.nih.gov
Tissue Procurement: Dr. Jamie Thompson, University of WI
cDNA Library Preparation: Gina Zastrow-Hayes
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Total number of hits satisfying chosen parameters: 1139956

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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18	74.4	5.4	1091	4	US-09-328-965-1
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ALIGNMENTS

RESULT 1

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; Patent No. 6348573
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; APPLICANT: Koseki, Takeyoshi
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
; TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
; FILE REFERENCE: UM-03333
; CURRENT APPLICATION NUMBER: US/09/069,023A
; CURRENT FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-069-023-33

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887 GTTGAGTGGAGAACTAAATTTGTTGCTCCAGATCAACTGGAATTTATTAGAAAATGC 946
841 GTTGAGTGGAGAACTAAATTTGTTGCTCCAGATCAACTGGAATTTATTAGAAAATGC 900
947 CTAAGAAGATCCACAGATAGACCTGAGAGCAAAATCCAGAGTACAAAGCTCTGTT 1006
901 CTAAGAAGATCCACAGATAGACCTGAGAGCAAAATCCAGAGTACAAAGCTCTGTT 960
1007 CAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1066
961 CAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1020
1067 GATCCTCAATAACTTCAGGAT 1089
1021 GATCCTCAATAACTTCAGGCT 1043

RESULT 2
US-08-795-088A-1
; Sequence 1, Application US/08795088A
; Patent No. 6242569
; GENERAL INFORMATION:
; APPLICANT: Sul Hong-Bing
; APPLICANT: Goeddel, David V.
; TITLE OF INVENTION: Regulators of Apoptosis
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Science & Technology Law Group
; STREET: 75 Denise Drive
; CITY: Hillsborough
; STATE: California
; COUNTRY: USA
; ZIP: 94010
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795.088A
; FILING DATE:
; CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-001
TELEPHONE: (650) 343-4341
TELEFAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2045 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-795-088A-1
Query Match 74.7%; Score 1025.2; DB 3; Length 2045;
Best Local Similarity 99.6%; Pred. No. 1.7e-226;
Matches 1038; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
48 GCGAGCTTGACGCCCTCACCGAGAGTCTCAACTAAAGGGACTCCCGAGAGCTAGGGTGG 107
78 GAGAGCTTGACGCCCTCACCGAGAGTCTCAACTAAAGGGACTCCCGAGAGCTAGGGTGG 137
108 GCATCGGCTCACAGAGTGTGCGGCTATTGAGCTTTTGTCCAGTGACAGCTGAGAC 167
138 GGACTCGGCTCACAGAGTGTGCGGCTATTGAGCTTTTGTCCAGTGACAGCTGAGAC 197
168 AACAGGACACCGGAGGAGGTGTAGGAGAGAGGCGCGGAGAGAGTCCCGCGGAGAGCAACT 227
198 AACAGGACACCGGAGGAGGTGTAGGAGAGAGGCGCGGAGAGAGTCCCGCGGAGAGCAACT 257
228 CAAGTCGGCTTCAGGCTTTCCGTTTCTTTCCTCCATCTGCGTCCGCTTCCCGGGCT 287
258 CAAGTCGGCTTCAGGCTTTCCGTTTCTTTCCTCCATCTGCGTCCGCTTCCCGGGCT 317
288 CTAGGAGAGCAAGGCTGAGGTGGCAGCGGAGGAGTCCCGCGGAGAGCAACT 347
318 CTAGGAGAGCAAGGCTGAGGTGGCAGCGGAGGAGTCCCGCGGAGAGCAACT 377
348 CCCCCACTGAAAGGATCTGAAAGAAATGAAGTCAAGCTCAGACCTCAGAAATCAAGTCACTGC 407
378 CCCCCACTGAAAGGATCTGAAAGAAATGAAGTCAAGCTCAGACCTCAGAAATCAAGTCACTGC 437
408 CTGCTGGCTTTCTGTTGACTGGCCGCGGAGTGTACTGCAAGACCCCTTGTGAGCTTCCCT 467
438 CTGCTGGCTTT-CTGTTGACTGGCCGCGGAGTGTACTGCAAGACCCCTTGTGAGCTTCCCT 496
468 AGTCTAAGAGTAGGATGCTGCTGAAGTCAATCAGTTCATCAGTTCAGAGCACTTGATACAG 527
497 AGTCTAAGAGTAGGATGCTGCTGAAGTCAATCAGTTCATCAGTTCAGAGCACTTGATACAG 556
528 ATGAGAAGGAGATGCTGCTCTTTTGTGCGGAGTGTGCTATAGATGTTGGTTCACCTA 587
557 ATGAGAAGGAGATGCTGCTCTTTTGTGCGGAGTGTGCTATAGATGTTGGTTCACCTA 616
588 ATGTCAGGACCTTCTGATATTTTACGGGAAAGAGTAAAGTGTGTCGTCGGGAGCTGG 647
617 ATGTCAGGACCTTCTGATATTTTACGGGAAAGAGTAAAGTGTGTCGTCGGGAGCTGG 676
648 CTGAAGTCTCTACAGAGTGAAGGATTTGACCTGCTCAACGCTATCTTGAAGATGGACA 707
677 CTGAAGTCTCTACAGAGTGAAGGATTTGACCTGCTCAACGCTATCTTGAAGATGGACA 736
708 GAAAAGCTGTGAGAGACCCCTGCTCAGAAACCCCTCACTTGTTCGGAGCTATAGAGTGC 767
737 GAAAAGCTGTGAGAGACCCCTGCTCAGAAACCCCTCACTTGTTCGGAGCTATAGAGTGC 796
768 TGATGGCAGAGATGCTGAGGATTTGGATAAATCTGATGTCCTCATTAATTTTCCCTCA 827
797 TGATGGCAGAGATGCTGAGGATTTGGATAAATCTGATGTCCTCATTAATTTTCCCTCA 856
828 TGAAGGATTACATGGCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 887

Patent No. 6063760
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Enad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: FADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF
; TITLE OF INVENTION: USING THE SAME, AND COMPOSITIONS FOR AND METHODS
; TITLE OF INVENTION: OF MAKING THE SAME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESS: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6063760ris
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: WINDOWS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/109,273
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/859,167
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1750 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 413..1750
; US-09-109-273-1
Query Match 73.5%; Score 1008.6; DB 3; Length 1750;
Best Local Similarity 99.5%; Pred. No. 1e-222;
Matches 1022; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
Qy 69 CGAGTCTCACTAAAGGAGCTCCCGGAGCTAGGGGTGGGACTCGGCTCACACAGTGA 128
Db 1 CGAGTCTCACTAAAGGAGCTCCCGGAGCTAGGGGTGGGACTCGGCTCACACAGTGA 60
Qy 129 GTCCGGCTATTGGACTTTTGTCCAGTGCAGCTGAGACAAAGGAGGAGGAGG 188
Db 61 GTCCGGCTATTGGACTTTTGTCCAGTGCAGCTGAGACAAAGGAGGAGGAGG 120
Qy 189 TGTAGGAGAGAGCGCGGAGACAGCGATCGCCGAGCAGGCTCGGCTTCAGGCTTC 248
Db 121 TGTAGGAGAGAGCGCGGAGACAGCGATCGCCGAGCAGGCTCGGCTTCAGGCTTC 180
Qy 249 GGTTCCTTTCCTCCATCTTGGTGGCGCTTCCCGGCTGTAGGGGAGGAGGCTGAGG 308
Db 181 GGTTCCTTTCCTCCATCTTGGTGGCGCTTCCCGGCTGTAGGGGAGGAGGCTGAGG 240
Qy 309 TGGCAGCGGAGAGAGTCCGGCGGAGCAGGAGCAGGCTCCCGCTGAAAGGATTCG 368
Db 241 TGGCAGCGGAGAGAGTCCGGCGGAGCAGGAGCAGGCTCCCGCTGAAAGGATTCG 300
Qy 369 AAGAAATGAAGTCAAGCTTCAGAAATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 428
Db 301 AAGAAATGAAGTCAAGCTTCAGAAATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 359

Qy 429 GGCCCGGAGCTGTACTGCAAGACCCCTTGTGAGCTTCCCTAGTCTAAGAGTAGGATGTCTG 488
Db 360 GGCCCGGAGCTGTACTGCAAGACCCCTTGTGAGCTTCCCTAGTCTAAGAGTAGGATGTCTG 419
Qy 489 CTGAAGTCAATCCATCAGGTTGAAGAGCATTGATACAGATGAGAGAGATGCTGCTCT 548
Db 420 CTGAAGTCAATCCATCAGGTTGAAGAGCATTGATACAGATGAGAGAGATGCTGCTCT 479
Qy 549 TTTTGTGCGGGATGTGTCTATAGATGTGGTTCACCTTAATGTCAAGGACCTTCTGGATA 608
Db 480 TTTTGTGCGGGATGTGTCTATAGATGTGGTTCACCTTAATGTCAAGGACCTTCTGGATA 539
Qy 609 TTTTACGGGAAAGAGTAACTGTCTGCGGGGACTTGGCTGAACCTGCTACAGAGTGA 668
Db 540 TTTTACGGGAAAGAGTAACTGTCTGCGGGGACTTGGCTGAACCTGCTACAGAGTGA 599
Qy 669 GCGGATTTGACCTGCTCAACCTTCTTGAAGATGAGACAGAAAGCTTGGAGACCCACC 728
Db 600 GCGGATTTGACCTGCTCAACCTTCTTGAAGATGAGACAGAAAGCTTGGAGACCCACC 659
Qy 729 TGCTCAGGAACCTCACCTTGTTCGGACTATAGAGTGTGATGCAGAGATTTGTGAGG 788
Db 660 TGCTCAGGAACCTCACCTTGTTCGGACTATAGAGTGTGATGCAGAGATTTGTGAGG 719
Qy 789 ATTTGGATTAATCTGATGTCTCTCAATTAATTTCTCATGAAGATTTACATGGCCGAG 848
Db 720 ATTTGGATTAATCTGATGTCTCTCAATTAATTTCTCATGAAGATTTACATGGCCGAG 779
Qy 849 GCAAGATAAGCAAGAGAGAGTTTCTTGGACCTTGTGTTGAGTTGGAGAACTAAAT 908
Db 780 GCAAGATAAGCAAGAGAGAGTTTCTTGGACCTTGTGTTGAGTTGGAGAACTAAAT 839
Qy 909 TGGTGGCCGAGATCAACTGGATTATTATAGAAAATGCTTAAGACATCCACAGATAG 968
Db 840 TGGTGGCCGAGATCAACTGGATTATTATAGAAAATGCTTAAGACATCCACAGATAG 899
Qy 969 ACCTGAAGACAAAATCCAGAGTACAAGCAGTCTTCAAGGAGAGGAGGAGGAGTACA 1028
Db 900 ACCTGAAGACAAAATCCAGAGTACAAGCAGTCTTCAAGGAGAGGAGGAGGAGTACA 959
Qy 1029 GGAATGTTCTCAAGCAGCAATCCAAAGAGTCTCAAGGATCTTCAAAATTAAGTTCAGGA 1088
Db 960 GGAATGTTCTCAAGCAGCAATCCAAAGAGTCTCAAGGATCTTCAAAATTAAGTTCAGGA 1019
Qy 1089 TGATAAC 1095
Db 1020 GCATACC 1026
RESULT 5
US-09-276-993-1
; Sequence 1, Application US/09276993
; Patent No. 6207801
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Enad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: FADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF
; TITLE OF INVENTION: USING THE SAME, AND COMPOSITIONS FOR AND METHODS
; TITLE OF INVENTION: OF MAKING THE SAME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESS: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6207801ris
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: WINDOWS
; SOFTWARE: WordPerfect

Dbb 121 TGTAGGAGAGAGCGCCGGAACAGCGATCGCCCAACACCAAGTCGCTTCAGAGCTTC 180


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; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: FARACI, C. J.
; REGISTRATION NUMBER: 32,350
; REFERENCE/DOCKET NUMBER: 2121-110P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1582 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; US-08-545-196B-12

Query Match          5.8%; Score 79.4; DB 3; Length 1582;
Best Local Similarity 73.7%; Pred. No. 3.9e-09;
Matches 101; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 1237 TTGCTGTATGTTAGATGCTTCCAAATCTTTTGTACTACTATATGCTATAAAATAAA 1296
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Db 1415 TGGCTGTTCTACTGTTTCTTCTATCTATATGTTTAAAGTATATATAATAAA 1474
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QY 1297 TATCCCTGTACTCTTAAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1356
    ||||| || ||||| || ||||| || ||||| || ||||| || ||||| || ||||| ||
Db 1475 TATTTAATTTTTTTTAAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1534
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QY 1357 AAAAAAAAAAAAAAAAAA 1373
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Db 1535 AAAAAAAAAAAAAAAAAA 1551
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RESULT 9
US-08-909-965C-7
; Sequence 7, Application US/08090965C
; Patent No. 5936078
; GENERAL INFORMATION:
; APPLICANT: Kuga Tetsuo
; APPLICANT: Nakagawa Satoshi
; APPLICANT: Sakaki Yoshiyuki
; APPLICANT: Zhao Nanding
; APPLICANT: Hashida Hideji
; TITLE OF INVENTION: NOVEL DNA, NOVEL POLYPEPTIDE
; TITLE OF INVENTION: AND NOVEL ANTIBODY
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FITZPATRICK, CELLA, HARPER AND SCINTO
; STREET: 277 Park Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10172-0194
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/909,965C
; FILING DATE: August 12, 1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JPT 322745/95
; APPLICATION NUMBER: PCT/JF96/03630
; FILING DATE: 12-No. 5936078-1995
; FILING DATE: 12-Dec-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Lawrence S. Perry
; REGISTRATION NUMBER: 31865
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-2400

; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: FARACI, C. J.
; REGISTRATION NUMBER: 32,350
; REFERENCE/DOCKET NUMBER: 2121-110P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1582 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; US-08-545-196B-12

Query Match          5.8%; Score 79.4; DB 3; Length 1582;
Best Local Similarity 73.7%; Pred. No. 3.9e-09;
Matches 101; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 1237 TTGCTGTATGTTAGATGCTTCCAAATCTTTTGTACTACTATATGCTATAAAATAAA 1296
    ||||| || ||||| || ||||| || ||||| || ||||| || ||||| || ||||| ||
Db 1415 TGGCTGTTCTACTGTTTCTTCTATCTATATGTTTAAAGTATATATAATAAA 1474
    ||||| || ||||| || ||||| || ||||| || ||||| || ||||| || ||||| ||
QY 1297 TATCCCTGTACTCTTAAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1356
    ||||| || ||||| || ||||| || ||||| || ||||| || ||||| || ||||| ||
Db 1475 TATTTAATTTTTTTTAAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1534
    ||||| || ||||| || ||||| || ||||| || ||||| || ||||| || ||||| ||
QY 1357 AAAAAAAAAAAAAAAAAA 1373
    ||||| || ||||| || ||||| || ||||| || ||||| || ||||| || ||||| ||
Db 1535 AAAAAAAAAAAAAAAAAA 1551
    ||||| || ||||| || ||||| || ||||| || ||||| || ||||| || ||||| ||

RESULT 10
US-09-372-422A-19
; Sequence 19, Application US/09372422A
; Patent No. 6313375
; GENERAL INFORMATION:
; APPLICANT: Rudolf Jung
; APPLICANT: Francois Barrieu
; TITLE OF INVENTION: Maize Aquaporins and Uses Thereof
; FILE REFERENCE: 0919
; CURRENT APPLICATION NUMBER: US/09/372,422A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: US 60/098,692
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 1454
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (224)...(1112)
; US-09-372-422A-19

Query Match          5.7%; Score 78; DB 4; Length 1454;
Best Local Similarity 73.9%; Pred. No. 8e-09;
Matches 99; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

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Db 1277 CTGTATGCTGCTGCTAGTGCTCCCAATATGATATGATATGATAGGCCATATATACCAAG 1336
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QY 1300 CCTTGCTACTCTTAAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1359
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Db 1337 GCCATTCTTAAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1396
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QY 1360 AAAAAAAAAAAAAA 1373
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Db 1397 AAAAAAAAAAAAAA 1410
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RESULT 12
US-08-821-994-63
US-08-821-994-63, Application US/08821994A
; Sequence 63,
; Patent No. 6228643
; GENERAL INFORMATION:
; APPLICANT: Greenland, Andrew J
; APPLICANT: Thomas, Didier RP
; APPLICANT: Jepson, Ian
; TITLE OF INVENTION: Promoters
; FILE REFERENCE: PPD 50108
; CURRENT APPLICATION NUMBER: US/08/821
; CURRENT FILING DATE: 1997-03-22
; EARLIER APPLICATION NUMBER: PCT/GB97
; EARLIER FILING DATE: 1997-03-18
; EARLIER APPLICATION NUMBER: GB 96060
; EARLIER FILING DATE: 1996-03-22
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 63
; LENGTH: 1441
; TYPE: DNA
; ORGANISM: Brassica napus
US-08-821-994-63
Query Match 5.6% Score
Best Local Similarity 62.5% Predicted

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	EARLIER APPLICATION NUMBER:	60/047,492
	EARLIER FILING DATE:	1997-05-23
	EARLIER APPLICATION NUMBER:	60/047,598
	EARLIER FILING DATE:	1997-05-23
	EARLIER APPLICATION NUMBER:	60/047,613
	EARLIER FILING DATE:	1997-05-23
	EARLIER APPLICATION NUMBER:	60/047,582
	EARLIER FILING DATE:	1997-05-23
	EARLIER APPLICATION NUMBER:	60/047,596
	EARLIER FILING DATE:	1997-05-23
	EARLIER APPLICATION NUMBER:	60/047,612
	EARLIER FILING DATE:	1997-05-23
	EARLIER APPLICATION NUMBER:	60/047,632
	EARLIER FILING DATE:	1997-05-23
	EARLIER APPLICATION NUMBER:	60/047,601
	EARLIER FILING DATE:	1997-05-23
	EARLIER APPLICATION NUMBER:	60/043,580
	EARLIER FILING DATE:	1997-04-11
	EARLIER APPLICATION NUMBER:	60/043,568
	EARLIER FILING DATE:	1997-04-11
	EARLIER APPLICATION NUMBER:	60/043,314
	EARLIER FILING DATE:	1997-04-11
	EARLIER APPLICATION NUMBER:	60/043,569
	EARLIER FILING DATE:	1997-04-11
	EARLIER APPLICATION NUMBER:	60/043,311
	EARLIER FILING DATE:	1997-04-11
	EARLIER APPLICATION NUMBER:	60/043,671
	EARLIER FILING DATE:	1997-04-11
	EARLIER APPLICATION NUMBER:	60/043,674
	EARLIER FILING DATE:	1997-04-11
	EARLIER APPLICATION NUMBER:	60/043,669
	EARLIER FILING DATE:	1997-04-11
	EARLIER APPLICATION NUMBER:	60/043,312
	EARLIER FILING DATE:	1997-04-11
	EARLIER APPLICATION NUMBER:	60/043,313
	EARLIER FILING DATE:	1997-04-11
	EARLIER APPLICATION NUMBER:	60/048,974
	EARLIER FILING DATE:	1997-06-06
	EARLIER APPLICATION NUMBER:	60/056,886
	EARLIER FILING DATE:	1997-08-22
	EARLIER APPLICATION NUMBER:	60/056,877
	EARLIER FILING DATE:	1997-08-22
	EARLIER APPLICATION NUMBER:	60/056,889
	EARLIER FILING DATE:	1997-08-22
	EARLIER APPLICATION NUMBER:	60/056,893
	EARLIER FILING DATE:	1997-08-22
	EARLIER APPLICATION NUMBER:	60/056,630
	EARLIER FILING DATE:	1997-08-22
	EARLIER APPLICATION NUMBER:	60/056,878
	EARLIER FILING DATE:	1997-08-22
	EARLIER APPLICATION NUMBER:	60/056,662
	EARLIER FILING DATE:	1997-08-22
	EARLIER APPLICATION NUMBER:	60/056,872
	EARLIER FILING DATE:	1997-08-22
	EARLIER APPLICATION NUMBER:	60/056,882
	EARLIER FILING DATE:	1997-08-22
	EARLIER APPLICATION NUMBER:	60/056,888
	EARLIER FILING DATE:	1997-08-22
	EARLIER APPLICATION NUMBER:	60/056,879
	EARLIER FILING DATE:	1997-08-22
	EARLIER APPLICATION NUMBER:	60/056,880
	EARLIER FILING DATE:	1997-08-22
	EARLIER APPLICATION NUMBER:	60/056,894
	EARLIER FILING DATE:	1997-08-22
	EARLIER APPLICATION NUMBER:	60/056,911

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 22, 2003, 11:36:53 ; Search time 312.115 Seconds
(without alignments)
9889.733 Million cell updates/sec

Title: US-09-380-546A-3

Perfect score: 1373

Sequence: 1 ggcagctcagcattacat.....aaaaaaaaaaaaaaaaaaaaa 1373

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1517243 seqs, 1124081882 residues

Total number of hits satisfying chosen parameters: 3034486

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications_NA.*
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3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
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5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
15: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
16: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
17: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1044.4	76.1	2352	11	US-09-471-749-2 Sequence 2, Appl
2	1025.2	74.7	2045	9	US-09-861-270-1 Sequence 1, Appl
3	975.8	71.1	2143	9	US-09-410-194-16 Sequence 16, Appl
4	860.8	62.7	2034	11	US-09-009-893-1 Sequence 1, Appl
5	858.2	62.5	1190	9	US-09-410-194-14 Sequence 14, Appl
6	431.4	31.4	495	11	US-09-918-995-26998 Sequence 26998, A
7	382.4	27.9	441	11	US-09-918-995-35401 Sequence 35401, A
8	373.8	27.2	2452	9	US-09-410-194-18 Sequence 18, Appl
9	354.2	25.8	490	10	US-09-833-381-436 Sequence 436, Appl
10	345	25.1	443	11	US-09-918-995-35271 Sequence 35271, A
11	337.8	24.6	2770	13	US-10-005-921-1 Sequence 1, Appl
12	324.4	23.6	1319	14	US-10-103-313-34 Sequence 34, Appl
13	324.4	23.6	1319	14	US-10-115-928-19 Sequence 19, Appl
14	324.4	23.6	2597	11	US-09-009-893-5 Sequence 5, Appl
15	313.4	22.8	414	11	US-09-009-893-23 Sequence 23, Appl
16	276	20.1	437	9	US-09-864-761-3120 Sequence 3120, Ap

17	245.4	17.9	324	11	US-09-009-893-27	Sequence 27, Appl
18	215.4	15.7	308	11	US-09-009-893-29	Sequence 29, Appl
19	206.4	15.0	297	11	US-09-009-893-30	Sequence 30, Appl
20	187.8	13.7	479	11	US-09-918-995-37866	Sequence 37866, A
C 21	177	12.9	177	9	US-09-864-761-19899	Sequence 19899, A
C 22	90	6.6	277	10	US-09-960-352-12673	Sequence 12673, A
C 23	88	6.4	200	13	US-10-005-921-4	Sequence 4, Appl
C 24	86.4	6.3	603	13	US-10-027-632-132228	Sequence 132228, A
C 25	81.2	5.9	6335	12	US-10-311-455-909	Sequence 909, App
C 26	80.4	5.9	506	11	US-09-918-995-7423	Sequence 7423, Ap
C 27	80.2	5.8	416	10	US-09-960-352-4584	Sequence 4584, Ap
C 28	79.4	5.8	312	10	US-09-960-352-8414	Sequence 8414, Ap
C 29	79.4	5.8	375	10	US-09-960-352-15014	Sequence 15014, A
C 30	79.4	5.8	424	10	US-09-960-352-11218	Sequence 11218, A
C 31	79.4	5.8	882	14	US-10-198-846-5958	Sequence 5958, Ap
C 32	79.2	5.7	272	10	US-09-960-352-6986	Sequence 6986, Ap
C 33	78.4	5.7	465	14	US-10-198-846-1482	Sequence 1482, Ap
C 34	78	5.7	393	10	US-09-960-352-4582	Sequence 4582, Ap
C 35	78	5.7	2165	15	US-10-176-306-19	Sequence 19, Appl
C 36	77.8	5.7	1092	14	US-10-106-698-1161	Sequence 1161, Ap
C 37	77.8	5.7	1727	14	US-10-205-823-320	Sequence 320, App
C 38	77.4	5.6	408	10	US-09-960-352-6263	Sequence 6263, Ap
C 39	77.2	5.6	373	10	US-09-960-352-836	Sequence 836, App
C 40	77.2	5.6	3899	9	US-09-745-763-107	Sequence 107, App
C 41	77.2	5.6	5001	14	US-10-198-846-11011	Sequence 11011, A
C 42	76.4	5.6	312	10	US-09-960-352-8414	Sequence 8414, Ap
C 43	76.4	5.6	364	10	US-09-960-352-9419	Sequence 9419, Ap
C 44	76.4	5.6	950	14	US-10-198-846-6625	Sequence 6625, Ap
C 45	76.4	5.6	1194	14	US-10-106-698-1692	Sequence 1692, Ap

ALIGNMENTS

RESULT 1

US-09-471-749-2
; Sequence 2, Application US/09471749
; Publication No. US20030124113A1
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Patterson, Chandra
; APPLICANT: Baughn, Mariah
; TITLE OF INVENTION: HUMAN APOPTOSIS ASSOCIATED PROTEINS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/471,749
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/078,402
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cerrone, Michael C.
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0519 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:

Mon Aug 25 09:11:09 2003

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; LENGTH: 2352 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: THP1PLB02
; CLONE: 157658
;

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Query Match	76.1%	Score 1044.4;	DB 11;	Length 2352;
Best Local Similarity	98.9%	Pred. No. 1.2e-210;		
Matches 1062; Conservative	0;	Mismatches 11;	Indels 1;	Gaps 1;

16	ACAAATCGCGAACC	RAGCCATAGCATGAAACAGCGAGCTTGCAGCCTCACCGACGAGTCT	75
147	ATACTCAGTCTACA	CAAGCCATAGCAGGAAACAGCGAGCTTGCAGCCTCACCGACGAGTCT	206
76	CAACTAAAAGGACT	CCCGGAGCTAGGGGTGGGAGCTCGGCCTCACACAGTGAAGTCCGG	135
207	CAACTAAAAGGACT	CCCGGAGCTAGGGGTGGGAGCTCGGCCTCACACAGTGAAGTCCGG	266
136	CTATTGGACTTTTG	TCCAGTGCACGCTGAGACAACAGGACACGGGAGGAGGTGTAGGA	195
267	CTATTGGACTTTTG	TCCAGTGCACGCTGAGACAACAGGACACGGGAGGAGGTGTAGGA	326
196	GAGAAGCGCGGAA	CACAGCGATCGCCAGCACCAAGTCCGCTTCCAGAGCTTTCGGTTTCT	255
327	GAGAAGCGCGGAA	CACAGCGATCGCCAGCACCAAGTCCGCTTCCAGAGCTTTCGGTTTCT	386
256	TTGGCTCCATCTTT	TGGGTGGCCCTTCCCGCGCTCTAGGGAGCGAAGGCTGAGGTGGCAGC	315
387	TTGGCTCCATCTTT	TGGGTGGCCCTTCCCGCGCTCTAGGGAGCGAAGGCTGAGGTGGCAGC	446
316	GGCAGGAGAGTCC	GGCGGACAGGACGACACTCCCCACTGGAGAAAGGATCTCTGAAGAAA	375
447	GGCAGGAGAGTCC	GGCGGACAGGACGACACTCCCCACTGGAGAAAGGATCTCTGAAGAAA	506
376	TGAAGTCAGCCCT	CAGAAATGAAGTTGACTGCGTGCCTTCTCGTTGACTGCGCCGG	435
507	TGAAGTCAGCCCT	CAGAAATGAAGTTGACTGCGTGCCTTCTCGTTGACTGCGCCGG	565
436	AGCTGTACTGCA	AGACCCTTGTGAGCTTCCCTAGTCTAAGAGTAGAGTCTGCTGAAAGT	495
566	AGCTGTACTGCA	AGACCCTTGTGAGCTTCCCTAGTCTAAGAGTAGAGTCTGCTGAAAGT	625
496	CATCCATCAGGTT	GAAAGACACTTGCATACAGATGAGAAGGAGATGCTGCTCTTTTGTG	555
626	CATCCATCAGGTT	GAAAGACACTTGCATACAGATGAGAAGGAGATGCTGCTCTTTTGTG	685
556	CCGGAGTGTTCAT	AGATGTGGTTCACCACTAATGTCAAGGACCTTCTGGATATTTACG	615
686	CCGGAGTGTTCAT	AGATGTGGTTCACCACTAATGTCAAGGACCTTCTGGATATTTACG	745
616	GGAAAGAGGTAA	GCTGTGTCGGGACTTGGCTGAACCTCTACAGAGTGAAGCGATT	675
746	GGAAAGAGGTAA	GCTGTGTCGGGACTTGGCTGAACCTCTACAGAGTGAAGCGATT	805
676	TCAGCTGCTCAAC	AGTATCTTGAAGATGGACAGAAAAGCTGTGGAGACCCACCTGCTCAG	735
806	TGACCTGCTCAAC	AGTATCTTGAAGATGGACAGAAAAGCTGTGGAGACCCACCTGCTCAG	865
736	GAACCCCTCACCT	TGTTTCGGACTATAGAGTGTCTATGGCAGAGATTGGTGAGATTGGA	795
866	GAACCCCTCACCT	TGTTTCGGACTATAGAGTGTCTATGGCAGAGATTGGTGAGATTGGA	925
796	TAAATCTGATGT	CTCATTAAATTTTCCCTCATGAAGGATTTACATGGCGCGAGCAAGAT	855
926	TAAATCTGATGT	CTCATTAAATTTTCCCTCATGAAGGATTTACATGGCGCGAGCAAGAT	985
856	AAGCAAGGAGAA	GAGTTTCTTGGACCTTGTGGTTGAGTTGAGAGAACTAAATTTGGTTGC	915
986	AAGCAAGGAGAA	GAGTTTCTTGGACCTTGTGGTTGAGTTGAGAGAACTAAATTTGGTTGC	1045

QY	228	CAAGTCGCGCTTCAGAGCTTTTCGGCTTTCTTTGCTCCATCTTTGGTGGGCGCTTCCCGCGCT	287
Db	258	CAAGTCGCGCTTCAGAGCTTTTCGGTTCCTTTGCTCCATCTTTGGTGGGCGCTTCCCGCGCT	317
QY	288	CTAGGGAGCGAAGGCTGAGTGGCAGCGCAGGAGAGTCCGGCCGCGACAGGACGAAC	347
Db	318	CTAGGGAGCGAAGGCTGAGTGGCAGCGCAGGAGTCCGGCCGCGACAGGACGAAC	377
QY	348	CCCCACTGAAAGGATTTCTGAAAGAAATGAAGTCAGCCCTCAGAAATGAAGTTGACTGC	407
Db	378	CCCCACTGGAAGAGATTTCTGAAAGAAATGAAGTCAGCCCTCAGAAATGAAGTTGACTGC	437
QY	408	CTGCTGGCTTTCTGTTGACTGCGCGGAGCTCTACTGCAAGACCCCTTGAGACTTCCCT	467
Db	438	CTGCTGGCTTT-CTGTTGACTGCGCGGAGCTGTACTGCAAGACCCCTTGAGACTTCCCT	496
QY	468	AGTCTAAGAGTAGGATGCTCTGCTGAAGTCATCCATCAGGTTGAAGAGCACTTTGATACAG	527
Db	497	AGTCTAAGAGTAGGATGCTCTGCTGAAGTCATCCATCAGGTTGAAGAGCACTTTGATACAG	556
QY	528	ATGAGAAGGAGATGCTGCTCTTTTGTGCGGGATGTGCTATAGATGTGGTTCCACCTA	587
Db	557	ATGAGAAGGAGATGCTGCTCTTTTGTGCGGGATGTGCTATAGATGTGGTTCCACCTA	616
QY	588	ATCTCAGGGACCTTCGGATATTTTACGGGAAAGAGGTAAAGCTCTCTGTCGGGACTTGG	647
Db	617	ATCTCAGGGACCTTCGGATATTTTACGGGAAAGAGGTAAAGCTCTCTGTCGGGACTTGG	676
QY	648	CTGAACCTGCTCTACAGAGTCAGGCGATTTGACCTGCTCAAAAGCTATCTTGAAGATGGACA	707
Db	677	CTGACCTGCTCTACAGAGTCAGGCGATTTGACCTGCTCAAAAGCTATCTTGAAGATGGACA	736
QY	708	GAAGAGCTGGAGAGCCACCCTGCTCAGGAACCCCTCACCTGTTTCGGACTATAGAGTGC	767
Db	737	GAAGAGCTGGAGAGCCACCCTGCTCAGGAACCCCTCACCTGTTTCGGACTATAGAGTGC	796
QY	768	TGATGGCAGAGATTGGTGAGGATTTGGATAAATCTGATGTCTCATTAATTTTCTCTCA	827
Db	797	TGATGGCAGAGATTGGTGAGGATTTGGATAAATCTGATGTCTCATTAATTTTCTCTCA	856
QY	828	TGAAGGATTACATGGGCCGAGGCAAGATAAGCAAGGAGAGAGTTCCTTGGACCTTTGTTG	887
Db	857	TGAAGGATTACATGGGCCGAGGCAAGATAAGCAAGGAGAGAGTTCCTTGGACCTTTGTTG	916
QY	888	TTGAGTTGGAGAACTAAATTTGGTTGCCCGCCAGATCAACTGAGATTTATTAGAAAAATGCC	947
Db	917	TTGAGTTGGAGAACTAAATTTGGTTGCCCGCCAGATCAACTGAGATTTATTAGAAAAATGCC	976
QY	948	TAAAGAACATCCACAGAAATAGACTGAAGACAAAAATCCAGAAGTCAACAGCACTCTGTTTC	1007
Db	977	TAAAGAACATCCACAGAAATAGACTGAAGACAAAAATCCAGAAGTCAACAGCACTCTGTTTC	1036
QY	1008	AAGGAGCAGGCAAGTTACAGGAATGTTCTCCAAGCAGCAATCCAAAAAGAGTCTCAAGG	1067
Db	1037	AAGGAGCAGGCAAGTTACAGGAATGTTCTCCAAGCAGCAATCCAAAAAGAGTCTCAAGG	1096
QY	1068	ATCCTTCAAATAACTTCAGGAT	1089
Db	1097	ATCCTTCAAATAACTTCAGGCT	1118

RESULT 3

US-09-410-194-16
; Sequence 16, Application US/09410194
; Patent No. US20020095030A1
; GENERAL INFORMATION:
; APPLICANT: Tschopp, Jurg
; APPLICANT: Thome, Margot
; APPLICANT: Burns, Kimberly
; APPLICANT: Imler, Marten
; APPLICANT: Hahne, Michael
; APPLICANT: Schroter, Michael

```

; APPLICANT: Schneider, Pascal
; APPLICANT: Bodmer, Jean- Luc
; APPLICANT: Steiner, Veronique
; APPLICANT: Rimoldi, Donata
; APPLICANT: Hofmann, Kay
; APPLICANT: French, E. Lars
; TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
; FILE REFERENCE: 11141-002001
; CURRENT APPLICATION NUMBER: US/09/410,194
; CURRENT FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: PCT/EP98/01857
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 2143
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (383)...(1822)
US-09-410-194-16

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Query Match	71.1%;	Score 975.8;	DB 9;	Length 2143;
Best Local Similarity	99.7%;	Pred. No. 3.4e-196;		
Matches 988; Conservative	0;	Mismatches 2;	Indels 1;	Gaps 1;

Qy	99	TAGGGTGGGACTCGCGCTCACACAGTGAAGTGC	CGGCTATTGGACTTTTGTCCAGTGAC	158
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Qy	159	AGCTGAGACAAAGGACCGGAGAGAGTGTAGGAG	AAGCGCCGCGCAACAGCGATC	218
Db				
Db	61	AGCTGAGACAAAGGACCGGAGAGAGTGTAGGAG	AAGCGCCGCGCAACAGCGATC	120
Qy	219	GCCCAGCACCAAGTCCGCTTCCAGGCTTTCCGGT	TTCTTGCCTCCATCTTTGGGTGCGCCT	278
Db	121	GCCCAGCACCAAGTCCGCTTCCAGGCTTTCCGGT	TTCTTGCCTCCATCTTTGGGTGCGCCT	180
Qy	279	TCCCGGGTCTTAGGGGAGCGAAGGCTCAGTGG	CGAGCGGAGAGCTCCGGCGCGGAC	338
Db	181	TCCCGGGTCTTAGGGGAGCGAAGGCTCAGTGG	CGAGCGGAGAGCTCCGGCGCGGAC	240
Qy	339	GGACGAATCCCCACTCGGAAGGATTCTCGAA	AGAAATGAAGTCAGCGCCTCAGAAATGAA	398
Db	241	GGACGAATCCCCACTCGGAAGGATTCTCGAA	AGAAATGAAGTCAGCGCCTCAGAAATGAA	300
Qy	399	GTTGACTGCGCTGCGGCTTTCCTGTTGACTGG	CGCGGAGCTGTACTCGAAGACCCCTTGTG	458
Db	301	GTTGACTGCGCTGCGGCTTTCCTGTTGACTGG	CGCGGAGCTGTACTCGAAGACCCCTTGTG	359
Qy	459	AGCTTCCTCTAGTCTAAGAGTAGGATGCTCT	GTAAGTCATCCATCAGTTGGAAGAAGCAC	518
Db	360	AGCTTCCTCTAGTCTAAGAGTAGGATGCTCT	GTAAGTCATCCATCAGTTGGAAGAAGCAC	419
Qy	519	TTGATACAGATGAGAAGGAGATGCTGCTCTT	TTTGTCCCGGATGTTGCTATAGATGG	578
Db	420	TTGATACAGATGAGAAGGAGATGCTGCTCTT	TTTGTCCCGGATGTTGCTATAGATGG	479
Qy	579	TTCCACCTAATGTCAGGACCTTCTGGATATTT	TACGGGAAGAGGTTAAGCTGCTGCTCG	638
Db	480	TTCCACCTAATGTCAGGACCTTCTGGATATTT	TACGGGAAGAGGTTAAGCTGCTGCTCG	539
Qy	639	GGGACTTTGGCTGAACTGCTCTACAGAGTGA	GGCGATTGTGACCTGCTCAACAGTATCTTGA	698
Db	540	GGGACTTTGGCTGAACTGCTCTACAGAGTGA	GGCGATTGTGACCTGCTCAACAGTATCTTGA	599
Qy	699	AGATGGACAGAAAGCTGTGGAGACCCACCTG	CTCAGGAACCCCTCAACCTTGTTCGGACT	758
Db	600	AGATGGACAGAAAGCTGTGGAGACCCACCTG	CTCAGGAACCCCTCAACCTTGTTCGGACT	659

Mon Aug 25 09:11:09 2003

Db 290 TTT-CTGTTGACGTCGGCGGAGGCTGACTGCAAGACCCCTTGAGCTTCCCTAGTCTAAG 348
 Qy 476 AGTAGGATGCTGCTGAAGTCATCCATCAGGTTGAAGAAGCACTTGTATACAGATGAGAAG 535
 Db 349 AGTAGGATGCTGCTGAAGTCATCCATCAGGTTGAAGAAGCACTTGTATACAGATGAGAAG 408
 Qy 536 GAGATGCTGCTCTTTTGTGTCGGGATGCTGCTATAGATGCTGCTCCACCTAATGTCAGG 595
 Db 409 GAGATGCTGCTCTTTTGTGTCGGGATGCTGCTATAGATGCTGCTCCACCTAATGTCAGG 468
 Qy 596 GACCTTCTGGATATTTTACGGGAAG 621
 Db 469 GACCTTCTGGATATTTTACGGGAAG 494

RESULT 7
 US-09-918-995-35401
 ; Sequence 35401, Application US/09918995
 ; Publication No. US20030073623A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hyseq, Inc.
 ; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
 ; FILE REFERENCE: 20411-756
 ; CURRENT APPLICATION NUMBER: US/09/918,995
 ; PRIOR FILING DATE: 2001-07-30
 ; PRIOR APPLICATION NUMBER: US/09/235,076
 ; NUMBER OF SEQ ID NOS: 38054
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 35401
 ; LENGTH: 441
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)...(441)
 ; OTHER INFORMATION: n = A,T,C or G
 US-09-918-995-35401

Query Match 27.9%; Score 382.4; DB 11; Length 441;
 Best Local Similarity 98.3%; Pred. No. 3,5e-71;
 Matches 397; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
 Qy 268 TGGGTGCGCTTCCCGGCTCTAGGGAGCGAGGCTGAGTGGCAGCGGAGGAGTC 327
 Db 39 TCGGTGGAATCCCGGCTCTAGGGAGCGAGGCTGAGTGGCAGCGGAGGAGTC 98
 Qy 328 CGGCCGCGACAGGACCACTCCCGGCTCTAGGGAGCGAGGCTGAGTGGCAGCGGAGGAGTC 387
 Db 99 CGGCCGCGACAGGACCACTCCCGGCTCTAGGGAGCGAGGCTGAGTGGCAGCGGAGGAGTC 158
 Qy 388 TCAGAAATGAAGTTGACTGCTGCTGCTTCCCTGTTGACTGCGCCGAGGCTGTACTGCA 447
 Db 159 TCAGAAATGAAGTTGACTGCTGCTGCTTCCCTGTTGACTGCGCCGAGGCTGTACTGCA 217
 Qy 448 AGACCCCTGTGAGCTTCCCTAGTCTTAAGATGAGTGTCTGCTGAGTCAATCCATCAGGT 507
 Db 218 AGACCCCTGTGAGCTTCCCTAGTCTTAAGATGAGTGTCTGCTGAGTCAATCCATCAGGT 277
 Qy 508 TGAAGAGCACTTGATACAGATGAGAAAGAGATGCTGCTCTTTTGTGCGCGGATGTTGC 567
 Db 278 TGAAGAGCACTTGATACAGATGAGAAAGAGATGCTGCTCTTTTGTGCGCGGATGTTGC 337
 Qy 568 TATAGATGTTGGTTCACCTAATGTCAGGACCTTCTGGATATTTTACGGGAAGAGGTAA 627
 Db 338 TATAGATGTTGGTTCACCTAATGTCAGGACCTTCTGGATATTTTACGGGAAGAGGTAA 397
 Qy 628 GCTGCTGTCGGGACTTGGCTGAAGTCTCTACAGATGAGGC 671
 Db 398 GCTGCTGTCGGGACTTGGCTGAAGTCTCTACAGATGAGGC 441

RESULT 8

US-09-410-194-18
 ; Sequence 18, Application US/09410194
 ; Patent No. US20020095030A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Tschoop, Jurg
 ; APPLICANT: Thome, Margot
 ; APPLICANT: Burns, Kimberly
 ; APPLICANT: Irmler, Marten
 ; APPLICANT: Hahne, Michael
 ; APPLICANT: Schroter, Michael
 ; APPLICANT: Schneider, Pascal
 ; APPLICANT: Bodmer, Jean-Luc
 ; APPLICANT: Steiner, Veronique
 ; APPLICANT: Rimoldi, Donata
 ; APPLICANT: Hofmann, Kay
 ; APPLICANT: French, E. Lars
 ; TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
 ; FILE REFERENCE: 11141-002001
 ; CURRENT APPLICATION NUMBER: US/09/410,194
 ; CURRENT FILING DATE: 1999-09-30
 ; PRIOR APPLICATION NUMBER: PCT/EP98/01857
 ; PRIOR FILING DATE: 1998-03-31
 ; PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2
 ; PRIOR FILING DATE: 1997-04-01
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 18
 ; LENGTH: 2452
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (172)...(1614)
 US-09-410-194-18

Query Match 27.2%; Score 373.8; DB 9; Length 2452;
 Best Local Similarity 68.8%; Pred. No. 5,5e-69;
 Matches 532; Conservative 0; Mismatches 232; Indels 9; Gaps 1;
 Qy 313 AGCGGAGGAGAGTCGGCGCGACAGGAGCACTCCCGACTGGAAAGNTCTGAAAG 372
 Db 9 AGGCTCTCAAGCGGCCACTTTAGGCGCGACAGAGTGTCTCTATTGCAAGAACTCTGAGAG 68
 Qy 373 AAATGAAGTCAGCCCTCAGAAATGAAGTTGACTGCTGCTGG-----CTTTCCTGT 423
 Db 69 AAATGAAGAGAGCTCTCAGCAATGATGTTGGCTTCTCGTGGTCCCGAGAGCCCTGCTAA 128
 Qy 424 TGACTGCGCGGAGCTGTACTGCAAGACCCCTTGTGAGCTTCCCTAGTCTTAAGAGTAGGAT 483
 Db 129 TGGATGAGAGCTGGACGAGAAACCTGGCTGCTGTGGTTCTGAACATGCCCGAGAGCCCTGT 188
 Qy 484 GTCGTGCTGAAGTCATCCATCAGGTTGAAGAGCACTTGTATACAGATGAGAGGAGATGCT 543
 Db 189 GTCTGCGGAGGTCAITCACCAGGTGGAAGAGTGTCTTTGATGAAGACGAGAGAGATGAT 248
 Qy 544 GCTCTTTTGTGCGGATGTTGCTATAGATGTTGGTTCACCTTAATGTCAGGAGCCCTTCT 603
 Db 249 GCTCTTCTGTGTAGATGCTGACTGAGAACCTGGCTGCACCTAACCTCAGGAGCCCTCT 308
 Qy 604 GGATATTTACGGGAAAGAGGTAAGCTGTCTGTCGGGAGCTTGGCTCAACTGCTCTACAG 663
 Db 309 GGATAGCTTAAAGTGAAGAGAGCCAGCTCTCTTTTGTCTACCTTGGCTGAATGCTCTACAG 368
 Qy 664 AGTGAGGCGATTTGACCTGCTCAACAGTATCTCAAGATGGACAGAGAAAGCTGTGGAGAC 723
 Db 369 AGTGAGGCGGTTTGACCTTCTCAGAGAGATCTTGAAGACAGACAGAAACCAACCGTGGAGGA 428
 Qy 724 CCACCTGCTCAGGAAACCTCACCTTGTGTCGAGATATAGAGTGTGTATGTCAGAGATGG 783
 Db 429 CCACCTGCGCAGAAACCTCACCTGTTCTCTGATTATAGGCTCTGCTGATGGAGATGG 488
 Qy 784 TGAGGATTTGGATAAATCTGATGCTCTCTCAATTTTCTCATGAAGGATTACATGGG 843

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Db      489  TGAAGCTTAGATCAGACGATGTATCTCTCTTAGTTTCCCTACAGGGATTACACAGG 548
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Db      549  CAGAGCAAGATAGCAAGGACAAGATTCTTGGATCTGGTGATTAATGATTCGAGAACT 608
QY      904  AAATTTGGTGGCCCGCAGATCAACTGGATTTATTAGAAAATCCCTAAAGAAATCCACAG 963
Db      609  GAATCTAATTTGCTTCAGACCAATTGAATTTGTTAGAAAAATGCCTGAAGAACATCCACAG 668
QY      964  AATAGACCTGGAAGACAAAATCCAGAGTACAGCAGTCTGTTCAAGGAGGAGGACACAG 1023
Db      669  AATAGACTTGAACACAAAGATCCAGAGTACACCCAGTCCAGCCAGGAGCAAGATCAAA 728
QY      1024 TTACAGGAATGTTCTCCAGCAGCAATCCAAAAGAGTCTCAAGGATCCCTTCAA 1076
Db      729  TATGAATACTCTCCAGGCTTCGCTCCCAAAATTTAGTATCAAGTATACTCAA 781

RESULT 9
US-09-833-381-436/c
; Sequence 436, Application US/09833381
; Patent No. US20020132090A1
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: No. US20020132090A1el Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833,381
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 436
; LENGTH: 490
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(490)
; OTHER INFORMATION: n = A,T,C or G
US-09-833-381-436

Query Match      25.8%; Score 354.2; DB 10; Length 490;
Best Local Similarity 82.4%; Pred. No. 3.3e-65;
Matches 404; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

QY      653  CTGCTCTACAGAGTGAGGCGATTGACCTGCTCAACAGTATCTTGAAGATGGACAGAAA 712
Db      490  CTGTTCTATAGAGTGAGGCGATTGATTGCTCTACATGCATCTCGCACATCGACACA 431
QY      713  GCTGTGGAGACCCACTGCTCAGGAACCTCACCTTGTTCGGACTATAGAGTGTCTGATG 772
Db      430  GCTGTGCAGATCCACNTGCTTAGCCATCTCACTTGTTCACATATACATGCTGATG 371
QY      773  GCAGAGATTGGTGGAGATTGGATAAATCTGATGTCTCATTAATTTCTCATGAAG 832
Db      370  GTAGAGATGGTGGAGCATTTTCGATCAATNCCATGTGTCTCATATTCTTTTATCAAG 311
QY      833  GATTACATGGGCGGAGCAAGATAAGCAGAGAGAGATTTCTTGACCTTGTGTGAG 892
Db      310  CATCCAATGGCTCAGGTGAAGATAACCCAGGAGAGAGTTTTTGGACTTTGTGTGTAG 251
QY      893  TTGGAGAACTAAATTTGGTTCGCCAGATCAACTGGATTATTAGAAAATGCGCTAAG 952
Db      250  TTGGAGAAATATACATCCGCTCGCCTCAGATTCTACATTCATTATGACAAATGCTTAAG 191
QY      953  AACATCCACAGATAGACTGAAGACAAAATCCAGAGTACAGACAGTCTCTTCAAGGA 1012
Db      190  AACATCCACAGATAGACTCAACCCAAAATCCAGAGTATAAGCAGTCTGTTCAGCA 131
QY      1013 GCAGGACAAAGTTACAGGAATGTTCTCCAGCAGCAATCCAAAAGAGTCTCAAGGATCCT 1072
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Db      130  GCAGGACAAGTCACACGAATGTTTCCACCAGCAATTAACACGAGTTTCCAGGATCCT 71
QY      1073  TCAATAAATCTTCAGATGATAACACCCATATGCCCATTTGCTGTGATCTGAAAAATTTCTTGA 1132
Db      70  TTAATAATATTTTCAGATGATCAACCCATATGCCCATTTGCTGTGATTTGAAAAATTTTGGC 11
QY      1133  AATTGTTCCA 1142
Db      10  CATTTGTTCCA 1

RESULT 10
US-09-918-995-35271
; Sequence 35271, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 35271
; LENGTH: 443
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(443)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-35271

Query Match      25.1%; Score 345; DB 11; Length 443;
Best Local Similarity 91.3%; Pred. No. 2.8e-63;
Matches 377; Conservative 0; Mismatches 35; Indels 1; Gaps 1;

QY      266  CTTGGTGCGCCTTCCCGCGTCTAGGGAGGAGGAGGCTGAGGTGGCAGCGGAGAGAG 325
Db      32  CTTGGTGCGGTAATTTCCAGCGTCTAGCGGAGGGAATGCTGAGGTGGCAGCGCTAGACAG 91
QY      326  TCCGCGCGGAGAGAGCAACTCCCGCACTGGAAGGATTTCTGAAAGAAATGAAGTCAGC 385
Db      92  TCCGCGCGGAGAGAGCAACTCCCGCACTGGAAGGATTTCTGAGAGAAATGAAGTCAGC 151
QY      386  CTTCAAGAAATGAAGTTGACTGCTGCTGCTTTCTGTTGACTGGCCCGGAGCTGTACTG 445
Db      152  CTTCAAGAAATGAAGTTGACTGCTGCTGCTTT-CTGTTGACTGGCCCGGAGCTGTACTG 210
QY      446  CAAGACCTTGTGAGCTTCCCTAGTCTAGAGTAGGATGCTGCTGCTGAAGTCAATCATCAG 505
Db      211  CAAGACCTTGTGAGCTTACCTAGTCTAGAGTAGGATGCTGCTGAGGTCTATCCATCT 270
QY      506  GTTGAAGAGCACTTGTATACAGATGAGAGGAGAGTCTGCTCTTTTGTGCGGGGATGTT 565
Db      271  GCTGAAGAGCACTTGTATCAATCAGAAGGAGATGCTCTTTTGTGCGGGGATGTT 330
QY      566  GCTATAGATGTGGTTCACCTAATGTGAGGGACCTTCTGATTTTACGGGAAAGAGGT 625
Db      331  GCTATATATGTGGATCCACCTAACGTTGAAGGACCTTCTGGATATTCTACTGGAAGAGGA 390
QY      626  AAGCTGCTCTCGGGAGCTTGGCTGAACCTGCTCTACAGAGTGAAGGCGATTTCGA 678
Db      391  AAACGTCTCTCGGGAGCTTGAACCTGCTCTACAAAGTGAAGGCGATTTCGA 443

RESULT 11
US-10-005-921-1
; Sequence 1, Application US/10005921
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Mon Aug 25 09:11:09 2003

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; Publication No. US20020174450A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJ207C1
; CURRENT APPLICATION NUMBER: US/10/103,313
; CURRENT FILING DATE: 2002-03-12
; NUMBER OF SEQ ID NOS: 653
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34
; LENGTH: 1319
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc.feature
; LOCATION: (1136)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-103-313-34

Query Match      23.6%; Score 324.4; DB 14; Length 1319;
Best Local Similarity 97.6%; Pred. No. 1.1e-58;
Matches 328; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 754 GGACTATAGAGTCTGATGGCAGAGATTGGTGGAGGATTTGGATAAATCTGTGTCTCC 813
DB 14 GCACGAGGAGTCTGATGGCAGAGATTGGTGGAGGATTTGGATAAATCTGTGTCTCC 73
QY 814 ATTAATTTCTCATGAAGATTACATGGCCGAGGCAAGATAAGCAAGAGAGTTT 873
DB 74 ATTAATTTCTCATGAAGATTACATGGCCGAGGCAAGATAAGCAAGAGAGTTT 133
QY 874 CTGGACCTTGTGGTGGTGGAGAACTAAATTTGGTGGCCAGATCAACTGGATTT 933
DB 134 CTGGACCTTGTGGTGGTGGAGAACTAAATTTGGTGGCCAGATCAACTGGATTT 193
QY 934 ATTAGAAAATGCTTAAAGAACATCCACAGATAGACCTGAGACAAAATCCAGAGTA 993
DB 194 ATTAGAAAATGCTTAAAGAACATCCACAGATAGACCTGAGACAAAATCCAGAGTA 253
QY 994 CAAGCAGCTGTTCAGGAGCAGGCAAGTTACAGAAATGTTCTCAAGCAGCAATCCA 1053
DB 254 CAAGCAGCTGTTCAGGAGCAGGCAAGTTACAGAAATGTTCTCAAGCAGCAATCCA 313
QY 1054 AAAGAGTCTCAAGGATCCTTCAATAACTTCCAGAT 1089
DB 314 AAAGAGTCTCAAGGATCCTTCAATAACTTCCAGCT 349

RESULT 13
US-10-115-928-19
; Sequence 19, Application US/10115928
; Publication No. US20030092615A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT204C1
; CURRENT APPLICATION NUMBER: US/10/115,928
; CURRENT FILING DATE: 2002-04-05
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 1319
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc.feature
; LOCATION: (1136)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-115-928-19

Query Match      23.6%; Score 324.4; DB 14; Length 1319;
Best Local Similarity 97.6%; Pred. No. 1.1e-58;
Matches 328; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 469 GTCTAAGAGTAGTGTCTGCTGAAGTCATCCATCAGTTGAAGAGCAGCTGTGATCAGA 528
DB 77 GCGCCAGAGCCCTGTCTGCGGAGTCAATTCACAGGTGGAAGAGTGTCTGTATGAAGA 136
QY 529 TGAGAAGAGATGTGCTCTTTTGTGCGGAGTGTGCTATAGATGTGTGTTCCACCTAA 588
DB 137 CGAGAAGAGATGTGCTCTTCTCTGTGTAGAGTGTGCTGAGAACCTGGCTGACCTAA 196
QY 589 TGTCTAGGAGACCTTCTGGATATTTTACGGGAAAGAGTAAAGTGTCTGTGCGGGACTTGGC 648
DB 197 CTTGAGGAGACCTTCTGGATATTTTAAAGTGAGAGGCGGAGCTCTCTTTTGTACCTTGGC 256
QY 649 TGAATCTGTCTACAGATGAGGCGATTTGACCTGCTCAAGCTATCTTGAAGATGGACAG 708
DB 257 TGAATCTGTCTACAGATGAGGCGATTTGACCTGCTCAAGAGATCTTGAAGATGGACAG 316
QY 709 AAAAGCTGTGGAGACCCCTCTCTCAGGAACCCCTCACCTTGTTCGGGACTATAGAGTGTCT 768
DB 317 AGCAACCTGTGGAGACCCCTCTCAGGAACCCCTCACCTTGTTCGGGACTATAGAGTGTCT 376
QY 769 GATGGCAGAGATTTGGATTAATCTCATGTGCTCCATTAATTTCC 824
DB 377 GCTGATGGAGATTTGGTGTAGAGCTTAGATCAGAACGATGTATCTCTCTTAGTTTCCCTTAC 436
QY 825 -----TCATGAAGGATTACATGGCGGCAAGATAAGCAAGAGAGAGTTTCTTGGGA 879
DB 437 AAGGATTCAAGGATTACAGGACAGGCAAGGCAAGATGCCAAGGACAGAGTTTCTTGGGA 496
QY 880 CTTGTGGTGTGATTTGGAGAACTAAATTTGTTGCTCCAGATCAACTGGATTTATTTAGA 939
DB 497 TCTGTGTGATTAATTTGGAGAACTAAATTTGTTGCTCCAGATCAACTGGATTTATTTAGA 556
QY 940 AATATCCTTAAGAACTACAGAGATACCTGAGCAAAAATCCAGAGTCAAGCA 999
DB 557 AATATCCTTAAGAACTACAGAGATACCTGAGCAAAAATCCAGAGTCAAGCA 616
QY 1000 GTCTGTTCAGGAGCAGGAGGATTTACAGAAATGTTCTTCCAGGAGCAATCCAAAGAG 1059
DB 617 GTCCAGCAGGAGGAGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 676
QY 1060 TCTCAAGGATCTTCAA 1076
DB 677 TATCAAGTATAACTCAA 693

RESULT 12
US-10-103-313-34
; Sequence 34, Application US/10103313
; Publication No. US20030082758A1
; GENERAL INFORMATION:
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Mon Aug 25 09:11:09 2003

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; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488,0970002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 414 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-09-009-893-23

Query Match          22.8%; Score 313.4; DB 11; Length 414;
Best Local Similarity .931%; Pred. No. 1.3e-56;
Matches 367; Conservative 0; Mismatches 20; Indels 7; Gaps 4;

QY   638 GGGGACTTGGCTGTGAAGCTCTACAGAGTCAGCGGATTTTGACCTGCTCAAAAGCTATCTTG 697
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    15 GNGGAGTTGGCTGTGAAGCTCTACAGAGTAGGGCGATTTGACCTGCTCAAAAGCTATCTTG 74
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY   698 AAGATGGACAGAAAAGCTGTGGAGACCACCTGCTCAGGAACCCCTCACCTTGTTCGGAC 757
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    75 AAGATGGACAGAAAAGCTGTGGAGACCACCTGCTCAGGAACCCCTCACCTTGTTCGGAC 134

QY   758 TATAGAGTCTGATGGCAGAGATTGGTGAGGATTTGGATAATCTCATGTGCTCCATTA 817
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    135 TATAGAGTCTGATGGCAGAGATTGGTGAGGATTTGGATAATCTCATGTGCTCCATTA 194

QY   818 ATTTTCCTCATGAAGATTACATGGCGGAGGCCAAGATAGAAGAGAGAGTTTCTTG 877
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    195 ATTTTCCTCATGAAGATTACATGGCGGAGGCCAAGATAGAAGAGAGAGTTTCTTG 254

QY   878 G--ACCTTGTGGTTGAGTT-GGAGAAACTAAATTTGG-TTGCCCCCAGATCAACTGG---A 930
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    255 GGACCTTGTGCTTGCAGTTGGGAGAAACTAAATCTGCTTTGCCCCAGATCAACTNGGGAT 314

QY   931 TTATTATGAAAAATGCCTTAAGAACATCCAGAAATAGACCTGNAGCAAATAATCCAGAA 990
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    315 TTNTTAGGAAAAATGCTTAAGAACATNCACAGGTATAGACCTGNAGCAAATAATCCAGNA 374

QY   991 GTACAAGCAGCTGTGTTCAAGGACGAGGACAAGT 1024
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    375 GTACAGCAGATTGTTTCAGGAGACGAGGACAATT 408
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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Search completed: August 22, 2003, 17:24:11
Job time : 316.115 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 13, 2003, 16:40:24 ; Search time 13.2411 Seconds
(without alignments)
706.188 Million cell updates/sec

Title: US-09-380-546A-4
Perfect score: 1114
Sequence: 1 MSAEVIHQVEEALDTDEKEM.....RMITPYAHCPDKILGNCSM 221

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Issued Patents:AA.*
- 1: /cgn2.6/ptodata/1/1aa/5A_COMB.pep.*
 - 2: /cgn2.6/ptodata/1/1aa/5B_COMB.pep.*
 - 3: /cgn2.6/ptodata/1/1aa/6A_COMB.pep.*
 - 4: /cgn2.6/ptodata/1/1aa/6B_COMB.pep.*
 - 5: /cgn2.6/ptodata/1/1aa/PCTUS_COMB.pep.*
 - 6: /cgn2.6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1114	100.0	221	3	US-09-382-155-17
2	1114	100.0	221	3	US-09-074-044A-17
3	1015	91.1	445	3	US-08-859-167-2
4	1015	91.1	445	3	US-09-109-273-2
5	1015	91.1	445	3	US-09-276-993-2
6	1015	91.1	445	4	US-09-723-450-2
7	1007	90.4	480	3	US-08-795-088A-2
8	987	88.6	480	4	US-09-069-023-34
9	417	37.4	84	3	US-09-074-044A-2
10	403	36.2	84	3	US-09-382-155-2
11	384	34.5	78	3	US-09-382-155-1
12	384	34.5	78	3	US-09-074-044A-1
13	218.5	19.6	241	3	US-09-382-155-21
14	218.5	19.6	241	3	US-09-074-044A-21
15	195	17.5	220	2	US-08-807-200-2
16	195	17.5	220	3	US-09-001-777-2
17	192.5	17.3	235	4	US-08-983-502-5
18	192.5	17.3	235	4	US-09-516-747-5
19	192.5	17.3	235	5	PCT-US96-10521-5
20	192.5	17.3	257	1	US-08-618-164-2
21	192.5	17.3	277	4	US-08-983-502-8
22	192.5	17.3	277	4	US-09-516-747-8
23	192.5	17.3	277	5	PCT-US96-10521-8
24	192.5	17.3	479	2	US-08-807-200-12
25	192.5	17.3	479	3	US-08-852-782-3
26	192.5	17.3	479	3	US-09-001-777-12
27	192.5	17.3	479	4	US-08-983-502-7

28	192.5	17.3	479	4	US-09-516-747-7	Sequence 7, Appl1
29	192.5	17.3	479	5	PCT-US96-10521-7	Sequence 7, Appl1
30	190	17.1	261	4	US-08-983-502-25	Sequence 25, Appl1
31	190	17.1	261	4	US-09-516-747-25	Sequence 25, Appl1
32	190	17.1	261	5	PCT-US96-10521-25	Sequence 25, Appl1
33	190	17.1	464	4	US-08-983-502-18	Sequence 18, Appl1
34	190	17.1	464	4	US-09-516-747-18	Sequence 18, Appl1
35	190	17.1	464	5	PCT-US96-10521-18	Sequence 18, Appl1
36	187.5	16.8	479	3	US-09-382-155-28	Sequence 28, Appl1
37	187.5	16.8	479	3	US-09-074-044A-27	Sequence 27, Appl1
38	187.5	16.8	479	3	US-09-074-044A-28	Sequence 28, Appl1
39	187	16.8	180	3	US-09-382-155-18	Sequence 18, Appl1
40	187	16.8	180	3	US-09-074-044A-18	Sequence 18, Appl1
41	184.5	16.6	479	3	US-09-074-044A-26	Sequence 26, Appl1
42	182.5	16.4	479	3	US-09-382-155-27	Sequence 27, Appl1
43	176.5	15.8	479	3	US-09-382-155-26	Sequence 26, Appl1
44	173	15.5	139	3	US-09-382-155-20	Sequence 20, Appl1
45	173	15.5	139	3	US-09-074-044A-20	Sequence 20, Appl1

ALIGNMENTS

RESULT 1
US-09-382-155-17
; Sequence 17, Application US/09382155B
; Patent No. 6160095
; GENERAL INFORMATION:
; APPLICANT: CHAUDHARY, PREET M
; APPLICANT: HOOD, LEROY
; TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NF-kB, JNK AND APOPTOSIS
; FILE REFERENCE: Chaudhary
; CURRENT APPLICATION NUMBER: US/09/382,155B
; EARLIER FILING DATE: 1999-08-24
; EARLIER APPLICATION NUMBER: 09/074,044
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 17
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-382-155-17

Query Match	100.0%	Score 1114;	DB 3;	Length 221;
Best Local Similarity	100.0%	Pred. No. 8.7e-105;		
Matches 221;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVYPPNVRDLDLILRERKGLSVGDLAELLY	60	
Db	1	MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVYPPNVRDLDLILRERKGLSVGDLAELLY	60	
QY	61	RVRRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIFLMKDYM	120	
Db	61	RVRRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIFLMKDYM	120	
QY	121	GRGKISKERSFLDVVLEKLNIVAPDQLDLEKLNKIHRIIDLKTKIQYKQSVQAGT	180	
Db	121	GRGKISKERSFLDVVLEKLNIVAPDQLDLEKLNKIHRIIDLKTKIQYKQSVQAGT	180	
QY	181	SYRNVQAQIKSLKDPSPNNFRMITPYAHCPDLKILGNCSM	221	
Db	181	SYRNVQAQIKSLKDPSPNNFRMITPYAHCPDLKILGNCSM	221	

RESULT 2
US-09-074-044A-17
; Sequence 17, Application US/09074044A
; Patent No. 6207458
; GENERAL INFORMATION:
; APPLICANT: CHAUDHARY, PREET M
; APPLICANT: HOOD, LEROY

517198

;; TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NK-KB, JNK AND
;; TITLE OF INVENTION: APOPTOSIS PATHWAYS AND METHODS OF USING THE SAME
;; NUMBER OF SEQUENCES: 28
;; CORRESPONDENCE ADDRESSES:
;; ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS
;; STREET: 2405 GRAND BLVD., SUITE 400
;; CITY: KANSAS CITY
;; STATE: MISSOURI
;; COUNTRY: USA
;; ZIP: 64108
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/074,044A
;; FILING DATE:
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: COLLINS, JOHN M
;; REGISTRATION NUMBER: 26,262
;; REFERENCE/DOCKET NUMBER: 26588
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 816/474-9050
;; TELEFAX: 816/474-9057
;; INFORMATION FOR SEQ ID NO: 17:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 221 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: not relevant
;; MOLECULE TYPE: protein
;; ORIGINAL SOURCE:
;; ORGANISM: Homo sapiens
;; US-09-074-044A-17
Query Match 100.0%; Score 1114; DB 3; Length 221;
Best Local Similarity 100.0%; Pred. No. 8.7e-105;
Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSAEVTHQVEEALDTDEKEMLLFLCRDVAIDVPPNVRDLIDLRLRERKLSVGDLAELLY 60
Db 1 MSAEVTHQVEEALDTDEKEMLLFLCRDVAIDVPPNVRDLIDLRLRERKLSVGDLAELLY 60
QY 61 RVRFFDLKRLKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIFLMKDYM 120
Db 61 RVRFFDLKRLKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIFLMKDYM 120
QY 121 GRGKISKESFSLDVLVVELEKLNVLVAPDQDLLEKLNHRIIDLTKTKIQYKQSVQAGT 180
Db 121 GRGKISKESFSLDVLVVELEKLNVLVAPDQDLLEKLNHRIIDLTKTKIQYKQSVQAGT 180
QY 181 SYRNVLAQAQKSLKDPSSNNFRMITPYAHCPLDKILGNCM 221
Db 181 SYRNVLAQAQKSLKDPSSNNFRMITPYAHCPLDKILGNCM 221
RESULT 3
US-08-859-167-2
; Sequence 2, Application US/08859167
; Patent No. 6037461
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: FADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF
; TITLE OF INVENTION: USING THE SAME, AND COMPOSITIONS FOR AND METHODS
; TITLE OF INVENTION: OF MAKING THE SAME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6037461iris
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia

;; STATE: PA
;; COUNTRY: USA
;; ZIP: 19103
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: WINDOWS
;; SOFTWARE: WordPerfect
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/859,167
;; FILING DATE:
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Deluca, Mark
;; REGISTRATION NUMBER: 33,229
;; REFERENCE/DOCKET NUMBER: TJU-
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (215) 568-3100
;; TELEFAX: (215) 568-3439
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 445 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-859-167-2
Query Match 91.1%; Score 1015; DB 3; Length 445;
Best Local Similarity 94.5%; Pred. No. 2.3e-94;
Matches 207; Conservative 1; Mismatches 11; Indels 0; Gaps 0;
QY 1 MSAEVTHQVEEALDTDEKEMLLFLCRDVAIDVPPNVRDLIDLRLRERKLSVGDLAELLY 60
Db 1 MSAEVTHQVEEALDTDEKEMLLFLCRDVAIDVPPNVRDLIDLRLRERKLSVGDLAELLY 60
QY 61 RVRFFDLKRLKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIFLMKDYM 120
Db 61 RVRFFDLKRLKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIFLMKDYM 120
QY 121 GRGKISKESFSLDVLVVELEKLNVLVAPDQDLLEKLNHRIIDLTKTKIQYKQSVQAGT 180
Db 121 GRGKISKESFSLDVLVVELEKLNVLVAPDQDLLEKLNHRIIDLTKTKIQYKQSVQAGT 180
QY 181 SYRNVLAQAQKSLKDPSSNNFRMITPYAHCPLDKILGNC 219
Db 181 SYRNVLAQAQKSLKDPSSNNFRMITPEERYKMKSKPLGIC 219
RESULT 4
US-09-109-273-2
; Sequence 2, Application US/09109273
; Patent No. 6063760
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: FADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF
; TITLE OF INVENTION: USING THE SAME, AND COMPOSITIONS FOR AND METHODS
; TITLE OF INVENTION: OF MAKING THE SAME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6063760rls
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: WINDOWS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/109,273

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; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/859,167
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 445 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-109-273-2

Query Match          91.1%; Score 1015; DB 3; Length 445;
Best Local Similarity 94.5%; Pred. No. 2.3e-94;
Matches 207; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPVPPNVRDLIDLRLRGKLSVGDLAELLY 60
DB 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPVPPNVRDLIDLRLRGKLSVGDLAELLY 60
QY 61 RVRFPDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMMAEIGEDLDKSDVSSLIPLMKDYM 120
DB 61 RVRFPDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMMAEIGEDLDKSDVSSLIPLMKDYM 120
QY 121 GRGKISKEKSFLLDVVVELEKLNLVAPDQLDLEKCLKNHRIIDLTKTIQKYKQSVQAGT 180
DB 121 GRGKISKEKSFLLDVVVELEKLNLVAPDQLDLEKCLKNHRIIDLTKTIQKYKQSVQAGT 180
QY 181 SYRNVLOAAIQSKLSDPSNFRMITPYAHCPDLKILGNC 219
DB 181 SYRNVLOAAIQSKLSDPSNFRSIPERYKMKSKPLGIC 219

RESULT 5
US-09-276-993-2
; Sequence 2, Application US/09276993
; Patent No. 6207801
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: FADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF
; TITLE OF INVENTION: USING THE SAME, AND COMPOSITIONS FOR AND METHODS
; TITLE OF INVENTION: OF MAKING THE SAME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6207801ris
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: WINDOWS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/276,993
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/859,167
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark

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; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 445 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-276-993-2

Query Match          91.1%; Score 1015; DB 3; Length 445;
Best Local Similarity 94.5%; Pred. No. 2.3e-94;
Matches 207; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPVPPNVRDLIDLRLRGKLSVGDLAELLY 60
DB 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPVPPNVRDLIDLRLRGKLSVGDLAELLY 60
QY 61 RVRFPDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMMAEIGEDLDKSDVSSLIPLMKDYM 120
DB 61 RVRFPDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMMAEIGEDLDKSDVSSLIPLMKDYM 120
QY 121 GRGKISKEKSFLLDVVVELEKLNLVAPDQLDLEKCLKNHRIIDLTKTIQKYKQSVQAGT 180
DB 121 GRGKISKEKSFLLDVVVELEKLNLVAPDQLDLEKCLKNHRIIDLTKTIQKYKQSVQAGT 180
QY 181 SYRNVLOAAIQSKLSDPSNFRMITPYAHCPDLKILGNC 219
DB 181 SYRNVLOAAIQSKLSDPSNFRSIPERYKMKSKPLGIC 219

RESULT 6
US-09-723-450-2
; Sequence 2, Application US/09723450
; Patent No. 6576751
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: Fadd-Like Anti-Apoptotic Molecules, Methods Of Using The Same,
; TITLE OF INVENTION: Compositions For And Methods Of Making The Same
; FILE REFERENCE: TJU2445
; CURRENT APPLICATION NUMBER: US/09/723,450
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/276,993
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 08/859,167
; PRIOR FILING DATE: 1997-05-20
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: No. 6576751el Sequence
; US-09-723-450-2

Query Match          91.1%; Score 1015; DB 4; Length 445;
Best Local Similarity 94.5%; Pred. No. 2.3e-94;
Matches 207; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPVPPNVRDLIDLRLRGKLSVGDLAELLY 60
DB 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPVPPNVRDLIDLRLRGKLSVGDLAELLY 60
QY 61 RVRFPDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMMAEIGEDLDKSDVSSLIPLMKDYM 120
DB 61 RVRFPDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMMAEIGEDLDKSDVSSLIPLMKDYM 120
QY 121 GRGKISKEKSFLLDVVVELEKLNLVAPDQLDLEKCLKNHRIIDLTKTIQKYKQSVQAGT 180

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Db 121 GRGKISKEKSFLLVVELEKLNVLAPDQLDLLEKCLKNHRIIDLTKIKYKQSVQAGT 180
Qy 181 SYRNVLQAAIQKSLKDPSSNNFRMTTPYAHCPDLKILGNC 219
Db 181 SYRNVLQAAIQKSLKDPSSNNFRSIPERYKMKSKPLGIC 219

RESULT 7
US-08-795-088A-2
; Sequence 2, Application US/08795088A
; Patent No. 6242569
; GENERAL INFORMATION:
; APPLICANT: Sul, Hong-Bing
; APPLICANT: Goeddel, David V.
; TITLE OF INVENTION: Regulators of Apoptosis
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Science & Technology Law Group
; STREET: 75 Denise Drive
; CITY: Hillsborough
; STATE: California
; COUNTRY: USA
; ZIP: 94010
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,088A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-001
; TELEPHONE: (650) 343-4341
; TELEFAX: (650) 343-4342
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 480 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
US-08-795-088A-2

Query Match 90.4%; Score 1007; DB 3; Length 480;
Best Local Similarity 99.5%; Pred. No. 1.6e-93;
Matches 202; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVPPNVRDLILRERKLSVGDIAELLY 60
Db 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVPPNVRDLILRERKLSVGDIAELLY 60
Qy 61 RVRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIPLMKDYM 120
Db 61 RVRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIPLMKDYM 120
Qy 121 GRGKISKEKSFLLVVELEKLNVLAPDQLDLLEKCLKNHRIIDLTKIKYKQSVQAGT 180
Db 121 GRGKISKEKSFLLVVELEKLNVLAPDQLDLLEKCLKNHRIIDLTKIKYKQSVQAGT 180
Qy 181 SYRNVLQAAIQKSLKDPSSNNFRM 203
Db 181 SYRNVLQAAIQKSLKDPSSNNFRM 203

RESULT 8
US-09-069-023-34
; Sequence 34, Application US/09069023A

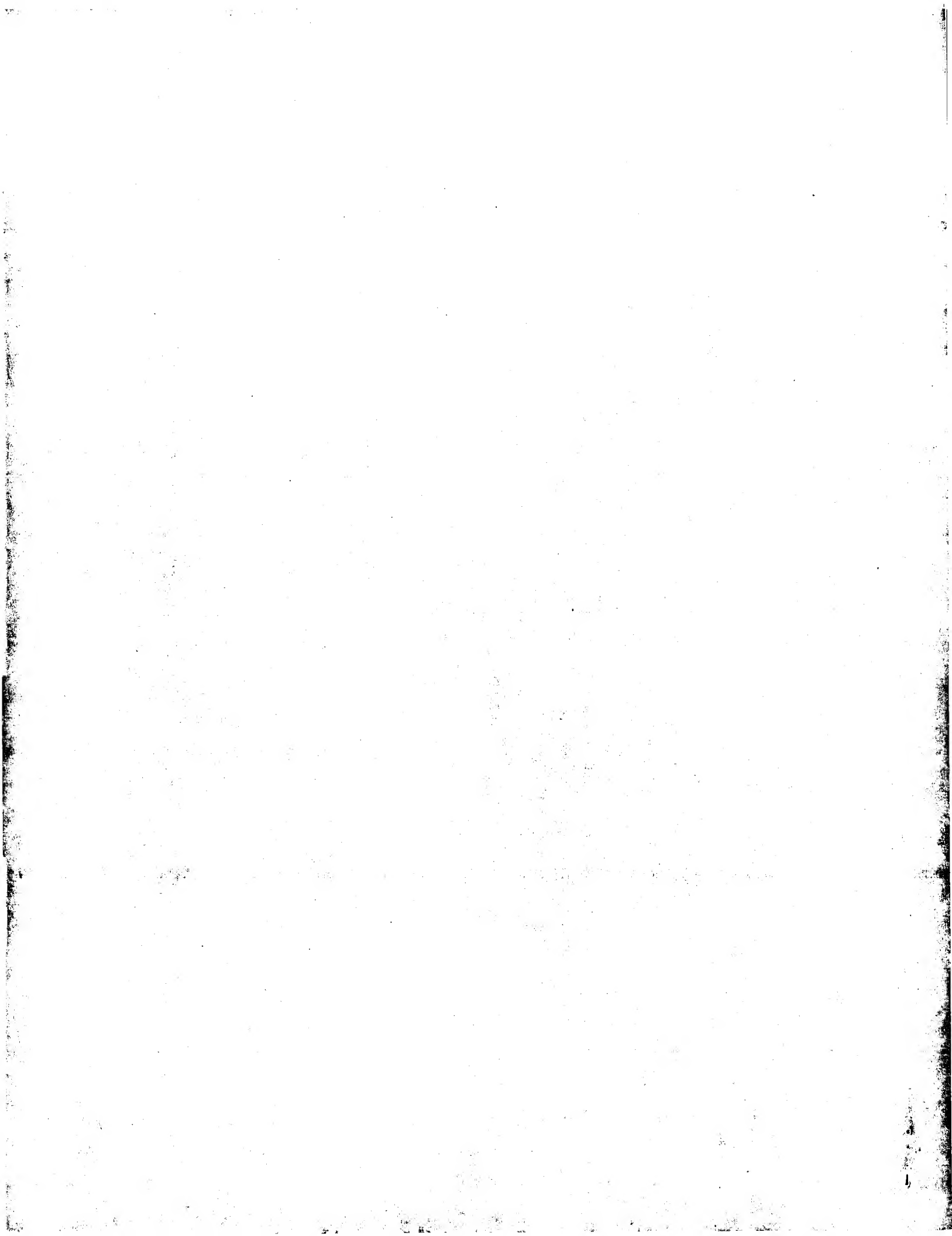
; Patent No. 6348573
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; APPLICANT: Koseki, Takeyoshi
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
; TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
; FILE REFERENCE: UM-03333
; CURRENT APPLICATION NUMBER: US/09/069,023A
; CURRENT FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-069-023-34
Query Match 88.6%; Score 987; DB 4; Length 480;
Best Local Similarity 98.0%; Pred. No. 1.7e-91;
Matches 199; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVPPNVRDLILRERKLSVGDIAELLY 60
Db 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVPPNVRDLILRERKLSVGDIAELLY 60
Qy 61 RVRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIPLMKDYM 120
Db 61 RVRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIPLMKDYM 120
Qy 121 GRGKISKEKSFLLVVELEKLNVLAPDQLDLLEKCLKNHRIIDLTKIKYKQSVQAGT 180
Db 121 GRGKISKEKSFLLVVELEKLNVLAPDQLDLLEKCLKNHRIIDLTKIKYKQSVQAGT 180
Qy 181 SYRNVLQAAIQKSLKDPSSNNFRM 203
Db 181 SYRNVLQAAIQKSLKDPSSNNFRM 203

RESULT 9
US-09-074-044A-2
; Sequence 2, Application US/09074044A
; Patent No. 6207458
; GENERAL INFORMATION:
; APPLICANT: CHAUDHARY, PREET M
; APPLICANT: HOOD, LEROY
; TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NK-KB, JNK AND
; TITLE OF INVENTION: APOPTOSIS PATHWAYS AND METHODS OF USING THE SAME
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS
; STREET: 2405 GRAND BLVD., SUITE 400
; CITY: KANSAS CITY
; STATE: MISSOURI
; COUNTRY: USA
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/074,044A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: COLLINS, JOHN M
; REGISTRATION NUMBER: 26,262
; REFERENCE/DOCKET NUMBER: 26588
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 816/474-9050
; TELEFAX: 816/474-9057
; INFORMATION FOR SEQ ID NO: 2:


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; SEQUENCE CHARACTERISTICS:
; LENGTH: 84 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; US-09-074-044A-2
Query Match 37.4%; Score 417; DB 3; Length 84;
Best Local Similarity 100.0%; Pred. No. 5.9e-35;
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 90 VSDYRLVMAEIGEDLDKSDVSSLIFLMKDYMGRGKISKESFLDLVVELEKLNVLAPDQL 149
Db 1 VSDYRLVMAEIGEDLDKSDVSSLIFLMKDYMGRGKISKESFLDLVVELEKLNVLAPDQL 60
QY 150 DLLEKCLKNHRIIDLTKTKQYKQ 173
Db 61 DLLEKCLKNHRIIDLTKTKQYKQ 84
RESULT 10
US-09-382-155-2
; Sequence 1, Application US/09382155B
; Patent No. 6160095
; GENERAL INFORMATION:
; APPLICANT: CHAUDHARY, PREET M
; TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NF-kB, JNK AND APOPTOSIS
; FILE REFERENCE: Chaudhary
; CURRENT APPLICATION NUMBER: US/09/382,155B
; CURRENT FILING DATE: 1999-08-24
; EARLIER APPLICATION NUMBER: 09/074,044
; EARLIER FILING DATE: 1998-05-07
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 84
; TYPE: PRT
; ORGANISM: HUMAN HERPESVIRUS 8
; US-09-382-155-2
Query Match 36.2%; Score 403; DB 3; Length 84;
Best Local Similarity 97.6%; Pred. No. 1.5e-33;
Matches 82; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Db 1 VSDYRLVMAEIGEDLDKSDVSSLIFLMKDYMGRGKISKESFLDLVVELEKLNVLAPDQL 60
QY 150 DLLEKCLKNHRIIDLTKTKQYKQ 173
Db 61 DLLEKCLKNHRIIDLTKTKQYKQ 84
RESULT 11
US-09-382-155-1
; Sequence 1, Application US/09382155B
; Patent No. 6160095
; GENERAL INFORMATION:
; APPLICANT: CHAUDHARY, PREET M
; TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NF-kB, JNK AND APOPTOSIS
; FILE REFERENCE: Chaudhary
; CURRENT APPLICATION NUMBER: US/09/382,155B
; CURRENT FILING DATE: 1999-08-24
; EARLIER APPLICATION NUMBER: 09/074,044
; EARLIER FILING DATE: 1998-05-07
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; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-382-155-1
Query Match 34.5%; Score 384; DB 3; Length 78;
Best Local Similarity 100.0%; Pred. No. 1.1e-31;
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVYPPNVRDLIDLREGRKLSVGDLAELLY 60
Db 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVYPPNVRDLIDLREGRKLSVGDLAELLY 60
QY 61 RVRFDLLKRLKMDRKA 78
Db 61 RVRFDLLKRLKMDRKA 78
RESULT 12
US-09-074-044A-1
; Sequence 1, Application US/09074044A
; Patent No. 6207458
; GENERAL INFORMATION:
; APPLICANT: CHAUDHARY, PREET M
; APPLICANT: HOOD, LEROY
; TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NF-kB, JNK AND APOPTOSIS
; FILE REFERENCE: Chaudhary
; CURRENT APPLICATION NUMBER: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS
; STREET: 2405 GRAND BLVD., SUITE 400
; CITY: KANSAS CITY
; STATE: MISSOURI
; COUNTRY: USA
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/074,044A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: COLLINS, JOHN M
; REGISTRATION NUMBER: 26,262
; REFERENCE/DOCKET NUMBER: 26588
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 816/474-9050
; TELEFAX: 816/474-9057
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 78 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; US-09-074-044A-1
Query Match 34.5%; Score 384; DB 3; Length 78;
Best Local Similarity 100.0%; Pred. No. 1.1e-31;
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVYPPNVRDLIDLREGRKLSVGDLAELLY 60
Db 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVYPPNVRDLIDLREGRKLSVGDLAELLY 60
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SUMMARIES			
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3	1114	100.0	221 20 AAY57455 Human FLICE-like i
4	1114	100.0	221 20 AAY05789 Human MACH related
5	1114	100.0	221 21 AAB03959 FLICE-like inhibit
6	1114	100.0	221 22 AAB84802 Human MRIT prodoma
7	1114	100.0	221 22 AAB61117 Human MRITalpha.
8	1114	100.0	221 22 AAB09293 Human FLIP-c prote
9	1015	91.1	270 23 AAE26110 Human FLAME-1b pro

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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13	1007	90.4	462	21	AAV67419	Usurpin-beta polyp
14	1007	90.4	480	19	AAW76631	Human CFLIP-L prot
15	1007	90.4	480	19	AAW78903	Human G1 protein i
16	1007	90.4	480	19	AAW69715	Human Casper prote
17	1007	90.4	480	19	AAW69229	I-FLICE-1 protein.
18	1007	90.4	480	19	AAW58578	Human FIN-1. Homo
19	1007	90.4	480	20	AAV57454	Human FLICE-like i
20	1007	90.4	480	20	AAV05787	Human MACH related
21	1007	90.4	480	21	AB03960	FLICE-like inhibit
22	1007	90.4	480	21	AAV67418	Usurpin-alpha polyp
23	1007	90.4	480	21	AAV57606	Human apoptosis as
24	1007	90.4	480	23	AB09294	Human FLIP-c prote
25	1007	90.4	491	21	AB03964	FLIP with detectab
26	987	88.6	480	21	AAV59414	Human CLARP protei
27	985.5	88.5	291	21	AAV67420	Usurpin-gamma poly
28	984.5	88.4	479	19	AAW76625	Human FLIP protein
29	713	64.0	481	19	AAW76632	Mouse CFLIP-L prot
30	713	64.0	481	21	AB03958	FLICE-like inhibit
31	713	64.0	481	23	AB09295	Mouse FLIP-c prote
32	701.5	63.0	218	23	AB09296	Mouse FLIP-c prote
33	701.5	63.0	484	23	AB09292	Mouse FLIP-c prote
34	701.5	63.0	484	24	AB09383	Amino acid sequenc
35	693	62.2	483	19	AAW76626	Murine FLIP protei
36	532	47.8	391	22	AAE09601	Human gene 9 encod
37	532	47.8	391	22	AU21591	Novel human neopla
38	532	47.8	391	23	AB078973	Human apoptosis re
39	529	47.5	366	20	AAV05788	Human MACH related
40	529	47.5	384	20	AAV05791	MRIT alpha 3 polyp
41	527	47.3	348	19	AAW69230	I-FLICE-2 protein.
42	499	44.8	104	19	AAW76215	Human FLIP protein
43	465	41.7	93	22	ABG50496	Human liver peptid
44	465	41.7	93	22	AB30476	Peptide #3127 enco
45	465	41.7	93	22	AB335643	Peptide #3149 enco

ALIGNMENTS

RESULT 1	
AAW76630	AAW76630 standard; Protein; 221 AA.
ID	AAW76630
XX	AC
XX	AAW76630;
DT	12-JUL-1999 (first entry)
XX	Human CFLIP-S protein.
DE	Death effector domain; human; murine; anti-apoptotic; treatment;
KW	HIV infection; autoimmune disease; FLIP protein.
XX	Homo sapiens.
OS	DE19713393-Al.
PN	08-OCT-1998.
XX	01-APR-1997; 97DE-1013393.
PF	01-APR-1997; 97DE-1013393.
XX	(TSCH/) TSCHOPP J.
PA	(APOT-) APOTECH SA.
XX	Bodmer J, Burns K, French EL, Hahne M, Hoffmann K;
PI	Irmeler M, Rimoldi D, Schneider P, Schroeter M, Steiner V;
PI	Thome M, Tschopp J, Hofmann K;
XX	WFI; 1998-532710/46.
DR	N-PSDB; AAV61936.

PT New DNA encoding isoforms of G1 protein which bind MORT-1 - and
PT regulate the effects of FAS and tumour necrosis factor receptors,
PT useful for killing of cells e.g. HIV and cancer cells
XX
XX
XX Claim 13; Fig 2; 132pp; English.
XX
XX This is the amino acid sequence of the beta isoform of novel
CC human G1 protein. The sequence is deduced from an isolated skin
CC fibroblast cDNA clone (see AAV52969). G1-beta (also called CASH beta,
CC CASH being caspase homologue) and a longer isoform, G1-alpha (see
CC AAV78903), represent 2 splice variants of the G1 protein. These G1
CC proteins are capable of binding to, or interacting directly or
CC indirectly, via their N-terminal MORT modules, with MORT-1 or with
CC MORT-binding proteins such as Mch4 (CASP-10) and MACH (CASP-8), and
CC thereby of binding to the intracellular domain of the FAS-R
CC receptor, to which MORT-1 binds, or of binding to the intracellular
CC domain of the p55 tumour necrosis factor (TNF) receptor, to which
CC TRADD binds and to which TRADD protein MORT-1 binds. Hence, they
CC are considered as mediators or modulators of FAS-R having a role in
CC e.g. the signalling process that is initiated by the binding of FAS
CC ligand to FAS-R, and also having a role in the signalling process
CC initiated by the binding of TNF to p55-R. The longer isoform also
CC has a C-terminal caspase activity region involved in cytotoxic
CC activity. G1 DNA (I) and polypeptide (II), vectors and fragments
CC are used to regulate cell death or inflammatory processes. (II) is
CC used to inhibit cell death, and its inhibitors augment/enhance the
CC processes. (I) and (II) regulate the FAS-R ligand or TNF effect on
CC cells carrying an FAS-R or p55-R. Tumour, HIV-infected or other
CC diseased cells can be treated using a viral vector encoding a viral
CC surface protein, which binds a specific cell surface receptor and a
CC sequence encoding (II), which kills the cell. Antisense
CC oligonucleotides, introduced using the above vector, block the
CC expression of (II) and can also regulate the above effects. These
CC effects can also be regulated using a vector encoding a ribozyme
CC that interacts with a cellular mRNA encoding (II), and allows (II)
XX expression.

XX Sequence 221 AA;
SQ

Query Match 100.0%; Score 1114; DB 19; Length 221;
Best Local Similarity 100.0%; Pred. No. 2.4e-95;
Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSAEVIHQVEALDTDEKEMLLFCRDVAIDVPPNVRDLILRERKLSVGDLAELLY 60
DB 1 MSAEVIHQVEALDTDEKEMLLFCRDVAIDVPPNVRDLILRERKLSVGDLAELLY 60
QY 61 RVRREFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIPLMKDYM 120
DB 61 RVRREFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIPLMKDYM 120
QY 121 GRGKISKEKSFLLDVLVELEKLNLYAPQDLLEKLNHRIIDLTKTIQYKQSVQAGT 180
DB 121 GRGKISKEKSFLLDVLVELEKLNLYAPQDLLEKLNHRIIDLTKTIQYKQSVQAGT 180
QY 181 SYRNVLOAAIQKSLKDPSSNNFRMITPYAHCPDLKILNCMSM 221
DB 181 SYRNVLOAAIQKSLKDPSSNNFRMITPYAHCPDLKILNCMSM 221

RESULT 3

AAV57455

ID AAV57455 standard; Protein: 221 AA.

XX AC AAV57455;

XX DT 25-FEB-2000 (first entry)

XX Human FLICE-like inhibitory protein short form protein sequence.
XX DE Human FLICE-like inhibitory protein long form; FLIP-L; FLIP-S;
XX KW FLICE-like inhibitory protein short form; apoptosis inhibitor;
XX KW arteriosclerosis; vascular wall inflammation; vascular injury;

XX New DNA encoding for anti-apoptotic gene product - used to treat HIV
PT infections and autoimmune diseases
XX
XX Claim 20; Fig 4A; 45pp; German.

XX This invention describes novel human and mouse anti-apoptotic gene
CC products which contain at least one death effector domain. The products
CC of the invention are used in the treatment of HIV infections and
CC autoimmune diseases.

XX Sequence 221 AA;
SQ

Query Match 100.0%; Score 1114; DB 19; Length 221;
Best Local Similarity 100.0%; Pred. No. 2.4e-95;
Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSAEVIHQVEALDTDEKEMLLFCRDVAIDVPPNVRDLILRERKLSVGDLAELLY 60
DB 1 MSAEVIHQVEALDTDEKEMLLFCRDVAIDVPPNVRDLILRERKLSVGDLAELLY 60
QY 61 RVRREFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIPLMKDYM 120
DB 61 RVRREFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIPLMKDYM 120
QY 121 GRGKISKEKSFLLDVLVELEKLNLYAPQDLLEKLNHRIIDLTKTIQYKQSVQAGT 180
DB 121 GRGKISKEKSFLLDVLVELEKLNLYAPQDLLEKLNHRIIDLTKTIQYKQSVQAGT 180
QY 181 SYRNVLOAAIQKSLKDPSSNNFRMITPYAHCPDLKILNCMSM 221
DB 181 SYRNVLOAAIQKSLKDPSSNNFRMITPYAHCPDLKILNCMSM 221

RESULT 2

AAV78904

ID AAV78904 standard; Protein: 221 AA.

XX AC AAV78904;

XX DT 11-JAN-1999 (first entry)

XX Human G1 protein isoform beta (CASH-beta).
XX G1 protein; CASH-beta; human; caspase homologue; Fas receptor;
XX modulator; apoptosis; cell death; inflammation; tumour; HIV;
XX therapy.

XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Domain 2..73
XX FT /note= "death domain/MORT module"
XX Domain 93..142
XX FT /note= "death domain/MORT module"

XX WO9839435-A1.

XX 11-SEP-1998.

XX 26-FEB-1998; 98WO-IL00098.

XX 01-MAY-1997; 97IL-0120759.

XX 03-MAR-1997; 97IL-0120367.

XX (YEDA) YEDA RES & DEV CO LTD.

XX Brodianski V, Goltsev Y, Kovalenko A, Varfolomeev E;

XX Wallach D;

XX WPI; 1998-495842/42.

XX N-PSDB; AAV52969.

KW Fas ligand-mediated apoptosis; atherosclerosis; transplant.

OS Homo sapiens.

PN W09942570-A1.

XX 26-AUG-1999.

XX 19-FEB-1999; 99WO-US03558.

XX 20-FEB-1998; 98US-0075471.

XX (SELL-) ST ELIZABETH'S MEDICAL CENT BOSTON INC.

XX Walsh K;

XX WPI; 1999-527469/44.

XX N-PSDB; AA239041.

XX Treating conditions characterized by vascular wall inflammation

XX Example 2; Page 72; 105pp; English.

XX The present sequence represents human FLICE-like inhibitory protein short form, designated FLIP-S. The present invention describes a new treatment of a condition characterised by vascular wall inflammation in a subject comprising administering a FLIP molecule to inhibit Fas ligand-mediated apoptosis of vascular endothelial cells in the subject. The method can be used to treat atherosclerosis, transplant arteriosclerosis and vascular injury.

XX Sequence 221 AA;

Query Match 100.0%; Score 1114; DB 20; Length 221;
Best Local Similarity 100.0%; Pred. No. 2.4e-95;
Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPVPPNVRDLDIRRGLKSLVGDIAELLY 60
DB 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPVPPNVRDLDIRRGLKSLVGDIAELLY 60
QY 61 RVRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIFFLMKDYM 120
DB 61 RVRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIFFLMKDYM 120
QY 121 GRGKISKEKSFLLDVVELEKLNIVAPDQLDLEKCLKNHRIIDLTKTKIQYKQSVQAGT 180
DB 121 GRGKISKEKSFLLDVVELEKLNIVAPDQLDLEKCLKNHRIIDLTKTKIQYKQSVQAGT 180
QY 181 SYRNVLQAAIQKSLKDPNSNFRMITPYAHCPDLKILNGCSM 221
DB 181 SYRNVLQAAIQKSLKDPNSNFRMITPYAHCPDLKILNGCSM 221

RESULT 4
AA05789
ID AAY05789 standard; Protein; 221 AA.

XX AAY05789;

XX 02-AUG-1999 (first entry)

XX Human MACH related inducer of toxicity MRIT beta 1.

XX MRIT beta 1; MACH related inducer of toxicity; human; apoptosis;
KW pro-apoptotic; cancer; autoimmune disease; infection; angiogenesis;
KW atherosclerosis; neurodegenerative disease; Alzheimer's disease;
KW Parkinson's disease; retinitis pigmentosa; stroke; AIDS;
KW aplastic anaemia; myocardial infarction; therapy.

OS Homo sapiens.

XX W09918230-A2.

XX 15-APR-1999.

XX 07-OCT-1998; 98WO-US21132.

XX 07-OCT-1997; 97US-0946226.

XX (UNIW) UNIV WASHINGTON.

XX Chaudhary PM;

XX WPI; 1999-277275/23.
XX N-PSDB; AA25510.

XX Identifying regulators of MACH-related inducer of toxicity

XX Example 1; Fig 1H; 78pp; English.

XX The present sequence represents novel human MACH-related inducer of toxicity (MRIT) isoform MRIT beta 1, a CED-4 homologue. Multiple isoforms of MRIT have been identified, some of which function to induce caspase dependent apoptosis in mammalian cells, e.g. MRIT alpha 1 (see AAY05787) and MRIT beta 1, while others have anti-apoptotic activity, e.g. MRIT alpha 2 (see AAY05788). MRIT beta 1 lacks the N-terminal death effector domain of MRIT alpha 1 but includes a C-terminal caspase ICE homology domain region. Selective enhancers and inhibitors of MRIT apoptotic activity can be identified and used to treat diseases mediated by the dysfunction of programmed cell death or proliferation. A cell accumulation disorder such as cancer, autoimmune disease, viral infection, angiogenesis or atherosclerosis is treated by administering an agent that selectively enhances MRIT apoptotic activity, thereby inducing apoptosis in a subject. A disorder of cell loss, such as a neurodegenerative disorder, including Alzheimer's disease, Parkinson's disease, retinitis pigmentosa, stroke, aplastic anaemia, myocardial infarction or AIDS can be treated by administering an agent that selectively inhibits MRIT apoptotic activity.

XX Sequence 221 AA;

Query Match 100.0%; Score 1114; DB 20; Length 221;
Best Local Similarity 100.0%; Pred. No. 2.4e-95;
Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPVPPNVRDLDIRRGLKSLVGDIAELLY 60
DB 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPVPPNVRDLDIRRGLKSLVGDIAELLY 60
QY 61 RVRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIFFLMKDYM 120
DB 61 RVRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIFFLMKDYM 120
QY 121 GRGKISKEKSFLLDVVELEKLNIVAPDQLDLEKCLKNHRIIDLTKTKIQYKQSVQAGT 180
DB 121 GRGKISKEKSFLLDVVELEKLNIVAPDQLDLEKCLKNHRIIDLTKTKIQYKQSVQAGT 180
QY 181 SYRNVLQAAIQKSLKDPNSNFRMITPYAHCPDLKILNGCSM 221
DB 181 SYRNVLQAAIQKSLKDPNSNFRMITPYAHCPDLKILNGCSM 221

RESULT 5
AAB03959
ID AAB03959 standard; Protein; 221 AA.

XX AAB03959;

XX 26-FEB-2001 (first entry)

XX FLICE-like inhibitor protein (Genbank Accession No. 2253681).

XX Chimeric protein; fusion protein; FLICE like inhibitor protein;

Adn

Abm

KW FLIP; Fas; TNF; apoptosis; caspase-8; ligand; T cell; thymocyte;
KW tumour specific antigen; immune response; therapy; prophylaxis;
KW diagnosis; HIV; human immunodeficiency syndrome; AIDS;
KW acquired immune deficiency syndrome; human.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200059935-A1.
XX
PD 12-OCT-2000.
XX
PF 05-APR-2000; 2000WO-US09002.
XX
XX 05-APR-1999; 99US-0127867.
PR 06-APR-1999; 99US-0128021.
XX
XX (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
PA (PAYA/) PAYA C.
PA (AGE/) ALGECIRAS-SCHMINICH A.
XX
XX Paya C, Algeciras-schminich A;
PI WPI; 2000-664988/64.
DR
XX Fusion polypeptide useful for inhibiting ligand-induced apoptosis,
PT comprises portion of anti-apoptotic polypeptide linked to a transport
PT group
XX
XX Disclosure; Page 78-79; 89pp; English.
XX
XX A chimeric group or fusion peptide which comprises a portion of an
CC anti-apoptotic polypeptide which inhibits apoptosis of lymphocytes in
CC combination with a transport group is described. The transport group
CC is capable of transporting the chimeric group or fusion peptide
CC across the cell membrane. The anti-apoptotic polypeptide is FLICE-like
CC inhibitor protein (FLIP) which inhibits Fas and TNF mediated apoptosis
CC by inhibiting binding of Caspase-8 to the Fas receptor complex, thus
CC shutting off the downstream Fas signalling pathway. The chimeric group
CC and fusion peptide are useful for inhibiting ligand-induced apoptosis
CC by bringing them into contact with T cells. The chimeric group is
CC useful for expanding T cells in vitro e.g. T cells specific for
CC particular antigens such as tumour-specific antigen, for enhancing
CC immune response and to inhibit the apoptosis of chronically activated
CC T cells e.g. activated CD4+ T cells in HIV infected patients. The
CC chimeric group is also useful for therapeutic, prophylactic or
CC diagnosis of intracellular delivery of small molecules and
CC macromolecules such as anti-apoptotic polypeptides and nucleic
CC acids encoding such polypeptides.
XX
SQ Sequence 221 AA;
Query Match 100.0%; Score 1114; DB 21; Length 221;
Best Local Similarity 100.0%; Pred. No. 2.4e-95;
Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSAEVIHQVEALDTDEKEMLLFLCRDVAIDVPPNVRDLILRERKLSVGDLAELLY 60
DB 1 MSAEVIHQVEALDTDEKEMLLFLCRDVAIDVPPNVRDLILRERKLSVGDLAELLY 60
QY 61 RVRFDDLKRLKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIFLMKDYM 120
DB 61 RVRFDDLKRLKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIFLMKDYM 120
QY 121 GRGKISKEKSFLLDVVELEKLNIVAPDQLDLEKLNHRIIDLTKIYKQSVQAGT 180
DB 121 GRGKISKEKSFLLDVVELEKLNIVAPDQLDLEKLNHRIIDLTKIYKQSVQAGT 180
QY 121 GRGKISKEKSFLLDVVELEKLNIVAPDQLDLEKLNHRIIDLTKIYKQSVQAGT 180
DB 121 GRGKISKEKSFLLDVVELEKLNIVAPDQLDLEKLNHRIIDLTKIYKQSVQAGT 180
QY 181 SYRNVLOAAIOKSLKDPSSNNFRMITPYAHCPLDKILGNCMS 221
DB 181 SYRNVLOAAIOKSLKDPSSNNFRMITPYAHCPLDKILGNCMS 221

RESULT 6
AAB84802
ID AAB84802 standard; Protein; 221 AA.
XX
AC AAB84802;
XX
DT 12-JUL-2001 (first entry)
XX
DE Huamn MRIT prodomain.
XX
KW NF-kappaB; JNK; apoptosis; death effector domain; DED.
XX
OS Homo sapiens.
XX
PN US6207458-B1.
PD 27-MAR-2001.
XX
XX 07-MAY-1998; 98US-0074044.
XX
XX 07-MAY-1998; 98US-0074044.
XX
XX (UNIW) UNIV WASHINGTON.
XX
XX Chaudhary PM, Hood L;
XX
XX WPI; 2001-342087/36.
XX
XX Testing candidate compound affecting cellular NFkappaB JNK, apoptosis
PT activity by comparing cell activity in presence and absence of
PT proteinaceous species having two death effector domain and test
PT compound
XX
XX Disclosure; Column 47-50; 62pp; English.
XX
XX The present invention relates to testing candidate compounds to
CC determine whether they affect NF-kappaB, JNK and apoptosis activity.
CC The method involves the use of 2 death effector domains (DED). The
CC compounds identified by the invention have therapeutic
CC applications and are useful for regulating cellular NFkappaB, JNK
CC and apoptosis activity. The assay is useful for identifying
CC pharmacological agents or lead compounds generally involved in
CC assaying for compounds which regulate or modulate a cell activity.
CC The present sequence is a prodomain used in the invention.
XX
SQ Sequence 221 AA;
Query Match 100.0%; Score 1114; DB 22; Length 221;
Best Local Similarity 100.0%; Pred. No. 2.4e-95;
Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSAEVIHQVEALDTDEKEMLLFLCRDVAIDVPPNVRDLILRERKLSVGDLAELLY 60
DB 1 MSAEVIHQVEALDTDEKEMLLFLCRDVAIDVPPNVRDLILRERKLSVGDLAELLY 60
QY 61 RVRFDDLKRLKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIFLMKDYM 120
DB 61 RVRFDDLKRLKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIFLMKDYM 120
QY 121 GRGKISKEKSFLLDVVELEKLNIVAPDQLDLEKLNHRIIDLTKIYKQSVQAGT 180
DB 121 GRGKISKEKSFLLDVVELEKLNIVAPDQLDLEKLNHRIIDLTKIYKQSVQAGT 180
QY 181 SYRNVLOAAIOKSLKDPSSNNFRMITPYAHCPLDKILGNCMS 221
DB 181 SYRNVLOAAIOKSLKDPSSNNFRMITPYAHCPLDKILGNCMS 221

RESULT 7
AAB61117
ID AAB61117 standard; protein; 221 AA.
XX
AC AAB61117;

```

XX DT 02-MAY-2001 (first entry)
XX DE Human MRITalpha.
XX KW Human; MRITalpha; apoptotic; nuclear factor-kappa B; NF-kB;
XX KW Jun N-terminal kinase; JUNK; apoptosis; Caspase-8 mutant.
XX OS Homo sapiens.
XX PN US6160095-A.
XX PD 12-DEC-2000.
XX PF 24-AUG-1999; 99US-0382155.
XX PR 07-MAY-1998; 98US-0074044.
XX PA (UNIW ) UNIV WASHINGTON.
XX PA (STOM-) STOMERS INST MEDICAL RES.
XX PI Hood L, Chaudhary PM;
XX PS WPI; 2001-101569/11.
XX PT Novel mutants D73A, L74A and L75A for Caspase 8 useful for regulating
XX PT nuclear factor-kappa B, Jun N-terminal kinase and apoptosis activities,
XX PT for therapeutic purposes
XX PS Example 8; Column 43-46; 60pp; English.
XX CC The present sequence has been shown to regulate the nuclear factor-kappa
XX CC B (NF-kB), Jun N-terminal kinase (JUNK) and apoptosis pathways. It
XX CC is provided in a specification relating to novel mutants (D73A, L74A and
XX CC L75A) for Caspase-8, which are also useful for regulating NF-kB, JUNK
XX CC and apoptosis activities. The Caspase-8 mutants are useful for
XX CC therapeutic purposes and in test methods or assays for determining
XX CC whether a candidate compound has a significant effect upon cell
XX CC activities, especially NF-kB, JUNK and apoptosis, so as to facilitate the
XX CC discovery and/or design of therapeutic agents.
XX SQ Sequence 221 AA;

Query Match 100.0%; Score 1114; DB 22; Length 221;
Best Local Similarity 100.0%; Pred. No. 2.4e-95;
Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSAEVIHQVEALDTDEKMLFLCRDVAIDVVPVPPNVRDLDLRLRERKLSVGDLAELLY 60
Db 1 MSAEVIHQVEALDTDEKMLFLCRDVAIDVVPVPPNVRDLDLRLRERKLSVGDLAELLY 60

Qy 61 RVRFRDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIFFLMKDYM 120
Db 61 RVRFRDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIFFLMKDYM 120

Qy 121 GRGKISKESFSDLVVELEKLNIVAPDQLLEKLNHRIIDLKTKIQYKOSVOGAGT 180
Db 121 GRGKISKESFSDLVVELEKLNIVAPDQLLEKLNHRIIDLKTKIQYKOSVOGAGT 180

Qy 181 SYRNLQAAIQKSLKDPNSNNFRMITPYAHCPLDKILGNCSM 221
Db 181 SYRNLQAAIQKSLKDPNSNNFRMITPYAHCPLDKILGNCSM 221

RESULT 8
ABB09293
ID ABB09293 standard; Protein; 221 AA.
XX AC ABB09293;
XX DT 15-JUL-2002 (first entry)
XX DE Human FLIP-c protein SEQ ID NO:10.

```

```

XX KW Human; FLIP-c; caspase 8 dominant negative regulator; antiinflammatory;
XX KW anti-tumour; FLIP-c inhibitor; apoptosis; antisense gene therapy;
XX KW phosphorothioate; antisense modulation; infection; inflammation;
XX OS Homo sapiens.
XX PN WO200224717-A1.
XX PD 28-MAR-2002.
XX PF 14-SEP-2001; 2001WO-US28732.
XX PR 20-SEP-2000; 2000US-0666269.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Ackermann EJ, Bennett CF, Zhang H, Watt AT, Ricketts W, Dean NM;
XX PS WPI; 2002-401983/43.
XX PT Novel antisense compound that hybridizes and inhibits nucleic acid
XX PT encoding a natural dominant negative regulator of caspase 8, FLIP-c,
XX PT useful for preventing or delaying infection, inflammation or tumor
XX PS formation
XX PS Example 13; Page 116-117; 154pp; English.
XX CC The present invention describes a compound (I) 8-50 nucleobases in length
XX CC targeted to a nucleic acid molecule (II) encoding a natural dominant
XX CC negative regulator of caspase 8, FLIP-c, where (I) specifically
XX CC hybridizes with and inhibits expression of the protein, or specifically
XX CC hybridizes with at least an 8-nucleobase portion of an active site on
XX CC (II). (I) has antiinflammatory and anti-tumour activities. (I) is an
XX CC inhibitor of FLIP-c expression, a modulator of apoptosis and can be used
XX CC in antisense gene therapy. (I) is useful for inhibiting the expression of
XX CC FLIP-c in cells or tissues, and for treating an animal having a disease
XX CC or condition associated with FLIP-c. (I) is also useful for modulating
XX CC apoptosis in a cell, where a caspase such as caspase 8, caspase 3 or
XX CC caspase 7 is activated, and the FLIP-c is the long form of FLIP-c. (I) is
XX CC also useful for diagnostics, therapeutics, prophylaxis, as research
XX CC reagents and kits, for distinguishing functions of various members of a
XX CC biological pathway, and in antisense gene therapy. (I) is also useful
XX CC prophylactically, e.g., to prevent or delay infection, inflammation or
XX CC tumour formation. The present sequence represents human FLIP-c as given
XX CC in an example from the present invention.
XX SQ Sequence 221 AA;

Query Match 100.0%; Score 1114; DB 23; Length 221;
Best Local Similarity 100.0%; Pred. No. 2.4e-95;
Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSAEVIHQVEALDTDEKMLFLCRDVAIDVVPVPPNVRDLDLRLRERKLSVGDLAELLY 60
Db 1 MSAEVIHQVEALDTDEKMLFLCRDVAIDVVPVPPNVRDLDLRLRERKLSVGDLAELLY 60

Qy 61 RVRFRDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIFFLMKDYM 120
Db 61 RVRFRDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIFFLMKDYM 120

Qy 121 GRGKISKESFSDLVVELEKLNIVAPDQLLEKLNHRIIDLKTKIQYKOSVOGAGT 180
Db 121 GRGKISKESFSDLVVELEKLNIVAPDQLLEKLNHRIIDLKTKIQYKOSVOGAGT 180

Qy 181 SYRNLQAAIQKSLKDPNSNNFRMITPYAHCPLDKILGNCSM 221
Db 181 SYRNLQAAIQKSLKDPNSNNFRMITPYAHCPLDKILGNCSM 221

RESULT 9

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Mon Aug 25 09:11:10 2003

AAE26110
ID AAE26110 standard; Protein; 270 AA.
AC AAE26110;
XX
XX
DT 14-NOV-2002 (first entry)
XX
XX Human FLAME-1b protein.
XX
XX Human; FADD-like apoptotic/anti-apoptotic protein; Alzheimer's disease;
KW gene therapy; human immunodeficiency virus; HIV infection; apoptosis;
KW FLAME-1b.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Region 232..270
FT /note= "FLAME-1b unique region"
FT
XX
XX US2002086983-A1.
XX
XX 04-JUL-2002.
XX
XX 22-AUG-2001; 2001US-0935223.
XX
XX 28-OCT-1997; 97US-0959167.
XX 26-MAR-1999; 98US-0276993.
XX 28-NOV-2000; 2000US-0723450.
XX
XX (UYJE-) UNIV JEFFERSON THOMAS.
XX
XX Alnemri ES;
XX
XX WPI; 2002-642259/69.
XX
XX Novel FADD-like apoptotic/anti-apoptotic proteins useful for inhibiting
PT apoptosis, treating diseases characterized by apoptosis e.g. HIV
PT infection and Alzheimer's disease, and for identifying modulators of
PT the protein
XX
XX Example; Fig 1A; 35pp; English.
XX
XX The invention relates to FADD-like apoptotic/anti-apoptotic proteins
CC (FLAME 1 or 2) and nucleic acid molecules encoding such proteins.
CC FLAME sequences are useful for inhibiting apoptosis and for gene
CC therapy of diseases characterised by apoptosis including HIV
CC infection and Alzheimer's disease. FLAME inhibitors are useful as
CC apoptotic agents and activators are useful as anti-apoptotic agents.
CC FLAME-1 is useful as a substrate for caspase in assays to identify
CC caspase inhibitors. The present sequence is human FLAME-1b protein.
XX
XX Sequence 270 AA;
SQ
Query Match 91.1%; Score 1015; DB 23; Length 270;
Best Local Similarity 94.5%; Pred. No. 4.7e-86;
Matches 207; Conservative 1; Mismatches 11; Indels 0; Gaps 0;
Oy 1 MSAEVIHQVEALDDEKMLFLCRDVAIDVPPNVDLLDLRGRKLSVGDIAELLY 60
Db 1 MSAEVIHQVEALDDEKMLFLCRDVAIDVPPNVDLLDLRGRKLSVGDIAELLY 60
Oy 61 RVRFDLLKRLKMDRAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIPLMKDYM 120
Db 61 RVRFDLLKRLKMDRAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIPLMKDYM 120
Oy 121 GRGKISKEKSPDLVLEKLNVLVAPDQLDLLEKCLKNTHRIDLTKYIKYKOSVQAGT 180
Db 121 GRGKISKEKSPDLVLEKLNVLVAPDQLDLLEKCLKNTHRIDLTKYIKYKOSVQAGT 180
Oy 181 SYRNVLAQIAQKSLKDSNNFRMITPYAHCPLDKILGNC 219
Db 181 SYRNVLAQIAQKSLKDSNNFRSIPERYKMKSKPLGIC 219

RESULT 10
AAW90107
ID AAW90107 standard; Protein; 445 AA.
XX
XX
AC AAW90107;
XX
XX 12-APR-1999 (first entry)
XX
XX Human FLAME-1 protein.
XX
XX FLAME-1; FADD-like apoptotic/anti-apoptotic molecule; human;
KW apoptosis; HIV; infection; Alzheimer's disease; cancer; therapy.
KW
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Domain 1..341
FT /note= "p39 subunit, specifically claimed in Claim
FT 3"
FT 342..445
FT /note= "p12 subunit, specifically claimed in Claim
FT 4"
FT 5..71
FT /note= "FADD-DED homology A"
FT 90..168
FT /note= "FADD-DED homology B"
FT 197..445
FT /note= "caspase-domain homology region"
FT 322..327
FT /note= "active site motif"
FT Cleavage-site 338..342
FT /note= "caspase cleavage site, generating p39 and
FT p12"
XX
XX WO9852963-A1.
XX
XX 26-NOV-1998.
XX
XX 20-MAY-1998; 98WO-US10200.
XX
XX 20-MAY-1997; 97US-0859167.
XX
XX (UYJE-) UNIV JEFFERSON THOMAS.
XX
XX Alnemri ES;
XX
XX WPI; 1999-045296/04.
XX N-PSDB; AAV74136.
XX
XX New isolated FADD-like anti-apoptotic molecules - used to develop
PT apoptotic and anti-apoptotic agents for treating, e.g. HIV
PT infection, Alzheimer's disease or neoplastic conditions
XX
XX Claim 2; Page 39-40; 68pp; English.
XX
XX This is the amino acid sequence of human FLAME-1, or FADD-like
CC apoptotic/anti-apoptotic molecule 1. FLAME-1 is a novel
CC anti-apoptotic protein that interacts specifically with FADD, Mch4,
CC Mch5 and FLAME-2. It is recruited to the Fas receptor complex and
CC can abrogate Fas/TNF-induced apoptosis upon expression in
CC Fas/TNF-sensitive MCF-7 cells. Despite having a caspase domain-like
CC region, it does not have caspase activity. The amino acid sequence
CC of FLAME-1 was deduced from the nucleotide sequence (see AAV74136) of
CC a Jurkat cell-derived cDNA clone. Host cells, recombinant vectors,
CC and methods of using FLAME-1 to identify substrates, activators or
CC inhibitors of FLAME-1 are provided. FLAME-1, FLAME-2 (see AAW90108)
CC and agonists can be used to inhibit apoptosis, e.g. for treating
CC HIV infection or Alzheimer's disease. Inhibitors can be used as
CC apoptotic agents.
XX
XX Sequence 445 AA;
SQ

Query Match 91.1%; Score 1015; DB 20; Length 445;
Best Local Similarity 94.5%; Pred. No. 8.8e-86;
Matches 207; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPVPPNVRDLTLRERGLSVGDLAELLY 60
Db 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPVPPNVRDLTLRERGLSVGDLAELLY 60

QY 61 RVRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIPLMKDYM 120
Db 61 RVRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIPLMKDYM 120

QY 121 GRGKISKEKSFLLVVELEKLNLPADQLDLEKLNHRIIDLTKTKIYKOSVOGAGT 180
Db 121 GRGKISKEKSFLLVVELEKLNLPADQLDLEKLNHRIIDLTKTKIYKOSVOGAGT 180

QY 181 SYRNVLQAAIQKSLKDPNSNNFRMITPYAHCPDLKILGNC 219
Db 181 SYRNVLQAAIQKSLKDPNSNNFRSIPERYKMKSKPLGIC 219

RESULT 11
AAE26086
ID AAE26086 standard; Protein; 445 AA.
AC AAE26086;
XX
XX 14-NOV-2002 (first entry)
XX Human FLAME-1 protein.
XX
KW Human; FADD-like apoptotic/anti-apoptotic protein; Alzheimer's disease;
KW gene therapy; human immunodeficiency virus; HIV infection; apoptosis;
KW FLAME-1.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FT Region 5..71
FT /note= "FADD-DED-Homology A (FDH-A) region"
FT Region 90..168
FT /note= "FADD-DED-Homology B (FDH-B) region"
FT Region 137..445
FT /note= "Caspase-domain homology (CDH) region"
FT Active-site 323..327
FT Cleavage-site 338..342
FT /note= "Caspase cleavage site"
XX
XX US2002086983-A1.
XX
XX 04-JUL-2002.
XX
XX 22-AUG-2001; 2001US-0935223.
XX
XX 28-OCT-1997; 97US-0959167.
XX 26-MAR-1999; 99US-0276993.
XX 28-NOV-2000; 2000US-0723450.
XX
XX (UYJE-) UNIV JEFFERSON THOMAS.
XX
XX Alnemri ES;
XX
XX WPI; 2002-642259/69.
XX N-PSDB; AAD43202.
XX
XX Novel FADD-like apoptotic/anti-apoptotic proteins useful for inhibiting
XX apoptosis, treating diseases characterized by apoptosis e.g. HIV
XX infection and Alzheimer's disease, and for identifying modulators of
XX the protein
XX
XX Claim 1; Page 14-15; 35pp; English.
XX
XX The invention relates to FADD-like apoptotic/anti-apoptotic proteins

CC (FLAME 1 or 2) and nucleic acid molecules encoding such proteins.
CC FLAME sequences are useful for inhibiting apoptosis and for gene
CC therapy of diseases characterised by apoptosis including HIV
CC infection and Alzheimer's disease. FLAME inhibitors are useful as
CC apoptotic agents and activators are useful as anti-apoptotic agents.
CC FLAME-1 is useful as a substrate for caspase in assays to identify
CC caspase inhibitors. The present sequence is human FLAME-1 protein.
XX
SQ Sequence 445 AA;
Query Match 91.1%; Score 1015; DB 23; Length 445;
Best Local Similarity 94.5%; Pred. No. 8.8e-86;
Matches 207; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPVPPNVRDLTLRERGLSVGDLAELLY 60
Db 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPVPPNVRDLTLRERGLSVGDLAELLY 60

QY 61 RVRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIPLMKDYM 120
Db 61 RVRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIPLMKDYM 120

QY 121 GRGKISKEKSFLLVVELEKLNLPADQLDLEKLNHRIIDLTKTKIYKOSVOGAGT 180
Db 121 GRGKISKEKSFLLVVELEKLNLPADQLDLEKLNHRIIDLTKTKIYKOSVOGAGT 180

QY 181 SYRNVLQAAIQKSLKDPNSNNFRMITPYAHCPDLKILGNC 219
Db 181 SYRNVLQAAIQKSLKDPNSNNFRSIPERYKMKSKPLGIC 219

RESULT 12
AAAY05795
ID AAAY05795 standard; Protein; 227 AA.
XX
XX AC AAAY05795;
XX
XX 02-AUG-1999 (first entry)
XX MRIT beta 2 polypeptide.
XX
XX MRIT beta 2; MACH related inducer of toxicity; human; apoptosis;
XX anti-apoptotic; cancer; autoimmune disease; angiogenesis;
XX atherosclerosis; neurodegenerative disease; Alzheimer's disease;
XX Parkinson's disease; retinitis pigmentosa; stroke; AIDS; infection;
XX aplastic anaemia; myocardial infarction; therapy; mutant.
XX
XX Homo sapiens.
XX OS Synthetic.
XX
XX WO9918230-A2.
XX
XX 15-APR-1999.
XX
XX 07-OCT-1998; 98WO-US21132.
XX PF
XX 07-OCT-1997; 97US-0946226.
XX PR
XX (UNIW) UNIV WASHINGTON.
XX PA
XX Chaudhary PM;
XX PI
XX WPI; 1999-277275/23.
XX DR
XX Identifying regulators of MACH-related inducer of toxicity
XX
XX Example 2; Page -; 78pp; English.
XX
XX The present sequence represents MRIT beta 2, comprising amino acid
XX residues 1-227 of novel human MACH-related inducer of toxicity
XX MRIT alpha 1 (see AAAY05787). This deletion mutant was used to
XX examine the interaction of MRIT alpha 1 with caspases. The results
XX indicated that the C-terminal 216 residues of MRIT are not

CC sufficient for FLICE-p20 interaction. The invention provides
 CC multiple isoforms of MRIT (see AAY05787-89), isolated active
 CC fragments of which have either pro-apoptotic or anti-apoptotic
 CC activity. Selective enhancers and inhibitors of MRIT apoptotic
 CC activity can be identified and used to treat diseases mediated by
 CC the dysfunction of programmed cell death or proliferation, such as
 CC cancer or a neurodegenerative disorder.
 CC Note: the present sequence is not shown in the specification but is
 CC derived from the MRIT alpha 1 sequence given in figure 1F.
 XX
 SQ Sequence 227 AA;
 Query Match 90.4%; Score 1007; DB 20; Length 227;
 Best Local Similarity 99.5%; Pred. No. 2.1e-85;
 Matches 202; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVPPNVRDLILRERKLSVGDIAELLY 60
 DB 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVPPNVRDLILRERKLSVGDIAELLY 60
 QY 61 RVRREFDLKRLKMDKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSLIFLMKDYM 120
 DB 61 RVRREFDLKRLKMDKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSLIFLMKDYM 120
 QY 121 GRGKISKEKSFIDLNVVELEKLNLPADQDLLEKLNHRIIDLTKTKIYKQSVQAGT 180
 DB 121 GRGKISKEKSFIDLNVVELEKLNLPADQDLLEKLNHRIIDLTKTKIYKQSVQAGT 180
 QY 181 SYRNVLOAAIQKSLKDPSSNNFRM 203
 DB 181 SYRNVLOAAIQKSLKDPSSNNFRM 203
 RESULT 13
 AAY67419
 ID AAY67419 standard; Protein: 462 AA.
 AC AAY67419;
 XX
 DT 12-MAY-2000 (first entry)
 DE Usurpin-beta polypeptide.
 KW Usurpin-alpha; death effector domain; DED; prodomain; usurpin-beta;
 KW usurpin-gamma; procaspase-8; CD95; apoptosis; cancer; immunosuppressive;
 KW caspase; cytostatic; antiparkinsonian; antidiabetic.
 XX
 OS Homo sapiens.
 XX WO200003023-A1.
 XX 20-JAN-2000.
 XX 07-JUL-1999; 99WO-CA00615.
 XX 08-JUL-1998; 98US-0092005.
 XX (MERI) MERCK FROSST CANADA INC.
 XX
 XX Nicholson DW, Rasper DM, Xanthoudakis S, Roy S;
 XX WPI; 2000-160929/14.
 XX N-PSDB; AAZ56988.
 XX Novel recombinant DNA molecules and polypeptides for treating apoptosis
 XX mediated diseases e.g. autoimmune diabetes, cancer and Parkinson's
 XX disease
 XX Claim 6; Fig 10B; 69pp; English.
 XX
 XX The invention provides recombinant nucleic acid molecules encoding
 XX usurpin-alpha (lacking the first death effector domain (DED) or its
 XX prodomain), usurpin-beta or usurpin-gamma. Usurpin polypeptides are

CC useful for in vitro and in vivo identification of usurpin-procaspase-8
 CC interaction inhibitor. Usurpin is useful as modulator of the sensitivity
 CC of cells to CD95(Fas/Apo-1) mediated apoptosis. Modulation of apoptosis
 CC is useful for treating diseases like autoimmune diabetes, cancer and
 CC Parkinson's disease. Activators and inhibitors of usurpin-procaspase-8
 CC interaction are also useful for treating various diseases mediated by
 CC apoptosis. Usurpin provides an attractive model for modulating caspase
 CC activation. Sensitivity of cells bearing CD95(Fas/Apo-1) receptor can
 CC be regulated at several levels in the presence of usurpin, conferring
 CC resistance to Fas-ligand cell death. The present sequence represents
 CC the usurpin-beta polypeptide.
 XX
 SQ Sequence 462 AA;
 Query Match 90.4%; Score 1007; DB 21; Length 462;
 Best Local Similarity 99.5%; Pred. No. 5.1e-85;
 Matches 202; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVPPNVRDLILRERKLSVGDIAELLY 60
 DB 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVPPNVRDLILRERKLSVGDIAELLY 60
 QY 61 RVRREFDLKRLKMDKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSLIFLMKDYM 120
 DB 61 RVRREFDLKRLKMDKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSLIFLMKDYM 120
 QY 121 GRGKISKEKSFIDLNVVELEKLNLPADQDLLEKLNHRIIDLTKTKIYKQSVQAGT 180
 DB 121 GRGKISKEKSFIDLNVVELEKLNLPADQDLLEKLNHRIIDLTKTKIYKQSVQAGT 180
 QY 181 SYRNVLOAAIQKSLKDPSSNNFRM 203
 DB 181 SYRNVLOAAIQKSLKDPSSNNFRM 203
 RESULT 14
 AAW76631
 ID AAW76631 standard; Protein: 480 AA.
 AC AAW76631;
 XX
 DT 12-JUL-1999 (first entry)
 DE Human CFLIP-L protein.
 KW Death effector domain; human; murine; anti-apoptotic; treatment;
 KW HIV infection; autoimmune disease; FLIP protein.
 XX
 OS Homo sapiens.
 XX DE19713393-A1.
 XX 08-OCT-1998.
 XX 01-APR-1997; 97DE-1013393.
 XX 01-APR-1997; 97DE-1013393.
 XX (TSCH/) TSCHOPP J.
 XX (APOT-) APOTECH SA.
 XX Bodmer J, Burns K, French EL, Hahne M, Hoffmann K;
 XX Irmler M, Rimoldi D, Schneider P, Schroeter M, Steiner V;
 XX Thome M, Tschoopp J, Hofmann K;
 XX WPI; 1998-532710/46.
 XX N-PSDB; AAV61937.
 XX New DNA encoding for anti-apoptotic gene product - used to treat HIV
 XX infections and autoimmune diseases
 XX Claim 20; Fig 4B; 45pp; German.

CC This invention describes novel human and mouse anti-apoptotic gene
 CC products which contain at least one death effector domain. The products
 CC of the invention are used in the treatment of HIV infections and
 CC autoimmune diseases.
 XX
 SQ Sequence 480 AA;

Query Match 90.4%; Score 1007; DB 19; Length 480;
 Best Local Similarity 99.5%; Pred. No. 5.4e-85;
 Matches 202; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPNNRDLILRERKLSVGDLAELLY 60
 DB 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPNNRDLILRERKLSVGDLAELLY 60
 QY 61 RVRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIFLMKDYM 120
 DB 61 RVRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIFLMKDYM 120
 QY 121 GRGKISKEKSFLLDVVELEKLNLVAPDQDLLEKLNTHRIDLTKTKIYKQSVQAGT 180
 DB 121 GRGKISKEKSFLLDVVELEKLNLVAPDQDLLEKLNTHRIDLTKTKIYKQSVQAGT 180
 QY 181 SYRNVLQAAIQKSLKDPSPNNFRM 203
 DB 181 SYRNVLQAAIQKSLKDPSPNNFRM 203

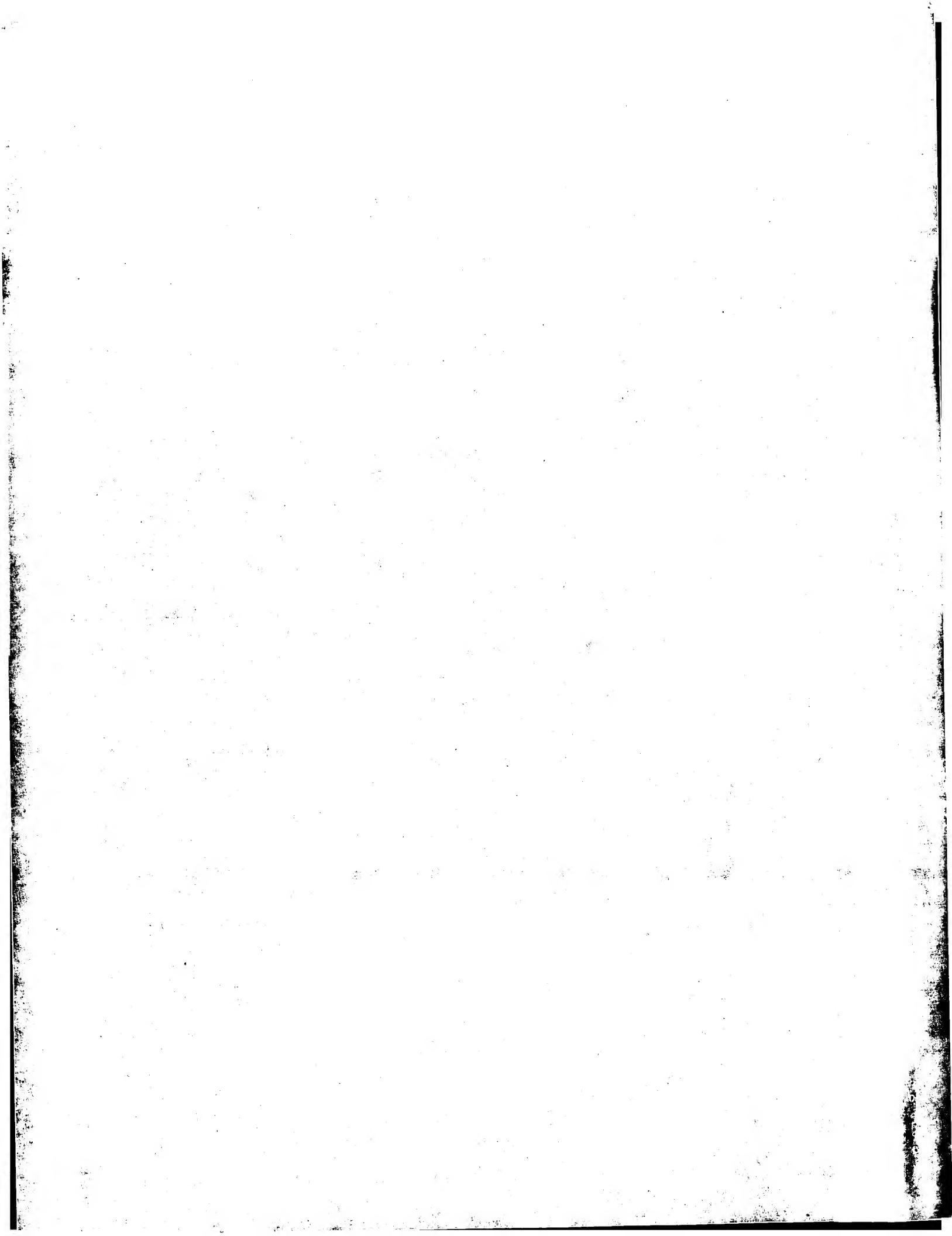
RESULT 15
 AAW78903
 ID AAW78903 standard; Protein; 480 AA.
 XX
 AC AAW78903;
 XX
 DT 11-JAN-1999 (first entry)
 XX
 DE Human G1 protein isoform alpha (CASH-alpha).
 XX
 KW G1 protein; CASH-alpha; human; caspase homologue; Fas receptor;
 KW modulator; apoptosis; cell death; inflammation; tumour; HIV;
 KW therapy.
 XX
 OS Homo sapiens.
 XX
 FH Key
 FT Domain Location/Qualifiers
 FT 2..73
 FT /note="death domain/MORT module"
 FT 93..142
 FT /note="death domain/MORT module"
 FT
 XX WO9839435-A1.
 XX
 PD 11-SEP-1998.
 XX
 PF 26-FEB-1998; 98WO-IL00098.
 XX
 PR 01-MAY-1997; 97IL-0120759.
 PR 03-MAR-1997; 97IL-0120367.
 XX
 PA (YEDA) YEDA RES & DEV CO LTD.
 XX
 XX Brodianski V, Goltsev Y, Kovalenko A, Varfolomeev E;
 PI Wallach D;
 XX
 DR WPI: 1998-495842/42.
 DR N-PSDB; AAV52968.
 XX
 PT New DNA encoding isoforms of G1 protein which bind MORT-1 - and
 PT regulate the effects of Fas and tumour necrosis factor receptors,
 PT useful for killing of cells e.g. HIV and cancer cells
 XX
 PS Claim 12; Fig 1B; 132pp; English.
 XX

CC This is the amino acid sequence of the alpha isoform of novel
 CC human G1 protein. The sequence is deduced from an isolated skin
 CC fibroblast cDNA clone (see AAV52968). G1-alpha (also called CASH
 CC alpha, CASH being caspase homologue) and a shorter isoform, G1-beta
 CC (see AAW78904), represent 2 splice variants of the G1 protein. These
 CC G1 proteins are capable of binding to, or interacting directly or
 CC indirectly, via their N-terminal MORT modules, with MORT-1 or with
 CC MORT-binding proteins such as Mch4 (CASP-10) and MACH (CASP-8), and
 CC thereby of binding to the intracellular domain of the FAS-R
 CC receptor, to which MORT-1 binds, or of binding to the intracellular
 CC domain of the p55 tumour necrosis factor (TNF) receptor, to which
 CC TRADD binds and to which TRADD protein MORT-1 binds. Hence, they
 CC are considered as mediators or modulators of FAS-R having a role in
 CC e.g. the signalling process that is initiated by the binding of FAS
 CC ligand to FAS-R, and also having a role in the signalling process
 CC initiated by the binding of TNF to p55-R. The longer isoform also
 CC has a C-terminal caspase activity region involved in cytotoxic
 CC activity. G1 DNA (I) and polypeptide (II), vectors and fragments
 CC are used to regulate cell death or inflammatory processes. (II) is
 CC used to inhibit cell death, and its inhibitors augment/enhance the
 CC processes. (I) and (II) regulate the FAS-R ligand or TNF effect on
 CC cells carrying an FAS-R or p55-R. Tumour, HIV-infected or other
 CC diseased cells can be treated using a viral vector encoding a viral
 CC surface protein, which binds a specific cell surface receptor and a
 CC sequence encoding (II), which kills the cell. Antisense
 CC oligonucleotides, introduced using the above vector, block the
 CC expression of (II) and can also regulate the above effects. These
 CC effects can also be regulated using a vector encoding a ribozyme
 CC that interacts with a cellular mRNA encoding (II), and allows (II)
 CC expression.
 XX
 SQ Sequence 480 AA;

Query Match 90.4%; Score 1007; DB 19; Length 480;
 Best Local Similarity 99.5%; Pred. No. 5.4e-85;
 Matches 202; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPNNRDLILRERKLSVGDLAELLY 60
 DB 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPNNRDLILRERKLSVGDLAELLY 60
 QY 61 RVRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIFLMKDYM 120
 DB 61 RVRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIFLMKDYM 120
 QY 121 GRGKISKEKSFLLDVVELEKLNLVAPDQDLLEKLNTHRIDLTKTKIYKQSVQAGT 180
 DB 121 GRGKISKEKSFLLDVVELEKLNLVAPDQDLLEKLNTHRIDLTKTKIYKQSVQAGT 180
 QY 181 SYRNVLQAAIQKSLKDPSPNNFRM 203
 DB 181 SYRNVLQAAIQKSLKDPSPNNFRM 203

Search completed: August 13, 2003, 16:36:32
 Job time : 39.1469 secs



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OM protein - protein search, using sw model

Run on: August 13, 2003, 16:33:14 ; Search time 9.45792 Seconds
(without alignments)
1098.857 Million cell updates/sec

Title: US-09-380-546A-4

Perfect score: 1114

Sequence: 1 MSAEVIHQVEALDTDEKEM.....RMTPYAHCPDLKILGNCNM 221

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1007	90.4	480	1 CFLA_HUMAN	015519 h casp8 and
2	701.5	63.0	484	1 CFLA_MOUSE	Q35732 m casp8 and
3	218.5	19.6	241	1 CFLA_MCV1	Q98325 molluscum c
4	197	17.7	480	1 ICE8_MOUSE	Q89110 mus musculus
5	192.5	17.3	479	1 ICE8_MOUSE	Q14790 h caspase-8
6	170.5	15.3	171	1 CFLA_HSV2	Q66674 equine herp
7	160	14.4	521	1 ICEA_HUMAN	Q92851 homo sapien
8	109.5	9.8	167	1 VG71_HSVSA	Q01044 herpesvirus
9	105	9.4	208	1 FADD_HUMAN	Q13158 homo sapien
10	103	9.2	1201	1 RPOC_LISIN	P77879 listeria in
11	103	9.2	1201	1 RPOC_LISMO	Q8Y996 listeria mo
12	99.5	8.9	989	1 RPOC_LEUPS	P94899 leuconostoc
13	99	8.9	2671	1 IP3T_HUMAN	Q14573 homo sapien
14	98.5	8.8	389	1 YC1M_ECOLI	P45576 escherichia
15	98	8.8	2670	1 IP3T_RAT	Q63269 rattus norv
16	97.5	8.8	989	1 RPOC_LEUME	P94892 leuconostoc
17	97	8.7	1199	1 RPOC_BACSU	P37871 bacillus su
18	95.5	8.6	1046	1 RPOC_WEIHE	P96177 weisella h
19	94	8.4	1639	1 LMGI_DROME	P15215 drosophila
20	93	8.3	1055	1 RPOC_PEDAC	P77917 pediococcus
21	93	8.3	1057	1 RPOC_STAAR	P47770 staphylococ
22	91.5	8.2	384	1 MTLD_CLOAB	Q65992 clostridium
23	91	8.2	313	1 VN34_ROTBU	P04514 bovine rota
24	90.5	8.1	391	1 KC21_MOUSE	Q60737 mus musculus
25	90	8.1	392	1 KC22_XENLA	P28020 xenopus lae
26	90	8.1	793	1 VAV_DROME	Q9nhv9 drosophila
27	90	8.1	1053	1 RPOC_LISGR	P77882 listeria gr
28	90	8.1	1169	1 EX5E_BORBU	Q51578 borrelia bu
29	90	8.1	1206	1 RPOC_BACHD	Q929m1 bacillus ha
30	89.5	8.0	535	1 TCPZ_SCHPO	Q94515 schizosacch
31	89.5	8.0	880	1 Y5A_ANASP	Q8Yud4 anabaena sp
32	89.5	8.0	903	1 YB56_METJA	Q58556 methanococ
33	89	8.0	350	1 KC22_CHICK	P21869 gallus gall

RESULT 1

ID	CFLA_HUMAN	STANDARD;	PRT;	480 AA.
AC	O15519; O14673; O14674; O15137; O15138; O15356; O15510;			P21868 gallus gall
AC	O43618; O43619; O43620; O60458; O60459; Q9UEW1;			P19138 homo sapien
DT	16-OCT-2001 (Rel. 40, Created)			P33674 oryctolagus
DT	16-OCT-2001 (Rel. 40, Last sequence update)			P19139 rattus norv
DT	15-SEP-2003 (Rel. 42, Last annotation update)			P52960 saccharomyc
DE	CASP8 and FADD-like apoptosis regulator precursor (Cellular FLICE-like inhibitory protein) (c-FLIP) (Caspase-eight-related protein) (Casper) (Caspase-like apoptosis regulatory protein) (CLARP) (MACH-related inducer of toxicity) (MRIT) (Caspase homolog) (CASH) (inhibitor of FLICE) (I-FLICE) (FADD-like antiapoptotic molecule 1) (flame-1) (Usurpin).			P77819 bacillus an
GN	CFLAR OR CLARP OR MRIT OR CASH.			Q9smh3 chlamydomon
OS	Homo sapiens (Human).			P52150 spiroplasma
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			O9J513 foripox vir
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			O49498 arabidopsis
OX	NCBI_TaxID=9606;			P96178 weisella p
RN	[1]			O9ze20 rickettsia
RP	SEQUENCE FROM N.A. (ISOFORMS 1; 13 AND 14), AND MUTAGENESIS OF TYR-360.			
RC	TISSUE=Embryonic kidney, and Umbilical vein endothelial cells; MEDLINE=97352452; PubMed=9208847;			
RA	Shu H.-B., Halpin D.R., Goeddel D.V.;			
RT	"Casper is a FADD- and caspase-related inducer of apoptosis.";			
RL	Immunity 6:751-763(1997).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).			
RX	MEDLINE=97470957; PubMed=9326610;			
RA	Han D.K.M., Chaudhary P.M., Wright M.E., Friedman C., Trask B.J., Riedel R.T., Baskin D.G., Schwartz S.M., Hood L.;			
RT	"MRIT, a novel death-effector domain-containing protein, interacts with caspases and BclxL and initiates cell death.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 94:11333-11338(1997).			
RN	[3]			
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).			
RC	TISSUE=Periphereal blood lymphocytes;			
RX	MEDLINE=97360133; PubMed=9217161;			
RA	Irmeler M., Thome M., Hahne M., Schneider P., Hofmann K., Steiner V., Bodmer J.-L., Schroeter M., Burns K., Mattmann C., Rimoldi D., French L.E., Tschopp J.;			
RT	"Inhibition of death receptor signals by cellular FLIP.";			
RL	Nature 388:190-195(1997).			
RN	[4]			
RP	SEQUENCE FROM N.A. (ISOFORMS 1; 8; 9 AND 10), AND MUTAGENESIS OF ASP-376.			
RC	TISSUE=T-cell;			
RX	MEDLINE=97373543; PubMed=9228018;			
RA	Srinivasula S.M., Ahmad M., O'Flaherty S., Bullrich F., Banks S., Wang Y., Fernandes-Alnemri T., Croce C.M., Litwack G., Tomaselli K.J., Armstrong R.C., Alnemri E.S.;			
RT	"FLAME-1, a novel FADD-like anti-apoptotic molecule that regulates Fas/TNFR1-induced apoptosis.";			
RL	J. Biol. Chem. 272:18542-18545(1997).			
RN	[5]			

RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Umbilical vein endothelial cells;
 RX MEDLINE=97362203; PubMed=9211860;
 RA Hu S., Vincenz C., Ni J., Gentz R., Dixit V.M.;
 RT "I-FLICE, a novel inhibitor of tumor necrosis factor receptor-1- and
 RL CD-95-induced apoptosis.";
 RN J. Biol. Chem. 272:17255-17257(1997).
 [6]
 RP SEQUENCE FROM N.A. (ISOFORMS 4; 5; 6 AND 7).
 RA Hu S., Dixit V.M.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 11 AND 12).
 RC TISSUE=Kidney;
 RX MEDLINE=99218584; PubMed=10200473;
 RA Raper D.M., Vaillancourt J.P., Hadano S., Rontzger V.M., Seiden I.,
 RA Keen S.L.C., Tava P., Xanthoudakis S., Nasir J., Martindale D.,
 RA Koop B.F., Peterson E.P., Thornberry N.A., Huang J., MacPherson D.P.,
 RA Black S.C., Hornung F., Lenardo M.J., Hayden M.R., Roy S.,
 RA Nicholson D.W.;
 RT "Cell death attenuation by 'Usurpin', a mammalian DED-caspase
 RL homologue that precludes caspase-8 recruitment and activation by the
 RT CD-95 (Fas, APO-1) receptor complex.";
 RL Cell Death Differ. 5:271-288(1998).
 RN [8]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC TISSUE=Skin fibroblast;
 RX MEDLINE=97426025; PubMed=9289491;
 RA Goltsev Y.V., Kovalenko A.V., Arnold E., Varfolomeev E.E.,
 RA Brodianskii V.M., Wallach D.;
 RT "CASH, a novel caspase homologue with death effector domains.";
 RL J. Biol. Chem. 272:19641-19644(1997).
 RN [9]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC TISSUE=Colon carcinoma;
 RX MEDLINE=98021435; PubMed=9380701;
 RA Inohara N., Koseki T., Hu Y., Chen S., Nunez G.;
 RT "CLARP, a death effector domain-containing protein interacts with
 RL caspase-8 and regulates apoptosis.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:10717-10722(1997).
 RN [10]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Lymph;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Diatchenko M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Hellon E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shcherenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RL human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [11]
 RP FUNCTION.
 RX MEDLINE=9909897; PubMed=9889531;
 RA Scaffidi C., Schmitz I., Kramer P.H., Peter M.E.;
 RT "The role of c-FLIP in modulation of CD95-induced apoptosis.";
 RL J. Biol. Chem. 274:1541-1548(1999).
 RN [12]
 RP INDUCTION.
 RX MEDLINE=99244884; PubMed=10227994;

RA Algecras-Schimmich A., Griffith T.S., Lynch D.H., Paya C.V.;
 RT "Cell cycle-dependent regulation of FLIP levels and susceptibility to
 RL Fas-mediated apoptosis.";
 RL J. Immunol. 162:5205-5211(1999).
 CC -I- FUNCTION: APOPTOSIS REGULATOR PROTEIN WHICH MAY FUNCTION AS A
 CC CRUCIAL LINK BETWEEN CELL SURVIVAL AND CELL DEATH PATHWAYS IN
 CC MAMMALIAN CELLS. ACTS AS AN INHIBITOR OF TNFRSF6 MEDIATED
 CC APOPTOSIS. A PROTEOLYTIC FRAGMENT (P43) IS LIKELY RETAINED IN THE
 CC DEATH-INDUCING SIGNALING COMPLEX (DISC) THEREBY BLOCKING FURTHER
 CC RECRUITMENT AND PROCESSING OF CASPASE-8 AT THE COMPLEX. FULL
 CC LENGTH AND SHORTER ISOFORMS HAVE BEEN SHOWN EITHER TO INDUCE
 CC APOPTOSIS OR TO REDUCE TNFRSF6 TRIGGERED APOPTOSIS. LACKS ENZYMATIC
 CC (CASPASE) ACTIVITY.
 CC -I- SUBUNIT: TNFRSF6 STIMULATION TRIGGERS RECRUITMENT TO THE DEATH-
 CC INDUCING SIGNALING COMPLEX (DISC) FORMED BY TNFRSF6, FADD AND
 CC CASPASE-8. A PROTEOLYTIC FRAGMENT (P43) STAYS ASSOCIATED WITH THE
 CC DISC. ALSO INTERACTS WITH CASPASE-10, CASPASE-3, TRAF1, TRAF2 AND
 CC BCL-X(L) (IN VITRO).
 CC -I- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=14;
 CC Name=1; Synonyms=FLIP-L, CLARP1, MRIT alpha-1, CASH alpha, I-FLICE
 CC 1, FLAME-1 gamma, Usurpin alpha;
 CC IsoId=O15519-1; Sequence=displayed;
 CC Name=2; Synonyms=FLIP-S, CLARP2, MRIT beta-1, CASH beta;
 CC IsoId=O15519-2; Sequence=VSP_000828, VSP_000829;
 CC Name=3; Synonyms=MRIT alpha-2;
 CC IsoId=O15519-3; Sequence=VSP_000830;
 CC Name=4; Synonyms=I-FLICE 2;
 CC IsoId=O15519-4; Sequence=VSP_000831;
 CC Name=5; Synonyms=I-FLICE 3;
 CC IsoId=O15519-5; Sequence=VSP_000832;
 CC Name=6; Synonyms=I-FLICE 4;
 CC IsoId=O15519-6; Sequence=VSP_000833;
 CC Name=7; Synonyms=I-FLICE 5;
 CC IsoId=O15519-7; Sequence=VSP_000834, VSP_000835;
 CC Name=8; Synonyms=Flame-1 alpha;
 CC IsoId=O15519-8; Sequence=VSP_000836;
 CC Name=9; Synonyms=Flame-1 beta;
 CC IsoId=O15519-9; Sequence=VSP_000837;
 CC Name=10; Synonyms=Flame-1 delta;
 CC IsoId=O15519-10; Sequence=VSP_000838;
 CC Name=11; Synonyms=Usurpin beta;
 CC IsoId=O15519-11; Sequence=VSP_000839;
 CC Name=12; Synonyms=Usurpin gamma;
 CC IsoId=O15519-12; Sequence=VSP_000840, VSP_000841;
 CC Name=13;
 CC IsoId=O15519-13; Sequence=VSP_000842;
 CC Name=14;
 CC IsoId=O15519-14; Sequence=VSP_000843;
 CC -I- TISSUE SPECIFICITY: WIDELY EXPRESSED. HIGHER EXPRESSION IN
 CC SKELETAL MUSCLE, PANCREAS, HEART, KIDNEY, PLACENTA, AND PERIPHERAL
 CC BLOOD LEUKOCYTES. ALSO DETECTED IN DIVERSE CELL LINES. ISOFORM 8
 CC IS PREDOMINANTLY EXPRESSED IN TESTIS AND SKELETAL MUSCLE.
 CC -I- INDUCTION: REPRESSION BY IL-2 AFTER TCR STIMULATION, DURING
 CC PROGRESSION TO THE S-PHASE OF THE CELL CYCLE.
 CC -I- DOMAIN: THE CASPASE DOMAIN LACKS THE ACTIVE SITES RESIDUES
 CC INVOLVED IN CATALYSIS.
 CC -I- PM: PROTEOLITICALLY PROCESSED; PROBABLY BY CASPASE-8. PROCESSING
 CC LIKELY OCCURS AT THE DISC, GENERATES SUBUNIT P43 AND P12.
 CC -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
 CC -I- SIMILARITY: Contains 2 death effector (DED) domains.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AF010127; AAB64110.1; -;
 CC EMBL; U85059; AAB82648.1; -;
 CC EMBL; U97074; AAC51622.1; -;

Query Match 90.4%; Score 1007; DB 1; Length 480;
Best Local Similarity 99.5%; Pred. No. 1.3e-64;
Matches 202; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSAEVIHQVEEALDTDEKEMLLFLCRDAIVDVPVPPNVRDLIDLIRGKLSVGDLAELLY 60
DB 1 MSAEVIHQVEEALDTDEKEMLLFLCRDAIVDVPVPPNVRDLIDLIRGKLSVGDLAELLY 60

QY 61 RYRREDLLKRLIKMDKRAVETHLLRNPHLVSDYRVLMIAEIGBDLKDSDVSSLIIFLMKDYM 120
DB 61 RYRREDLLKRLIKMDKRAVETHLLRNPHLVSDYRVLMIAEIGBDLKDSDVSSLIIFLMKDYM 120

QY 121 GRGKISKESKSFLLVVELEKLNVLAPDQDLLEKCLKNHRIIDLTKTKQYKQSVQAGT 180
DB 121 GRGKISKESKSFLLVVELEKLNVLAPDQDLLEKCLKNHRIIDLTKTKQYKQSVQAGT 180

QY 181 SYRNVLRQAIOKSLKDPNSNFRM 203
DB 181 SYRNVLRQAIOKSLKDPNSNFRM 203

RESULT 2

CFLA_MOUSE STANDARD; PRT: 484 AA.

AC 035732; 035707; 035733;
DT 16-OCT-2001 (Rel. 40, Created)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE CASP8 and FADD-like apoptosis regulator precursor (Cellular FLICE-like
inhibitory protein) (c-FLIP) (Caspase-eight-related protein) (Casper)
DE (Caspase-like apoptosis regulatory protein) (CLARP) (MACH-related
inducer of toxicity) (MRIT) (Caspase homolog) (CASH) (Inhibitor of
FLICE) (I-FLICE) (FADD-like antiapoptotic molecule 1) (Flame-1)
DE (Usurpin).
GN CFLAR OR CASH.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Liver;
RX MEDLINE=97426025; PubMed=9289491;
RA Goldsiev Y.V., Kovalenko A.V., Arnold E., Varfolomeev E.E.,
RA Brodianskii V.M., Wallach D.;
RT "CASH, a novel caspase homologue with death effector domains.";
RL J. Biol. Chem. 272:19641-19644 (1997).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Heart;
RX MEDLINE=97360133; PubMed=9217161;
RA Irmiler M., Thome M., Hahne M., Schneider P., Hofmann K., Steiner V.,
RA Bodner J.-L., Schroeter M., Burns K., Mattmann C., Rimoldi D.,
RA French L.E., Tschoopp J.;
RT "Inhibition of death receptor signals by cellular FLIP.";
RL Nature 388:190-195 (1997).
RN [3]
RP FUNCTION.
RX MEDLINE=20350661; PubMed=10894163;
RA Yeh W.-C., Itie A., Elia A.-J., Ng M., Shu H.-B., Wakeham A.,
RA Mirtsos C., Suzuki N., Bonnard M., Goeddel D.V., Mak T.W.;
RT "Requirement for Casper (c-FLIP) in regulation of death
receptor-induced apoptosis and embryonic development.";
RL Immunity 12:633-642 (2000).
RN [4]
RP FUNCTION.
RX MEDLINE=20069388; PubMed=10602037;
RA Wang J., Lobito A.A., Shen F., Hornung F., Winoto A., Lenardo M.J.;
RT "Inhibition of Fas-mediated apoptosis by the B cell antigen receptor
through c-FLIP.";
RL Eur. J. Immunol. 30:155-163 (2000).
CC -1- FUNCTION: APOPTOSIS REGULATOR PROTEIN WHICH MAY FUNCTION AS A

CRUCIAL LINK BETWEEN CELL SURVIVAL AND CELL DEATH PATHWAYS IN
MAMMALIAN CELLS. ACTS AS AN INHIBITOR OF TNFRSF6 MEDIATED
APOPTOSIS. A PROTEOLYTIC FRAGMENT (P43) IS LIKELY RETAINED IN THE
DEATH-INDUCING SIGNALING COMPLEX (DISC) THEREBY BLOCKING FURTHER
RECRUITMENT AND PROCESSING OF CASPASE-8 AT THE COMPLEX. FULL
LENGTH AND SHORTER ISOFORMS HAVE BEEN SHOWN EITHER TO INDUCE
APOPTOSIS OR TO REDUCE TNFRSF-TRIGGERED APOPTOSIS. LACKS ENZYMATIC
(CASPASE) ACTIVITY (BY SIMILARITY).
CC -1- SUBUNIT: TNFRSF6 STIMULATION TRIGGERS RECRUITMENT TO THE DEATH-
INDUCING SIGNALING COMPLEX (DISC) FORMED BY TNFRSF6, FADD AND
CASPASE-8. A PROTEOLYTIC FRAGMENT (P43) STAYS ASSOCIATED WITH THE
DISC (BY SIMILARITY).
CC -1- ALTERNATIVE PRODUCTS:
Event-Alternative splicing; Named isoforms=2;
Name=1; Synonyms=FLIP-L, CASH alpha;
IsoId=035732-1; Sequence=Displayed;
Name=2; Synonyms=FLIP-S, CASH beta;
IsoId=035732-2; Sequence=VSP_000842, VSP_000843;
CC -1- TISSUE SPECIFICITY: Highly expressed in heart.
CC -1- DEVELOPMENTAL STAGE: AT EMBRYONIC DAYS E9.5 AND E10.5 HIGHEST
EXPRESSION IN DEVELOPPING HEART.
CC -1- INDUCTION: ISOFORM 1 BUT NOT ISOFORM 2 IS ACTIVATED BY BCR CROSS-
LINKING IN PRIMARY B-CELLS.
CC -1- DOMAIN: THE CASPASE DOMAIN LACKS THE ACTIVE SITES RESIDUES
INVOLVED IN CATALYSIS.
CC -1- PTM: PROTEOLYTICALLY PROCESSED; PROBABLY BY CASPASE-8. PROCESSING
LIKELY OCCURS AT THE DISC, GENERATES SUBUNIT P43 AND P12 (BY
SIMILARITY).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
CC -1- SIMILARITY: Contains 2 death effector (DED) domains.

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or send an email to license@isb-sib.ch).

DR EMBL; Y14041; CAA74368.1; -
DR EMBL; Y14042; CAA74369.1; -
DR EMBL; U97076; AAC53281.1; -
DR HSP; Q15806; IQDD.
DR MEROPS; C14.974; -
DR MGD; MGI:1336166; Cflar.
DR InterPro; IPR001875; DED.
DR InterPro; IPR002398; ICE.
DR InterPro; IPR001309; ICE_p20.
DR Pfam; PF01335; DED; 2.
DR Pfam; PF00656; Peptidase_C14; 1.
DR SMART; SM00115; CASC; 1.
DR SMART; SM00031; DED; 2.
DR PROSITE; PS0208; CASPASE_P20; 1.
DR PROSITE; PS0168; DED; 2.
KW Apoptosis; Repeat; Alternative splicing.
FT CHAIN 1 380 CASP8 AND FADD-LIKE APOPTOSIS REGULATOR
SUBUNIT P43 (BY SIMILARITY).
FT CHAIN 381 484 CASP8 AND FADD-LIKE APOPTOSIS REGULATOR
SUBUNIT P12 (BY SIMILARITY).
FT DOMAIN 6 78 DED 1.
FT DOMAIN 97 175 DED 2.
FT DOMAIN 268 363 CASPASE.
FT DOMAIN 421 425 POLY-SER.
FT VARSPIC 208 218 LONGRSKEPRF -> VSLEPVYGVPA (in isoform
2).
FT /FTId=VSP_000842.
FT VARSPIC 219 480 Missing (in isoform 2).
FT /FTId=VSP_000843.
FT CONFLICT 123 125 MISSING (IN REF. 2).
FT SEQUENCE 484 AA; 55245 MW; 0BF7A92CB09F5F1F CRC64;
SQ
Query Match 63.0%; Score 701.5; DB 1; Length 484;
Best Local Similarity 73.4%; Pred. No. 6.8e-43;

[illegible]

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Caspase-8 precursor (EC 3.4.22.-) (ICE-like apoptotic protease 5)

DE (MORT1-associated CED-3 homolog) (MACH) (FADD-homologous ICE/CED-3-like protease)

DE (Apoptotic protease Mch-5) (CAP4).

GN CASP8 OR MCH5.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3; 5; 6; 7 AND 8).

RC TISSUE=B-cell, and Thymus;

RA MEDLINE=96279826; PubMed=8681376;

RA Boldin M.P., Goncharov T.M., Goltsev Y.V., Wallach D.;

RT "Involvement of MACH, a novel MORT1/FADD-interacting protease, in Fas/APO-1- and TNF receptor-induced cell death.";

RL Cell 85:803-815(1996).

RN [2]

RP SEQUENCE FROM N.A. (ISOFORM 1), AND PARTIAL SEQUENCE.

RX MEDLINE=96279827; PubMed=8681377;

RA Muzio M., Chinnaiyan A.M., Kischkel F.C., O'Rourke K., Shevchenko A., Ni J., Scaffidi C., Bretz J.D., Zhang M., Gentz R., Mann M., Krammer P.H., Peter M.E., Dixit V.M.;

RT "FLICE, a novel FADD-homologous ICE/CED-3-like protease, is recruited to the CD95 (Fas/APO-1) death-inducing signaling complex.";

RL Cell 85:817-827(1996).

RN [3]

RP SEQUENCE FROM N.A. (ISOFORM 4).

RC TISSUE=T-cell;

RX MEDLINE=96353638; PubMed=8755496;

RA Fernandes-Alnemri T., Armstrong R.C., Krebs J.F., Srinivasula S.M., Wang L., Bullrich F., Fritz L.C., Trapani J.A., Tomaselli K.J., Litwack G., Alnemri E.S.;

RT "In vitro activation of Cpp32 and Mch3 by Mch4, a novel human apoptotic cysteine protease containing two FADD-like domains.";

RL Proc. Natl. Acad. Sci. U.S.A. 93:7464-7469(1996).

RN [4]

RP SEQUENCE FROM N.A.

RX MEDLINE=99132295; PubMed=9931493;

RA Grenet J., Teitz T., Wei T., Valentine V., Kidd V.J.;

RT "Structure and chromosome localization of the human CASP8 gene.";

RL Gene 226:225-232(1999).

RN [5]

RP SEQUENCE FROM N.A. (ISOFORM 2).

RX MEDLINE=97373543; PubMed=9228018;

RA Srinivasula S.M., Ahmad M., Otilili S., Bullrich F., Banks S., Fernandes-Alnemri T., Croce C.M., Litwack G., Tomaselli K.J., Armstrong R.C., Alnemri E.S.;

RT "FLAME-1, a novel FADD-like anti-apoptotic molecule that regulates Fas/TNFR1-induced apoptosis.";

RL J. Biol. Chem. 272:18542-18545(1997).

RN [6]

RP SEQUENCE FROM N.A.

RX MEDLINE=21100893; PubMed=11161814;

RA Hadano S., Yanagisawa Y., Skaug J., Fichter K., Nasir J., Martindale D., Koop B.F., Scherer S.W., Nicholson D.W., Rouleau G.A., Ikeda J.-E., Hayden B.R.;

RT "Cloning and characterization of three novel genes, ALS2CR1, ALS2CR2, and ALS2CR3, in the juvenile amyotrophic lateral sclerosis (ALS2) critical region at chromosome 2q33-q34: Candidate genes for ALS2.";

RL Genomics 71:200-213(2001).

RN [7]

RP SEQUENCE FROM N.A. (ISOFORM 7), AND FUNCTION OF ISOFORM 7.

RC TISSUE=Leukocyte;

RX MEDLINE=22005982; PubMed=12010809;

RA Himeji D., Horiuchi T., Tsukamoto H., Hayashi K., Watanabe T., Harada M.;

RT "Characterization of caspase-8L: a novel isoform of caspase-8 that behaves as an inhibitor of the caspase cascade.";

RL Blood 99:4070-4078(2002).

RN [8]

RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 9), AND INTERACTION OF ISOFORM 9 WITH BCAP31 AT THE ENDOPLASMIC RETICULUM.

RX MEDLINE=21927603; PubMed=11917123;

RA Breckenridge D.G., Nguyen M., Kuppig S., Reth M., Shore G.C.;

RT "The procaspase-8 isoform, procaspase-8L, recruited to the BAP31 complex at the endoplasmic reticulum.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:4331-4336(2002).

RN [9]

RP SEQUENCE FROM N.A. (ISOFORM 7).

RC TISSUE=Leukocyte;

RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D., Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grumwood J., Schmutz J., Myers R.M., Butterfield A.S.N., Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [10]

RP PARTIAL SEQUENCE, AND PROCESSING.

RX MEDLINE=97121412; PubMed=8962078;

RA Srinivasula S.M., Ahmad M., Fernandes-Alnemri T., Litwack G., Alnemri E.S.;

RT "Molecular ordering of the Fas-apoptotic pathway: the Fas/APO-1 protease Mch5 is a CrmA-inhibitable protease that activates multiple Ced-3/ICE-like cysteine proteases.";

RL Proc. Natl. Acad. Sci. U.S.A. 93:14486-14491(1996).

RN [11]

RP FUNCTION.

RX MEDLINE=97160607; PubMed=9006941;

RA Muzio M., Salvesen G.S., Dixit V.M.;

RT "FLICE induced apoptosis in a cell-free system. Cleavage of caspase zymogens.";

RL J. Biol. Chem. 272:2952-2956(1997).

RN [12]

RP PROCESSING.

RX MEDLINE=97327557; PubMed=9184224;

RA Medema J.P., Scaffidi C., Kischkel F.C., Shevchenko A., Mann M., Krammer P.H., Peter M.E.;

RT "FLICE is activated by association with the CD95 death-inducing signaling complex (DISC)."

RL EMBO J. 16:2794-2804(1997).

RN [13]

RP CHARACTERIZATION OF ISOFORM 7.

RX MEDLINE=20318377; PubMed=10860845;

RA Horiuchi T., Himeji D., Tsukamoto H., Harashima S., Hashimura C., Hayashi K.;

RT "Dominant expression of a novel splice variant of caspase-8 in human peripheral blood lymphocytes.";

RL Biochem. Biophys. Res. Commun. 272:877-881(2000).

RN [14]

RP INTERACTION WITH BCL2; BCL2L1 AND BCAP31.

RX MEDLINE=97477382; PubMed=9334338;

RA Ng F.W.H., Nguyen M., Kwan T., Branton P.E., Nicholson D.W., Cronin J.A., Shore G.C.;

RT "p28 Bap31, a Bcl-2/Bcl-XL- and procaspase-8-associated protein in the endoplasmic reticulum.";

RL J. Cell Biol. 139:327-338(1997).

RN [15]

CFILA_HSV2	STANDARD;	PRT;	171 AA.
ID	CFILA_HSV2		
AC	Q66674;		
DT	16-OCT-2001 (Rel. 40, Created)		
DT	16-OCT-2001 (Rel. 40, Last sequence update)		
DT	15-SEP-2003 (Rel. 42, Last annotation update)		
DE	Viral CasP8 and FADD-like apoptosis regulator (V-CFLAR) (Viral		
DE	FLICE-inhibitory protein) (V-FLIP).		
GN	EB.		
OS	Equine herpesvirus type 2 (strain 86/87) (EHV-2).		
OC	Viruses; dsDNA viruses, no RNA stage; Herpesviridae;		
OC	Gammapherpesvirinae.		
OX	NCBI_TaxID=82831;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RP	MEDLINE=97242415; PubMed=9087414;		
RX	Thome M., Schneider P., Hofmann K., Fickenscher H., Meinel E.,		
RA	Wang C.-H., Senkevich T.G., Alnemri E.S., Moss B., Lenardo M.J.,		
RA	Tomasselli K.J., Cohen J.I.;		
RA	"Death effector domain-containing herpesvirus and poxvirus proteins		
RT	inhibit both Fas- and TNF α -induced apoptosis";		
RT	Proc. Natl. Acad. Sci. U.S.A. 94:1172-1176(1997).		
RL	[1]		
CC	-1- FUNCTION: INHIBITS TNFRSF1A, TNFRSF6, TNFRSF10 AND TNFRSF12		
CC	INDUCED APOPTOSIS. MAY INTERFERE WITH CASPASE-8 RECRUITMENT AND		
CC	ACTION AT THE DEATH-INDUCING SIGNALING COMPLEX (DISC). MAY		
CC	LEAD TO HIGHER VIRUS PRODUCTION AND CONTRIBUTE TO VIRUS		
CC	PERSISTENCE AND ONCOGENICITY.		
CC	-1- SUBUNIT: ASSOCIATES WITH THE DEATH-INDUCING SIGNALING COMPLEX		
CC	(DISC) FORMED BY TNFRSF6, FADD AND CASPASE-8. INTERACTS WITH FADD.		
CC	-1- SIMILARITY: Contains 2 death effector (DED) domains.		
CC	-----		
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/		
CC	or send an email to license@isb-sib.ch).		
CC	-----		
DR	EMBL: U20824; AAC13862.1;		
DR	PIR: S55668; S55668.		
DR	PDB: 1LGJ; 01-MAY-02.		
DR	InterPro: IPR001875; DED.		
DR	Pfam: PF01335; DED: 1.		
DR	SMART: SM00031; DED: 2.		
DR	PROSITE: PS00168; DED: 2.		
KW	Apoptosis; Repeat; 3D-structure.		
FT	DOMAIN 1 74 DED 1.		
FT	DOMAIN 92 171 DED 2.		
SQ	SEQUENCE 171 AA; 19925 MW; 4CEAF9D0EE04D9AE CRC64;		
Query Match	15.3%; Score 170.5; DB 1; Length 171;		
Best Local Similarity	32.7%; Pred. No. 1.2e-05;		
Matches 55; Conservative	22; Mismatches 72; Indels 19; Gaps 5;		

db 12 S I D E F E T E T Y I Y I C R D L I K N K C E E O C T R D A E K E I S D V A C I S A A N O M E I I E R V C B I . 66

QY 66 DLLKRLKMDKAVETHLLRNPHLVSDYRVLMATGEDLDKSDYSSLIPL----MKDYMG 121
DQ 67 DLIRIFGQTWTPDSCPRYPMP-ICSPFRCLMALVNDFLSDKEVEYFLCAPRLSHLE 125
QY 122 RGSISKEKSLDVLVELEKLNIVAPDQDLLEKCLKNHTRDLDKTKIQ 169
DQ 126 PG---SKASFLKSLASLLELLELGGDKLTFELRHLLTTIGRADLVKNLQ 170

RESULT 7

ICEA_HUMAN
ID ICEA_HUMAN STANDARD: PRT: 521 AA.
AC Q92851; Q8WQ8; Q92845; Q9Y2U6; Q9Y2U7;
DT 01-NOV-1997 (Rel. 35; Created)
DT 01-NOV-1997 (Rel. 35; Last sequence update)
DT 15-SEP-2003 (Rel. 42; Last annotation update)
DE Caspase-10 precursor (EC 3.4.22.-) (ICE-like apoptotic protease 4)
DE (Apoptotic protease Mch-4) (FAS-associated death domain protein
DE Interleukin-1B-converting enzyme 2) (FLICE2).
GN CASP10 OR MCH4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM A).
RC TISSUE=T-cell;
RX MEDLINE=96353838; PubMed=8755496;
RA Fernandes-Alnemri T., Armstrong R.C., Krebs J., Srinivasula S.M.,
RA Wang L., Bullrich F., Fritz L.C., Trapani J.A., Tomaselli K.J.,
RA Litwack G., Alnemri E.S.;
RT "In vitro activation of CPP32 and Mch3 by Mch4, a novel human
RT apoptotic cysteine protease containing two FADD-like domains."
RL Proc. Natl. Acad. Sci. U.S.A. 93:7464-7469(1996).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM B).
RX MEDLINE=97197836; PubMed=9045686;
RA Vincenz C., Dixit V.M.;
RT "Fas-associated death domain protein interleukin-1beta-converting
RT enzyme 2 (FLICE2), an ICE/Ced-3 homologue, is proximally involved in
RT CD95- and p55-mediated death signaling."
RL J. Biol. Chem. 272:6578-6583(1997).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS B AND C), AND VARIANT ILE-410.
RC TISSUE=Spleen, and Thymus;
RX MEDLINE=99214592; PubMed=10187817;
RA Ng P.W., Porter A.G., Janicke R.U.;
RT "Molecular cloning and characterization of two novel pro-apoptotic
RT isoforms of caspase-10."
RL J. Biol. Chem. 274:10301-10308(1999).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORMS A AND B).
RX MEDLINE=21100893; PubMed=81161814;
RA Hadano S., Yanagisawa Y., Skaug J., Fichter K., Nasir J.,
RA Martindale D., Koop B.F., Scherer S.W., Nicholson D.W., Rouleau G.A.,
RA Ikeda J.-E., Hayden M.R.;
RT "Cloning and characterization of three novel genes, ALS2CR1, ALS2CR2,
RT and ALS2CR3, in the juvenile amyotrophic lateral sclerosis (ALS2)
RT critical region at chromosome 2q33-q34: candidate genes for ALS2."
RL Genomics 71:200-213(2001).
RN [5]
RP PARTIAL SEQUENCE, AND PROCESSING.
RX MEDLINE=97121412; PubMed=8962078;
RA Srinivasula S.M., Ahmad M., Fernandes-Alnemri T., Litwack G.,
RA Alnemri E.S.;
RT "Molecular ordering of the Fas-apoptotic pathway: the Fas/APO-1
RT protease Mch5 is a Crma-inhibitable protease that activates multiple
RT Ced-3/ICE-like cysteine proteases."
RL Proc. Natl. Acad. Sci. U.S.A. 93:14486-14491(1996).
RN [6]
RP VARIANT ALPS2 PHE-285, AND VARIANT ILE-410.
RX MEDLINE=99339325; PubMed=10412980;

RA Wang J., Zheng L., Lobito A., Chan F.K., Dale J., Sneller M., Yao X.,
RA Puck J.M., Straus S.E., Lenardo M.J.;
RT "Inherited human caspase 10 mutations underlie defective lymphocyte
RT and dendritic cell apoptosis in autoimmune lymphoproliferative
RT syndrome type II";
RL Cell 98:47-58(1999).
CC -!- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
CC RESPONSIBLE FOR APOPTOSIS EXECUTION. RECRUITED TO BOTH FAS- AND
CC TNFR-1 RECEPTORS IN A FADD DEPENDENT MANNER. MAY PARTICIPATE IN
CC THE GRANZYME B APOPTOTIC PATHWAYS. CLEAVES AND ACTIVATES CASPASE-
CC 3, -4, -6, -7, -8, AND -9. HYDROLYZES THE SMALL- MOLECULE
CC SUBSTRATES, TYR-VAL-ALA-ASP-|-AMC AND ASP-GLU-VAL-ASP-|-AMC.
CC -!- FUNCTION: ISOFORM C IS PROTEOLYTICALLY INACTIVE.
CC -!- SUBUNIT: HETERODIMER OF A 23/17 kDa (P23/17) DEPENDENT ON THE
CC SPLICING EVENTS AND A 12 kDa (P12) SUBUNIT.
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=3;
CC Name=A; Synonyms=10-A;
CC IsoId=Q92851-1; Sequence=Displayed;
CC Name=B; Synonyms=10-B;
CC IsoId=Q92851-2; Sequence=VSP_000819, VSP_000820;
CC Name=C; Synonyms=10-C;
CC IsoId=Q92851-3; Sequence=VSP_000821, VSP_000822;
CC TISSUE SPECIFICITY: DETECTABLE IN MOST TISSUES. LOWEST EXPRESSION
CC IS SEEN IN BRAIN, KIDNEY, PROSTATE, TESTIS, AND COLON.
CC -!- PTM: CLEAVAGE BY GRANZYME B AND AUTOCATALYTIC ACTIVITY GENERATE
CC THE TWO ACTIVE SUBUNITS.
CC -!- DISEASE: Defects in CASP10 are the cause of type II autoimmune
CC lymphoproliferative syndrome (ALPS2) [MIM:60309]. ALPS2 is
CC characterized by abnormal lymphocyte and dendritic cell
CC homeostasis and immune regulatory defects.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
CC -!- SIMILARITY: Contains 2 death effector (DED) domains.
CC -----
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CC -----
DR EMBL; U60519; AAC50644.1; -;
DR EMBL; U86214; AB46730.1; -;
DR EMBL; AF111344; AAD28402.1; -;
DR EMBL; AF111345; AAD28403.1; -;
DR EMBL; AB038978; BAB32553.1; -;
DR EMBL; AB038973; BAB32553.1; JOINED.
DR EMBL; AB038974; BAB32553.1; JOINED.
DR EMBL; AB038975; BAB32553.1; JOINED.
DR EMBL; AB038977; BAB32553.1; JOINED.
DR EMBL; AB038979; BAB32554.1; -;
DR EMBL; AB038973; BAB32554.1; JOINED.
DR EMBL; AB038974; BAB32554.1; JOINED.
DR EMBL; AB038975; BAB32554.1; JOINED.
DR EMBL; AB038976; BAB32554.1; JOINED.
DR EMBL; AB038977; BAB32554.1; JOINED.
DR HSSP; Q15806; IQDU.
DR MEROPS; C14.011; -;
DR Genew; HGNC:1500; CASP10.
DR MIM; 601762; -;
DR MIM; 603909; -;
DR GO; GO:0004199; F:caspase activity; TAS.
DR GO; GO:0004206; F:caspase-10 activity; TAS.
DR GO; GO:0006917; P:induction of apoptosis; TAS.
DR InterPro; IPR001875; DED.
DR InterPro; IPR002398; ICE.
DR InterPro; IPR002139; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR Pfam; PF01335; DED; 2.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; IL1BCNZYME.
DR SMART; SM00115; CASC; 1.


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DR 231 LPVIPPEIRPMVQL--EGGRFATSGLNDLYRVRINRNRRLKRLDLGAPNLIIVQNEKRL 288
QY 76 RKAVE-----THLLRNPPLVSDYRVLMAEIGEDLDRSDVSSL 112
DB 289 QEAVDALINDGRRGPRVTPGPNRPLKLSLMLKG-----KQGRFRQNLGKRVDSYGRSVI 344
QY 113 I-----FLMKDYMGGRKISKEKSFGLDVLVELEKLNVLAPDQL 149
DB 345 VVGNLKMVQGLPKEMALELFKPFVVKELYVGRGLAHNIKS-----AKRKIERMAPEIW 398
QY 150 DLLLEKCLK-----NIHRDLKTKIQYKOS-VQAG-----TSYR----- 183
DB 399 DYLEEVIREHPVLLNRAPTLHLRG-----IQAFETLVGEAIRLHPLVCTAYNAFDGQ 454
QY 184 -----NVQAAIQSLKDPNSNFRMITPYAHCPLKILGN 218
DB 455 MAVHVPLSAEAQAEARILMLAAQNIL-NPKDKPVTVP---SQDM-VLGN 499

RESULT 12
RPOC_LEUPS
ID AC P94899; STANDARD; PRT; 989 AA.
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DE DNA-directed RNA polymerase beta' chain (EC 2.7.7.6) (Transcriptase
DE beta' chain) (RNA polymerase beta' subunit) (Fragment).
GN RPOC.
OS Leuconostoc pseudomesenteroides.
OC Bacteria; Firmicutes; Lactobacillales; Leuconostoc.
OX NCBI_taxid=33968;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=NCDO 768;
RX MEDLINE=97016803; PubMed=8863429;
RA Morse R., Collins M.D., O'Hanlon K., Wallbanks S., Richardson P.T.;
RT "Analysis of the beta' subunit of DNA-dependent RNA polymerase does
RT not support the hypothesis inferred from 16S rRNA analysis that
RT Oenococcus oeni (formerly Leuconostoc oenos) is a tachytelic
RT (fast-evolving) bacterium."
RL Int. J. Syst. Bacteriol. 46:1004-1009(1996).
CC -1- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
CC SUBSTRATES.
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC {RNA}(N).
CC -1- SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE
CC ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND 1
CC BETA' CHAIN.
CC -1- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.
CC -----
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CC -----
CC EMBL; X95812; CAA65079.1; -.
CC HSSP; Q9KWU6; 1HQM.
CC InterPro; IPR000722; RNA_pol.A.
CC InterPro; IPR007080; RNA_pol_Rpb1_1.
CC InterPro; IPR007066; RNA_pol_Rpb1_3.
CC InterPro; IPR007083; RNA_pol_Rpb1_4.
CC InterPro; IPR007081; RNA_pol_Rpb1_5.
CC InterPro; IPR006592; RNA_pol.N.
CC Pfam; PF04997; RNA_pol_Rpb1_1.
CC Pfam; PF00623; RNA_pol_Rpb1_2.
CC Pfam; PF04983; RNA_pol_Rpb1_3.
CC Pfam; PF05000; RNA_pol_Rpb1_4.
CC Pfam; PF05000; RNA_pol_Rpb1_4; 1.

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DR Pfam; PF04998; RNA_pol_Rpb1_5; 1.
DR SMART; SM00663; RPOLA_N; 1.
KW Transferase; DNA-directed RNA polymerase; Transcription.
FT NON_TER 1 989
FT NON_TER 989
SQ SEQUENCE 989 AA; 109914 MW; 55BICD8CA8739D06 CRC64;

Query Match
Best Local Similarity 8.9%; Score 99.5; DB 1; Length 989;
Matches 45; Conservative 50; Mismatches 76; Indels 37; Gaps 11;

QY 9 VEEALDTDEKEMILFLCHRDVAIDVVPNVRDLDIRRGKLSVGDIAELLYRV-RRPDL 67
DB 147 VEALQSNKPE--WMVMDV-VPIPPDLRPMVQL--EGGRFATSGLNDLYRVRINRNR 201
QY 68 LKRILKMDRKAVETHLLRNPPLVSDYRVLMAEIGEDLKS-----DYSSLIFL 115
DB 202 LKRLLDLNAPGI---IVQN-----EKRLQEAVALINDGRRGPRVAGPNRPLKLSLHM 253
QY 116 MKDYMGGRK-----ISKE-----KSFGLD--VVELEKLNVLAPDQLDLEK-CLKNIRHIDL 164
DB 254 LKGRQGRFRQNLGKRVDSYGRSVIDVGFLLKMNQMGLPVPMATELFRPFIMKELTRKL 313
QY 165 KTKIQYKOSVOGAGTSYRNVLQAAIOR 192
DB 314 AGNVKSARKKIDKADGDVMDVLEVDIKE 341

RESULT 13
IP3T_HUMAN
ID IP3T_HUMAN STANDARD; PRT; 2671 AA.
AC Q14573; Q14649;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Inositol 1,4,5-trisphosphate receptor type 3 (Type 3 inositol 1,4,5-
DE trisphosphate receptor) (Type 3 insp3 receptor) (IP3 receptor isoform
DE 3) (insp3R3).
GN ITPR3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_taxid=9606;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=94363219; PubMed=8081734;
RA Yamamoto-Hino M., Sugiyama T., Hikiti K., Mattei M.-G., Hasegawa K.,
RA Sekine S., Sakurada K., Miyawaki A., Furuichi T., Hasegawa M.,
RA Mikoshiba K.;
RT "Cloning and characterization of human type 2 and type 3 inositol
RT 1,4,5-trisphosphate receptors."
RL Recept. Channels 2:9-22(1994).
RN [2]
SEQUENCE FROM N.A.
RX MEDLINE=94117432; PubMed=8288584;
RA Maranto A.R.;
RT "Primary structure, ligand binding, and localization of the human type
RT 3 inositol 1,4,5-trisphosphate receptor expressed in intestinal
RT epithelium."
RL J. Biol. Chem. 269:1222-1230(1994).
CC -1- FUNCTION: RECEPTOR FOR INOSITOL 1,4,5-TRISPHOSPHATE, A SECOND
CC MESSENGER THAT MEDIATES THE RELEASE OF INTRACELLULAR CALCIUM.
CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY). INTERACTS WITH TRPC1,
CC TRPC3 AND TRPC4.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
CC reticulum.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN INTESTINAL CRYPT AND VILLUS
CC EPITHELIAL CELLS.
CC -1- DOMAIN: THE RECEPTOR CONTAINS A CALCIUM CHANNEL IN ITS C-TERMINAL
CC EXTREMITY. ITS LARGE N-TERMINAL CYTOPLASMIC REGION HAS THE LIGAND-
CC BINDING SITE IN THE N-TERMINUS AND MODULATORY SITES IN THE MIDDLE
CC PORTION IMMEDIATELY UPSTREAM OF THE CHANNEL REGION.
CC -1- PTM: PHOSPHORYLATED ON TYROSINE RESIDUES (BY SIMILARITY).

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CC CC -1- SIMILARITY: BELONGS TO THE INSP3 RECEPTOR FAMILY.
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CC CC ENBL; D26351; BAA05385.1; -
CC CC EMBL; U01062; AAC50064.1; -
CC CC PIR; A49873; A49873
CC CC Genew; HGNC:16182; ITPR3.
CC CC MIM; 147267; -
CC CC InterPro; IPR000699; Ca-rel_channel.
CC CC InterPro; IPR001682; Ca/Na_pore.
CC CC InterPro; IPR005821; Ion_pore.
CC CC InterPro; IPR003608; MIR_trans.
CC CC Pfam; PF00520; Ion_trans; 1.
CC CC Pfam; PF02815; MIR; 4.
CC CC Pfam; PF01365; RYDR_IPTR; 2.
CC CC SMART; SM00472; MIR; 4.
CC CC Receptor; Transmembrane; Phosphorylation; Endoplasmic reticulum;
CC CC Ionic channel; Ion transport; Calcium channel.
CC CC DOMAIN 1 2202
CC CC TRANSMEM 2203 2223
CC CC DOMAIN 2224 2235
CC CC TRANSMEM 2236 2256
CC CC DOMAIN 2257 2264
CC CC TRANSMEM 2265 2285
CC CC DOMAIN 2286 2325
CC CC TRANSMEM 2326 2346
CC CC DOMAIN 2347 2368
CC CC TRANSMEM 2369 2389
CC CC DOMAIN 2390 2495
CC CC TRANSMEM 2497 2517
CC CC DOMAIN 2518 2671
CC CC TRANSMEM 2583 2583
CC CC MOD_RES 524 524
CC CC CONFLICT 524 524
CC CC CONFLICT 562 562
CC CC CONFLICT 989 989
CC CC CONFLICT 1143 1143
CC CC CONFLICT 1391 1391
CC CC CONFLICT 1496 1497
CC CC CONFLICT 1674 1674
CC CC CONFLICT 2436 2436
CC CC CONFLICT 2671 2671
CC CC SEQUENCE 2671 AA; 304036 MW; 69F618CF27B681D7 CRC64;

Query Match 8.9%; Score 99; DB 1; Length 2671;
Best Local Similarity 20.3%; Pred. No. 31;
Matches 47; Conservative 52; Mismatches 73; Indels 60; Gaps 11;

QY 1 MSAEVTQVVEEA-LDTDEKMLFLICRDVAIDY--VPPNVRDLDDL--RERGL-- 50
Db 451 MLASAVEKUNEGFISQNDRRFVQLLEDVFFVSDVPNNQGVLDIVTPNREKRLMR 510
QY 51 -----SVGLAELLYRVRFDLLKRLKMDRKAVET 81
Db 511 EQNILKQVFGILKAPPRKGGEGPLVRLLELSQKNAPYQ-HMFLCYRVL---RHSDQ 566
QY 82 HLLRNPHLVSDYRVLMAGTEGDLKSD-VSSLF-----LMKYWGKGI-----SK 127
Db 567 YRKNQEHIAQFGQMOSQIGYDILAEEDTITALLHNNRKLKLEKHITKTEVTFVSLVRKNR 626
QY 128 EKSFLLVVELEKLNVA-PDQLDLLEKCLKNLHRID--LKTXYQKQSVQ 176
Db 627 EPRFLDLSLCVSNHIAIPVPTQELICKCVLPDKNPSDILIRTELPRPKMAQ 678

RESULT 14
YCID_ECOLI STANDARD; PRT; 389 AA.
ID YCID_ECOLI

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AC P45576; P76836;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein yCIM precursor.
GN YCIM OR B1280 OR C1749 OR Z2526 OR ECS1853.
OS Escherichia coli,
OS Escherichia coli O6, and
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562, 217992, 83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12."
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97251357; PubMed=9097039;
RA Aliba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,
RA Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T., Saito N.,
RA Sempel G., Seki Y., Sivasubram S., Tagami H., Takeda J.,
RA Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;
RT "A 570-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 28.0-40.1 min region on the linkage map."
RL DNA Res. 3:363-377(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=O6:H1 / CFT073 / ATCC 700928;
RX MEDLINE=22388234; PubMed=12471157;
RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
RA Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
RT "Extensive mosaic structure revealed by the complete genome sequence
of uropathogenic Escherichia coli."
RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai D., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7."
RL Nature 409:529-533(2001).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / RMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
O157:H7 and genomic comparison with a laboratory strain K-12."
RL DNA Res. 8:11-22(2001).
RN [6]
RP SEQUENCE OF 308-389 FROM N.A.
RX MEDLINE=89028656; PubMed=3052852;
RA Hidaka M., Akiyama M., Horiuchi T.;

```

RT "A consensus sequence of three DNA replication terminus sites on the
RT E. coli chromosome is highly homologous to the terR sites of the R6K
RT plasmid.";
RL Cell 55:467-475(1988).
RN [7]
RP IDENTIFICATION.
RX MEDLINE=96032851; PubMed=7567469;
RA Borodovsky M., McIninch J., Koonin E.V., Rudd K.E., Medigue C.,
RA Danchin A.;
RT "Detection of new genes in a bacterial genome using Markov models for
RT three gene classes.";
RL Nucleic Acids Res. 23:3554-3562(1995).
CC -1- SIMILARITY: STRONG. TO H.INFLUENZAE H11223
CC
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CC
CC EMBL; AE000226; AAC74362.1; -
DR EMBL; D90766; BAA14834.1; -
DR EMBL; AE016760; AAN80215.1; -
DR EMBL; AE005379; AAG56533.1; -
DR EMBL; AP002556; BAB35276.1; -
DR EMBL; M23250; -; NOT_ANNOTATED_CDS.
DR PIR; A85759; A85759.
DR PIR; C64876; C64876.
DR PIR; E90860; E90860.
DR EcoGene; EG12691; ycim.
DR InterPro; IPR001440; TPR.
DR Pfam; PF00515; TPR; 2.
KW Hypothetical protein; Zinc-finger; Signal; Complete proteome.
FT SIGNAL 1 16 POTENTIAL.
FT CHAIN 17 389 HYPOTHETICAL PROTEIN YCIM.
FT ZN_FING 357 374 C4-TYPE (POTENTIAL).
FT SEQUENCE 389 AA; 44531 MW; F4D1B9E2A526BCC3 CRC64;
Query Match 8.8%; Score 98.5; DB 1; Length 389;
Best Local Similarity 22.6%; Pred. No. 3.9;
Matches 47; Conservative 44; Mismatches 78; Indels 39; Gaps 11;
Qy 6 IQH--VEALDTDEKMLF--LCRDVAIDVPPNVRDLDLRERKLSVGLAEIL-- 59
Db 91 IQHLMESASITYQRLAIQQLGRDYMAGLYDRAEDMFNQLYDFTDFRIGALQQLLI 150
Qy 60 YRV-----RRFDLLKRLKM--DRKAVE--THL---LRNPHLVS---DYRVLMAEIGEDLD 105
Db 151 YQATSEWQKADVAERLVKLGKQKQVEIAHFYCELAHQHMASDLDLRAMTLKKGAAD 210
Qy 106 KSDVSSLLFMKDYMGKGIKSEKSEFLDLVVELEKLNIVAPDQDLLEKCLKNTHRIDLK 165
Db 211 KNSARVSTIMMGVFMKGEYAKAVESLQVRISODR-ELVS-ETLEMLQTCYQOL----- 262
Qy 166 TKIQKYSQVAGTSYRNVLQAAIKS 193
Db 263 -----GKTAWEAEFLQRAVEN 279
RESULT 15
IP3T_RAT
ID IP3T_RAT STANDARD; PRT; 2670 AA.
AC Q63269;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Inositol 1,4,5-trisphosphate receptor type 3 (Type 3 inositol 1,4,5-
DE trisphosphate receptor) (Type 3 Insp3 receptor) (IP3 receptor isoform
DE 3) (Insp3R3) (IP3R-3).
GN ITPR3.
OS Rattus norvegicus (Rat).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93266594; PubMed=8388391;
RA Blondel O., Takeda J., Janssen H., Seino S., Bell G.I.;
RT "Sequence and functional characterization of a third inositol
RT triphosphate receptor subtype, IP3R-3, expressed in pancreatic
RT islets, kidney, gastrointestinal tract, and other tissues.";
RL J. Biol. Chem. 268:11356-11363(1993).
CC -1- FUNCTION: RECEPTOR FOR INOSITOL 1,4,5-TRISPHOSPHATE, A SECOND
CC MESSENGER THAT MEDIATES THE RELEASE OF INTRACELLULAR CALCIUM.
CC
CC -1- SUBUNIT: HOMOTETRAMER (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
CC reticulum (By similarity).
CC -1- DOMAIN: THE RECEPTOR CONTAINS A CALCIUM CHANNEL IN ITS C-TERMINAL
CC EXTREMITY. ITS LARGE N-TERMINAL CYTOPLASMIC REGION HAS THE LIGAND-
CC BINDING SITE IN THE N-TERMINUS AND MODULATORY SITES IN THE MIDDLE
CC PORTION IMMEDIATELY UPSTREAM OF THE CHANNEL REGION.
CC -1- PTM: PHOSPHORYLATED ON TYROSINE RESIDUES (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE INSP3 RECEPTOR FAMILY.
CC
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CC
CC EMBL; L06096; AAA41446.1; -
DR PIR; A46719; A46719.
DR InterPro; IPR000699; Ca-rel_channel.
DR InterPro; IPR001682; Ca/Na_pore.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR003608; MIR.
DR Pfam; PF00520; Ion_trans; 1.
DR Pfam; PF02815; MIR; 4.
DR Pfam; PF01365; YDR_ITPR; 2.
DR SMART; SM00472; MIR; 4.
KW Receptor; Transmembrane; Phosphorylation; Endoplasmic reticulum;
KW Ionic channel; Ion transport; Calcium channel.
FT DOMAIN 1 2201 CYTOPLASMIC (POTENTIAL).
FT TRANSEM 202 2222 POTENTIAL.
FT DOMAIN 2223 2233 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 2234 2254 POTENTIAL.
FT DOMAIN 2255 2264 CYTOPLASMIC (POTENTIAL).
FT TRANSEM 2264 2284 POTENTIAL.
FT DOMAIN 2285 2324 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 2325 2345 POTENTIAL.
FT DOMAIN 2346 2367 CYTOPLASMIC (POTENTIAL).
FT TRANSEM 2368 2388 POTENTIAL.
FT DOMAIN 2389 2495 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 2496 2516 POTENTIAL.
FT DOMAIN 2517 2670 CYTOPLASMIC (POTENTIAL).
FT MOD_RES 2582 2582 PHOSPHORYLATION (POTENTIAL).
SQ SEQUENCE 2670 AA; 304284 MW; 13C787E4C2886E45 CRC64;
Query Match 8.8%; Score 98; DB 1; Length 2670;
Best Local Similarity 20.3%; Pred. No. 37;
Matches 47; Conservative 52; Mismatches 73; Indels 60; Gaps 11;
Qy 1 MSAEVIHQVEEA-LDTDEKEMLLFLCRDVAIDV--VPPNVRDLDL--REKGL-- 50
Db 451 MLASAVEKLNKGFISQNDREVIQLLEDLVFVSDFVPPNNGQNVLDIMVTKENRERQKLMR 510
Qy 51 -----SVGDLAELLYRVRFDLLKRLKMDRKAVET 81
Db 511 DENTLKQIFGLKAPFRDKGEGEGLVRLLEUSDQKNAPQY-MFLCYRVL---RHSQED 566
Qy 82 HLLRNHLVSDYRVLMAEIGEDLDKSD--VSSLIF----LMKDYMGKGI-----SK 127
OS Rattus norvegicus (Rat).

Db 567 YRKNQEHIAKQFCGMSQIGYDILAEDTITALLHNRKLEKHITTEVETFSVLRKNR 626

Qy 128 EKSFLDLVVELEKLNVA-PQQLDLLEKCLKNIHRID--LKTKIQKYKQSVQ 176

Db 627 EPRFLDYLSDLCVSNRIAPVTOELICKCVLDPKNSDILILQTELPRPKEMAQ 678

Search completed: August 13, 2003, 16:40:21
Job time : 11.4579 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 13, 2003, 16:34:29 ; Search time 38.7775 Seconds
(without alignments)
1470.690 Million cell updates/sec

Title: US-09-380-546A-4

Perfect score: 1114

Sequence: 1 MSAEVHQVEEALDTDEKEM.....RMITPAHCPDLKILGNCSM 221

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_23.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp Vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1007	90.4	462	4	Q96TE4
2	718	64.5	218	11	Q99MZ5
3	342	30.7	418	13	Q8UVG5
4	245	22.0	182	12	Q99CX0
5	234	21.0	188	12	P88961
6	224	20.1	476	13	Q918J3
7	208	18.7	482	13	Q90WU1
8	201	18.0	482	11	Q9JHX4
9	177	15.9	500	13	Q9IB64
10	161	14.5	520	13	Q9IB62
11	160	14.4	522	4	Q8IUP5
12	159	14.3	369	12	O11300
13	157	14.1	371	12	Q98326
14	157	14.1	479	4	Q8WYQ8
15	143.5	12.9	174	12	Q9WRM4
16	143.5	12.9	174	12	Q9J2H2

17	105	9.4	78	6	Q8MJ18
18	103.5	9.3	422	1	O93666
19	102.5	9.2	167	12	O56959
20	101.5	9.1	772	2	P94866
21	99.5	8.9	801	16	O8EMP6
22	99.5	8.9	979	5	O8I469
23	99.5	8.9	1157	11	Q8BWE0
24	99	8.9	1203	16	Q8ETY7
25	99	8.9	1256	5	O8SVZ5
26	99	8.9	2664	6	Q8WN95
27	98.5	8.8	313	12	O85014
28	98.5	8.8	399	17	Q973B7
29	98	8.8	1297	10	Q945S6
30	97	8.7	572	16	O8PQA6
31	96.5	8.7	607	10	O8C9N6
32	96	8.6	313	12	O85015
33	96	8.6	345	2	O54085
34	96	8.6	700	10	O8RZ04
35	95.5	8.6	310	16	O66556
36	95.5	8.6	345	16	O8E620
37	95.5	8.6	345	16	O8E0E6
38	95.5	8.6	445	17	O9YDV0
39	95	8.5	541	2	P95688
40	95	8.5	833	16	O9X2F5
41	95	8.5	1207	16	O99W64
42	94.5	8.5	313	12	O82053
43	94.5	8.5	698	2	O8GE65
44	93.5	8.4	313	12	O82048
45	93.5	8.4	394	5	O8MSB1

ALIGNMENTS

RESULT 1

ID	Q96TE4	PRELIMINARY;	PRT;	462 AA.
AC	Q96TE4;			
DT	01-DEC-2001 (TREMBLrel. 19, Created)			
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)			
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)			
DE	Usurpin beta.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-21100893; PubMed-11161814;			
RA	Hadano S., Yanagisawa Y., Skaug J., Fichter K., Nasir J.,			
RA	Martindale D., Koop B.F., Scherer S.W., Nicholson D.W., Rouleau G.A.,			
RA	Ikeda J.-E., Hayden M.R.;			
RT	"Cloning and characterization of three novel genes; ALS2CR1, ALS2CR2,			
RT	and ALS2CR3, in the juvenile amyotrophic lateral sclerosis (ALS2)			
RL	Genomics 71:200-213(2001).			
DR	EMBL; AB038972; BAB32552.1; JOINED.			
DR	ENBL; AB038967; BAB32552.1; JOINED.			
DR	ENBL; AB038968; BAB32552.1; JOINED.			
DR	ENBL; AB038969; BAB32552.1; JOINED.			
DR	ENBL; AB038970; BAB32552.1; JOINED.			
DR	ENBL; AB038971; BAB32552.1; JOINED.			
DR	InterPro; IPR001875; DED.			
DR	InterPro; IPR002398; ICE.			
DR	InterPro; IPR001309; ICE_P20.			
DR	Pfam; PF01335; DED; 2.			
DR	Pfam; PF00656; ICE_P20; 1.			
DR	SMART; SM00115; CASC; 1.			
DR	SMART; SM00031; DED; 2.			
DR	PROSITE; PS50208; CASPASE_P20; 1.			
DR	PROSITE; PS50168; DED; 2.			
SQ	SEQUENCE 462 AA; 52550 MW; D4E0109CBA47EAA3 CRC64;			

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Query Match 90.4%; Score 1007; DB 4; Length 462;
Best Local Similarity 99.5%; Pred. No. 1.7e-67;
Matches 202; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSAEVIHOVERALDTDEKEMLEFLCRDVAIDVPPNVRDLADILRLRERKLSVGDIAELLY 60
DB 1 MSAEVIHOVERALDTDEKEMLEFLCRDVAIDVPPNVRDLADILRLRERKLSVGDIAELLY 60
QY 61 RVRRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIFFLMKDYM 120
DB 61 RVRRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIFFLMKDYM 120
QY 121 GRGKISKEKSFLLDWVELEKLNVLAPQDLDLLEKLNHRIIDLTKTIQKYQSVQAGT 180
DB 121 GRGKISKEKSFLLDWVELEKLNVLAPQDLDLLEKLNHRIIDLTKTIQKYQSVQAGT 180
QY 181 SYRNVLAQAIOKSLKDPNSNFRM 203
DB 181 SYRNVLAQAIOKSLKDPNSNFRM 203

RESULT 2
Q99MZ5 PRELIMINARY; PRT; 218 AA.
AC Q99MZ5;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-OCT-2001 (Tremblrel. 18, Last annotation update)
DE FLIP short form.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RA Xiao C.W., Asselin E., Tsang B.K.;
RT "FLIP mRNA expression in rat ovarian granulosa cells.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF244366; AAK28338.1; -.
DR InterPro; IPR001875; DED.
DR Pfam; PF01335; DED; 2.
DR SMART; SM00031; DED; 2.
DR PROSITE; PS0168; DED; 2.
SQ SEQUENCE 218 AA; 24718 MW; 9DA9EBAF3441967B CRC64;

Query Match 64.5%; Score 718; DB 11; Length 218;
Best Local Similarity 72.5%; Pred. No. 3.1e-46;
Matches 148; Conservative 24; Mismatches 30; Indels 2; Gaps 2;

QY 1 MSAEVIHOVERALDTDEKEMLEFLCRDVAIDVPPNVRDLADILRLRERKLSVGDIAELLY 60
DB 6 VSAEVIHOVERSLDEKEMLEFLCRDVTENLAPPNVRDLDCLSERGQLSFAALAEILY 65
QY 61 RVRRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIFFLMKDYM 120
DB 66 RVRRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMAEIGENLNQSDVSSLIFFLTQDYT 125
QY 121 GRGKISKEKSFLLDWVELEKLNVLAPQDLDLLEKLNHRIIDLTKTIQKYQSVQAGT 180
DB 126 GRGKAVKDKSFLDWVIELEKLNIGSDQLNLEKCLKSIHRIIDLTKTIQKYQSSQEA-R 184
QY 181 SYRNVLAQAIOK-SLKDPNSNFRM 203
DB 185 SNMNAQASLPKLSIKELHNSRV 208

RESULT 3
Q8UVG5 PRELIMINARY; PRT; 418 AA.
ID Q8UVG5
AC Q8UVG5;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
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DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE Clarpi.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98021435; PubMed=9380701;
RA Inohara N., Koseki T., Hu Y., Chen S., Nunez G.;
RT "CIARP, a death effector domain-containing protein interacts with
caspase-8 and regulates apoptosis.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:10717-10722(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20373792; PubMed=10917738;
RA Inohara N., Nunez G.;
RT "Genes with homology to mammalian apoptosis regulators identified in
zebrafish.";
RL Cell Death Differ. 7:509-510(2000).
RN [3]
RP SEQUENCE FROM N.A.
RA Inohara N., Nunez G.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF448261; AAL41007.1; -.
DR InterPro; IPR001875; DED.
DR InterPro; IPR002398; ICE.
DR InterPro; IPR001309; ICE_p20.
DR Pfam; PF01335; DED; 1.
DR SMART; SM00115; CASC; 1.
DR SMART; SM00031; DED; 2.
DR PROSITE; PS0208; CASPASE_P20; 1.
DR PROSITE; PS0168; DED; 2.
SQ SEQUENCE 418 AA; 47619 MW; C2ECB3AE571E0237 CRC64;

Query Match 30.7%; Score 342; DB 13; Length 418;
Best Local Similarity 41.9%; Pred. No. 9.1e-18;
Matches 75; Conservative 46; Mismatches 50; Indels 8; Gaps 4;

QY 5 VHQVEEALDTDEKEMLEFLCRDVAIDVPPNVR-DLLDLRLR-GLSVGD--LAE 57
DB 8 LVNKVTASLSSDESKILYLCITDLFNCSVEELGDLALFAQNPQAGQPHSGNALLME 67
QY 58 LLYRVRRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIFFLMK 117
DB 68 LMPQMKRYDILLRKVFGTNKQVE-GILRKERVISDYRVLMADVSENLDKQLSLIFLLS 126
QY 118 DYMGKGISKEKSFLLDWVELEKLNVLAPQDLDLLEKLNHRIIDLTKTIQKYQSVQ 176
DB 127 SILPKERSTRATSFLLDWVELEKLNVEVSECKLDFLEKLNRRNDLVKKIQAYNRQ 185

RESULT 4
Q99CX0 PRELIMINARY; PRT; 182 AA.
ID Q99CX0
AC Q99CX0;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-OCT-2001 (Tremblrel. 18, Last annotation update)
DE V-FLIP.
OS Bovine herpesvirus 4.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae.
OX NCBI_TaxID=10385;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20583805; PubMed=11152491;
RA Zimmermann W., Brohl H., Ehlers B., Buhk H.-J., Rosenthal A.,
RA Goitz M.;
RT "Genome Sequence of Bovine Herpesvirus 4, a Bovine Rhadinovirus, and
RT Identification of an Origin of DNA Replication.";
RL J. Virol. 75:1186-1194(2001).
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DR EMBL; AF318573; AAK07993.1; -.
DR InterPro; IPR001875; DED.
DR Pfam; PF01335; DED; 1.
DR SMART; SM00031; DED; 2.
DR PROSITE; PS00168; DED; 2.
SQ SEQUENCE 182 AA; 21792 MW; 73BF1ADD9B0FE6A6 CRC64;

Query Match      22.0%; Score 245; DB 12; Length 182;
Best Local Similarity 32.4%; Pred. No. 6.4e-11;
Matches 57; Conservative 44; Mismatches 67; Indels 8; Gaps 4;

QY 1 MSAEVIHOVEALDTDEKEMLLFCRDVAIDVVPNVRDL---LDILBERGKLSVGDIAE 57
DB 2 VTRDVLIAETHLNQNEKTFVMYFLD---PYIPKECEDFPLTLENLHSHKRIIYPIIE 58
QY 58 LLYRVRREDLKRILKMDRKAVETHLLRNP-HLVSDYRVLMIAEIGEDLDKSDVSSLIFLM 116
DB 59 LMYILQRLDLSRIFLLOHFRVKDQITSSHWNYISPYKQLIFSIGNIDDELDLSIKRIS 118
QY 117 KDYMGKGKISKEKSFLLDLYVELEKLNVLVAPDQLDLEKCLKNHRIIDLTKTKYK 172
DB 119 MNYICKSP-SKIKNYLDNVRALKVAMVGPNDLDFETLKFQIHRMDIVKMIKNYR 173

RESULT 5
ID P88961 PRELIMINARY; PRT; 188 AA.
AC P88961;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE FLICE Inhibitory protein.
GN ORF 71.
OS Kaposi's sarcoma-associated herpesvirus (KSHV) (Human herpesvirus 8).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Rhadinovirus.
OX NCBI_TaxID=37296;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97121480; PubMed=8962146;
RA Russo J.J., Bohenzky R.A., Chien M.C., Chen J., Yan M., Maddalena D.,
RA Parry J.P., Peruzzi D., Edelman I.S., Chang Y., Moore P.S.;
RA "Nucleotide sequence of the Kaposi sarcoma-associated herpesvirus
RT (HHV8).";
RL Proc. Natl. Acad. Sci. U.S.A. 93:14862-14867(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97094384; PubMed=8939871;
RA Moore P.S., Bashoff C., Weiss R.A., Chang Y.;
RA "Molecular mimicry of human cytokine and cytokine response pathway
RT genes by KSHV.";
RL Science 274:1739-1744(1996).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=97094384; PubMed=8939871;
RA Russo J.J., Bohenzky R.A., Chien M.C., Chen J., Yan M., Maddalena D.,
RA Parry J.P., Peruzzi D., Edelman I.S., Chang Y., Moore P.S.;
RA Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=97094384; PubMed=8939871;
RA Neipel F., Albrecht J., Fleckenstein B.;
RA Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=97242415; PubMed=9087414;
RA Thome M., Schneider P., Hofmann K., Fickenscher H., Meinel E.,
RA Neipel F., Matmann C., Burns K., Bodmer J.L., Schroter M.,
RA Scalfidi C., Krammer P.H., Peter M.E., Tschopp J.;
RT "Viral FLICE-inhibitory proteins (FLIPs) prevent apoptosis induced by
RT death receptors.";
RL Nature 386:517-521(1997).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE=97296220; PubMed=9151804;

RA Neipel F., Albrecht J.C., Fleckenstein B.;
RT "Cell-homologous genes in the Kaposi's sarcoma-associated rhadinovirus
RT human herpesvirus 8: determinants of its pathogenicity?";
RL J. Virol. 71:4187-4192(1997).
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=GK18;
RX MEDLINE=99329221; PubMed=10400794;
RA Glenn M., Rainbow L., Aurade F., Davison A., Schulz T.F.;
RT "Identification of a Spliced Gene from Kaposi's Sarcoma-Associated
RT Herpesvirus Encoding a Protein with Similarities to Latent Membrane
RT Proteins 1 and 2A of Epstein-Barr Virus.";
RL J. Virol. 73:6953-6963(1999).
DR EMBL; U75698; AAC57156.1; -.
DR EMBL; U90534; AAB51072.1; -.
DR EMBL; U93872; AAB62643.1; -.
DR EMBL; AF148805; AAD46498.1; -.
DR InterPro; IPR001875; DED.
DR Pfam; PF01335; DED; 2.
DR SMART; SM00031; DED; 2.
DR PROSITE; PS00168; DED; 2.
SQ SEQUENCE 188 AA; 21474 MW; 37CFE147EAE45371 CRC64;

Query Match      21.0%; Score 234; DB 12; Length 188;
Best Local Similarity 34.3%; Pred. No. 4.4e-10;
Matches 58; Conservative 39; Mismatches 64; Indels 8; Gaps 3;

QY 4 EVIHOVEALDTDEKEMLLFCRDVAIDVVPNVRDLDIR---ERGKLSVGDIAELLY 60
DB 5 EVLCEVARKLGTDREVLFL---LNVFIPQTLAQIALRALKEGRLTFLAECFLF 61
QY 61 RYRFRDLKRILKMDRKAVETHLLRNP-HLVSDYRVLMIAEIGEDLDKSDVSSLIFLMKDYM 120
DB 62 RAGRDLRLDLHLPFLERHLAGTMSYFSPQLTVLHVDGELCARDIRSLIFLSKDTI 121
QY 121 GRGKISKEKSFLLDLYVELEKLNVLVAPDQLDLEKCLKNHRIIDLTKTKIQ 169
DB 122 --GSRSTPQTFLHWYCMENLDLGLPTDVLDMLSRLSRVLDLQRVQ 168

RESULT 6
QY18J3 PRELIMINARY; PRT; 476 AA.
ID QY18J3
AC QY18J3;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Caspase-8.
DE CASP8.
GN Brachydanio rerio (Zebrafish) (Danio rerio).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20373792; PubMed=10917738;
RA Inohara N., Nunez G.;
RT "Genes with homology to mammalian apoptosis regulators identified in
RT zebrafish.";
RL Cell Death Differ. 7:509-510(2000).
DR EMBL; AF273220; AAF79207.1; -.
DR HSSP; Q15806; 1QDU.
DR MEROPS; C14.009; -.
DR 2FIN; ZDB-GENE-000713-1; casp8.
DR InterPro; IPR001875; DED.
DR InterPro; IPR002398; ICE.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR Pfam; PF01335; DED; 2.
DR Pfam; PF00655; ICE_p10; 1.
DR Pfam; PF00656; ICE_p20; 1.
DR PRINTS; PR00376; IL1BCEN2YME.
```

DR SMART; SM00115; CASC; 1.
 DR PROSITE; PS01122; CASPASE_CYS; 1.
 DR PROSITE; PS50207; CASPASE_P10; 1.
 DR PROSITE; PS50208; CASPASE_P20; 1.
 DR PROSITE; PS50168; DED; 2.
 SQ SEQUENCE 476 AA; 54890 MW; FD9DF4B3C3C1FB9 CRC64;

Query Match 20.1%; Score 224; DB 13; Length 476;
 Best Local Similarity 28.7%; Pred. No. 7.2e-09;
 Matches 71; Conservative 47; Mismatches 85; Indels 44; Gaps 10;

QY 1 MSAEVIHQVEALDTDEKEMLLFLCRDVAIDVDP-----PNVRDLDDLRLRERKLSVG 53
 DB 1 MDPIGFHEIDENLSGVDQKFLC-----LDFIPRLLESVTDKADLILRLDEOGLLEDE 56
 QY 54 DL-AELLYRVRRFDLLKRLKMDRKAVETHLLRNPHL---VSDYRVLMMAETGEIDLDKSDV 109
 DB 57 LLEPELLIAIGRIDLE-ILKKSKEEVERNLLRCDNSRKGVSAVRKMLLKISEDMTEENF 115
 QY 110 SSLFLMKDYMGRGKISKESKESFLDLVVELEKLNVLAPDQLD-----LLEKCLKNHIHRLDLK 165
 DB 116 RAARFLDL--LPRAKGLRSTSFELDALIEMERQRLGPDNLDELRYILEKCDKQLAVMIER 173
 QY 166 TKIKYKQSGVGACTSY-----RNVLQAAIQKSLKDP--SNFRMIT 205
 DB 174 FRNSHRDQEGGRLPLEEVFLNPVSDTMRERRRRSSAGAITTDAETPLNPNEYILT 233
 QY 206 --PYAHC 210
 DB 234 QRPLGYC 240

RESULT 7
 Q90WU1 ID Q90WU1 PRELIMINARY; PRT; 482 AA.
 AC Q90WU1;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Caspase 8.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Barton S., Bridgham J.T., Johnson A.L.;
 RT "Caspase-8 and -9 expression in the hen ovary";
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY057939; AAL23700.1; -;
 DR MEROPS; C14.009; -;
 DR InterPro; IPR001875; DED.
 DR InterPro; IPR002398; ICE.
 DR InterPro; IPR002138; ICE_P10.
 DR InterPro; IPR001309; ICE_P20.
 DR Pfam; PF01335; DED; 2.
 DR Pfam; PF00655; ICE_P10; 1.
 DR Pfam; PF00656; ICE_P20; 1.
 DR PRINTS; PR00376; ILIBCENZYME.
 DR SMART; SM00115; CASC; 1.
 DR SMART; SM00031; DED; 2.
 DR PROSITE; PS01122; CASPASE_CYS; 1.
 DR PROSITE; PS01121; CASPASE_HIS; 1.
 DR PROSITE; PS50207; CASPASE_P10; 1.
 DR PROSITE; PS50208; CASPASE_P20; 1.
 DR PROSITE; PS50168; DED; 2.
 SQ SEQUENCE 482 AA; 54645 MW; 8E3936B6EE090BEF CRC64;

Query Match 18.7%; Score 208; DB 13; Length 482;
 Best Local Similarity 29.2%; Pred. No. 1.1e-07;
 Matches 66; Conservative 46; Mismatches 96; Indels 18; Gaps 8;

QY 3 AEVTHQVEEALDTDEKEMLLFLCRDVAI---DVVPPNVRDLDDLRLRERKLSVG--- 54
 DB 4 SOLLFVISEALDRTELASLKLSLEHVTVRKREDIEP--KAFTQALQEKGMIEVDLFF 61
 QY 55 LAELLYRVRRFDLLKRLKMDRKAVETHL-LRNPHLYSDYRVLMMAETGEIDLDKSDVSLI 113
 DB 62 LKELLYRINRIDLLASYLGSSREMERELQVPGRRVSPFRYLLFQLSENITKDDMKCFK 121
 QY 114 FLMDYMGGRGKISKESKESFLDLVVELEKLNVLAPDQLDLEKCLKNHIHRLDLTKTKYKQ 173
 DB 122 FLGKELPKCKLSPETMPDVFIEWKKGILKEDNLVTKTCGKVDKSLK-KIEDYEL 180
 QY 174 SVQGAGSYRVNLOAAIQKSLKDPNSNFRMITPYAHCPLDKILGNC 219
 DB 181 NLLGEG----EMLVTEGQSSGTGAPSAIWLAASSVAPD--SLGNC 220

RESULT 8
 Q9JHX4 ID Q9JHX4 PRELIMINARY; PRT; 482 AA.
 AC Q9JHX4;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Caspase-8.
 GN CASP8.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RA Itoh T., Itoh A., Pleasure D.;
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Cerebellum;
 RA Cao G., Graham S.H., Chen D., Chen J.;
 RT "Molecular cloning and characterization of rat caspase-8: Its
 RL implication in delayed neuronal cell death after ischemia";
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF279308; AAR87778.1; -;
 DR EMBL; AF288372; AAR83055.1; -;
 DR HSP; Q15806; IQDU.
 DR MEROPS; C14.009; -;
 DR InterPro; IPR001875; DED.
 DR InterPro; IPR002398; ICE.
 DR InterPro; IPR002138; ICE_P10.
 DR InterPro; IPR001309; ICE_P20.
 DR Pfam; PF01335; DED; 2.
 DR Pfam; PF00655; ICE_P10; 1.
 DR Pfam; PF00656; ICE_P20; 1.
 DR PRINTS; PR00376; ILIBCENZYME.
 DR SMART; SM00115; CASC; 1.
 DR SMART; SM00031; DED; 2.
 DR PROSITE; PS01122; CASPASE_CYS; 1.
 DR PROSITE; PS01121; CASPASE_HIS; 1.
 DR PROSITE; PS50207; CASPASE_P10; 1.
 DR PROSITE; PS50208; CASPASE_P20; 1.
 DR PROSITE; PS50168; DED; 2.
 SQ SEQUENCE 482 AA; 55339 MW; 82B4A29330C53264 CRC64;

Query Match 18.0%; Score 201; DB 11; Length 482;
 Best Local Similarity 31.2%; Pred. No. 3.8e-07;
 Matches 55; Conservative 31; Mismatches 75; Indels 8; Gaps 4;

QY 6 IHQVEEALDTDEKEMLLFLCRDVAIDVVPNVRDLDI---LRERKLSVGDLA---ELL 59
 DB 7 LYDIAERLGNELAAALFKLCIDHIPPQKQESINDVLVLFQRLQEGMLEEDNLSFLKELL 66
 QY 60 YRVRFDLLKRLKMDRKAVETHL-LRNPHLYSDYRVLMMAETGEIDLDKSDVSLIFLMKD 118

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Db      67 PHSRDLSRLKSPPEENVRELQVLGKAQVSAIRVLMFLKSEDMKEDLKSKFKLLIT 126
QY      119 YMGGRKISKEKSFSLDVLVVELEKLNVLAPDQLDLLEKLNHRIIDLKTKIYKQS 174
Db      127 EIPKCKLQDNSSLLDIFVEMEKRTILAEENLVTKSICFRVNR-SLLGRIDDYERS 181

RESULT 9
Q91B64
ID      Q91B64      PRELIMINARY;      PRT;      500 AA.
AC      Q91B64;
DT      01-OCT-2000 (TReMBLrel. 15, Created)
DT      01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DE      Caspase-8.
GN      01-MAR-2003 (TReMBLrel. 23, Last annotation update)
OS      Xenopus laevis (African clawed frog).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Amphibia; Batrachia; Anura; Mesobatrachia; Piploidea; Pipidae;
OC      Xenopodinae; Xenopus.
OX      NCBI_TaxID=8355;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=20209426; PubMed=10744739;
RA      Nakajima K., Takahashi A., Tachita Y.;
RT      "Structure, expression and function of the Xenopus laevis caspase
RT      family.";
RL      J. Biol. Chem. 275:10484-10491(2000).
DR      EMBL; AB038173; BAA94751.1;
DR      HSSP; Q15806; IODU.
DR      InterPro; IPR001875; DED.
DR      InterPro; IPR002398; ICE.
DR      InterPro; IPR002138; ICE_p10.
DR      InterPro; IPR001309; ICE_p20.
DR      Pfam; PF01335; DED; 2.
DR      Pfam; PF00655; ICE_p10; 1.
DR      Pfam; PF00656; ICE_p20; 1.
DR      PRINTS; PR00376; ILIBCEZYME.
DR      SMART; SM00115; CASC; 1.
DR      SMART; SM00031; DED; 2.
DR      PROSITE; PS01122; CASPASE_CYS; 1.
DR      PROSITE; PS01121; CASPASE_HIS; 1.
DR      PROSITE; PS0207; CASPASE_P10; 1.
DR      PROSITE; PS0208; CASPASE_P20; 1.
DR      PROSITE; PS0168; DED; 2.
DR      PROSITE; PS0255; INTERLEUKIN_7_9; 1.
SQ      SEQUENCE 500 AA; 57623 MW; AE138D4145108AE2 CRC64;

Query Match      15.9%; Score 177; DB 13; Length 500;
Best Local Similarity 28.4%; Pred. No. 2.5e-05;
Matches 50; Conservative 44; Mismatches 72; Indels 10; Gaps 5;

QY      4 EVHVEALDTDEKEMFLFCLRDVAIDVVPVNRD---LLDLRERGLKSVGDLA---E 57
Db      19 KLFSELDLKTETLAFIFCEKRYTAQEKENIKDAKTLFLCLKKDLICYNDFSFLKE 78
QY      58 LLYRVRRFDLLKRLKMDRKAVETHLLRNPHLSYDYRLVMAEIGEDLDKSYSLIFLMK 117
Db      79 LLYRGRNLLRKLGRVVEEIKRIEVSQ-ISPYRILLYDSQGLSKVEEDLKLYLD 137
QY      118 DYMGGRKISKEKSFSLDVLVVELEKLNVLAPDQLDLLEKLNHRIIDLKTKIYKQS 173
Db      138 --LSTAK--TENASILEIFELEKVGKLPDQLQKLADLETIGCKKNLSRNIEDYER 190

RESULT 10
Q91B62
ID      Q91B62      PRELIMINARY;      PRT;      520 AA.
AC      Q91B62;
DT      01-OCT-2000 (TReMBLrel. 15, Created)

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DT      01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT      01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE      Caspase-10.
GN      XCASPASE-10.
OS      Xenopus laevis (African clawed frog).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Amphibia; Batrachia; Anura; Mesobatrachia; Piploidea; Pipidae;
OC      Xenopodinae; Xenopus.
OX      NCBI_TaxID=8355;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=20209426; PubMed=10744739;
RA      Nakajima K., Takahashi A., Tachita Y.;
RT      "Structure, expression and function of the Xenopus laevis caspase
RT      family.";
RL      J. Biol. Chem. 275:10484-10491(2000).
DR      EMBL; AB038173; BAA94751.1;
DR      HSSP; Q15806; IODU.
DR      InterPro; IPR001875; DED.
DR      InterPro; IPR002398; ICE.
DR      InterPro; IPR002138; ICE_p10.
DR      InterPro; IPR001309; ICE_p20.
DR      Pfam; PF01335; DED; 2.
DR      Pfam; PF00655; ICE_p10; 1.
DR      Pfam; PF00656; ICE_p20; 1.
DR      PRINTS; PR00376; ILIBCEZYME.
DR      SMART; SM00115; CASC; 1.
DR      SMART; SM00031; DED; 2.
DR      PROSITE; PS01122; CASPASE_CYS; 1.
DR      PROSITE; PS01121; CASPASE_HIS; 1.
DR      PROSITE; PS0207; CASPASE_P10; 1.
DR      PROSITE; PS0208; CASPASE_P20; 1.
DR      PROSITE; PS0168; DED; 2.
SQ      SEQUENCE 520 AA; 59626 MW; 33164A5A09CA6615 CRC64;

Query Match      14.5%; Score 161; DB 13; Length 520;
Best Local Similarity 27.5%; Pred. No. 0.00041;
Matches 52; Conservative 34; Mismatches 57; Indels 46; Gaps 7;

QY      8 QVEEALDTDEKEMFLFCLRDVAIDVVPVNRDLDLRLRERGLKSVGD----- 54
Db      9 RIDDGLGREIDIEALKFLCRDV-----LRKNKLLSVQSGHFLFOOLMTEDL 53
QY      55 -----LAELLYRVRRFDLLKRLKMDRKAVETHLLRNPH--LVSDYRVLMAEIGEDL 104
Db      54 INEDNYFLGELLYIINHSL--HDLGTNKVEQKAL---PHWKISPYRQMLYELSENV 109
QY      105 DKSDVSLFLMKDYNGRGKISKEKSFSLDVLVVELEKLNVLAPDQLDLLEKLNHRIIDL 164
Db      110 TGEDEKRILFILPLHK---KHENKTFDLVLCLEKENAITDENVKLEEVFRKVP-DL 165
QY      165 KTKIYKQ 173
Db      166 LKTIKYKE 174

RESULT 11
Q81UP5
ID      Q81UP5      PRELIMINARY;      PRT;      522 AA.
AC      Q81UP5;
DT      01-MAR-2003 (TReMBLrel. 23, Created)
DT      01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DE      Caspase 10, apoptosis-related cysteine protease.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Brain;
RA      Strausberg R.;
RL      Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.

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DR EMBL: BC042844; AAHA2844.1; -
KW Protease.
SQ SEQUENCE 522 AA; 58993 MW; 34847E07B3DFA688 CRC64;

Query Match
Best Local Similarity 14.4%; Score 160; DB 4; Length 522;
Matches 64; Conservative 33; Mismatches 78; Indels 40; Gaps 9;

QY 9 VEEALDTDEKEMLLFLCRDVAIDVVP-----PNVRDLIDLRRGKLSVGD---LAEL 58
D : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 59 LYVRRPDLRLKRLKMDKAVETHLLRNPHLYSDYRVLMAEIGEDLDKSDVSSLIPLMKD 118
D : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 83 LYIIRKQLLQH-LNCTKEEVE-RLLPTRQVRVLFRLNLYELSEGIDSENKDMIFLKD 140
QY 119 YMGGRKISKSEKSFLLDVLVELEKLNIVAPDQDLLE-----KCLNKHRIIDLTKIQ- 169
D : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 141 SLPK-----TEMSTLSFLAFLEKQKIDEDNTCTLEDLCKTVVPKLLRNIEKYKREKAIQI 196
QY 170 -----KYKQSVQG-----AGTSYRNVLQAAIQKS 193
D : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 197 VTPPVDKAEYSQGEELVQSOTDKVTFLEALPQES 231

RESULT 12
QI1300 PRELIMINARY; PRT; 369 AA.
AC OI1300;
AC OI1300;
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Hypothetical 38.4 kDa protein (Fragment).
GN H-K.1.
OS Molluscum contagiosum virus subtype 1 (MCV1).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Molluscipoxvirus.
OX NCBI_TaxID=10280;
RN [1]
RP SEQUENCE FROM N.A.
RA Lopez-Esteban J.L., Esteban M., Martin-Gallardo A.;
RA "A Random DNA Sequencing, Computer-Based Approach for the Generation
RT of a Gene Map of Molluscum Contagiosum Virus.";
RL Virus Genes 0:0-(1997).
DR EMBL: U86889; AAB57924.1; -
DR InterPro; IPR001875; DED.
DR SMART; SM00031; DED; 2.
DR PROSITE; PS0168; DED; 2.
KW Hypothetical protein.
FT NON_TER 369
SQ SEQUENCE 369 AA; 38403 MW; FFCDD119A576FF001 CRC64;

Query Match
Best Local Similarity 14.3%; Score 159; DB 12; Length 369;
Matches 52; Conservative 26; Mismatches 80; Indels 16; Gaps 5;

QY 13 LDTDEKEMLLFLCRDVAIDVVPNNVRDLIDLRRGKLSVGDLAELLYRVRFFDLKRL 72
D : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 18 LDASEHEVLELCRDVA--PASKTAEDALRALQRRLTLTSSMAELLCALRRFDVLKVF 75
QY 73 KMDKAVETHLLRNPHLYSDYRVLMAEIGEDLDKSDVSSLIPLMKDYGSKI-----SKE 128
D : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 76 GMTRECAGR--LLGHGFLSQYRLQVAAINNMGVSEDLRVMC-----LCAGKLLPPSCTP 127
QY 129 KSFDLVVLEKLNIVAPDQDLLEKCLKNTHRIDLTKIQ--KYKQSVQAGT 180
D : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 128 RCLVDLNSALEDVGAISPDQVSVLVTLLHVAVCYDLSVALSAVAHGHTVGVGT 181

RESULT 13
Q98326 PRELIMINARY; PRT; 371 AA.
ID Q98326
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AC Q98326;
DT 01-FEB-1997 (TREMBlrel. 02, Created)
DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE MC160L.
GN MC160L.
OS Molluscum contagiosum virus subtype 1 (MCV1).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Molluscipoxvirus.
OX NCBI_TaxID=10280;
RN [1]
RP SEQUENCE FROM N.A.
RA Senkevich T.G., Bugert J.J., Sisler J.R., Koonin E.V., Darai G.,
RA Moss B.;
RA "Genome sequence of a human tumorigenic poxvirus: Prediction of
RT specific host response-evasion genes.";
RL Science 273:813-816(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Senkevich T.G., Bugert J.J., Sisler J.R., Koonin E.V., Darai G.,
RA Moss B.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U60315; AAC55288.1; -
DR InterPro; IPR001875; DED.
DR SMART; SM00031; DED; 2.
DR PROSITE; PS0168; DED; 2.
SQ SEQUENCE 371 AA; 38625 MW; 48123BADD29667AB CRC64;

Query Match
Best Local Similarity 14.1%; Score 157; DB 12; Length 371;
Matches 52; Conservative 25; Mismatches 81; Indels 16; Gaps 5;

QY 13 LDTDEKEMLLFLCRDVAIDVVPNNVRDLIDLRRGKLSVGDLAELLYRVRFFDLKRL 72
D : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 18 LDASEHEVLELCRDVA--PASKTAEDALRALQRRLTLTSSMAELLCALRRFDVLKVF 75
QY 73 KMDKAVETHLLRNPHLYSDYRVLMAEIGEDLDKSDVSSLIPLMKDYGSKI-----SKE 128
D : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 76 GMTRECAGR--LLGHGFLSQYRLQVAAINNMGVSEDLRVMC-----LCAGKLLPPSCTP 127
QY 129 KSFDLVVLEKLNIVAPDQDLLEKCLKNTHRIDLTKIQ--KYKQSVQAGT 180
D : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 128 RCLVDLNSALEDVGAISPDQVSVLVTLLHVAVCYDLSVALSAVAHGHTVGVGT 181

RESULT 14
Q8WYQ8 PRELIMINARY; PRT; 479 AA.
ID Q8WYQ8
AC Q8WYQ8;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Caspase-10a.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-21100893; PubMed-11161814;
RA Hadano S., Yanagisawa Y., Skaug J., Fichter K., Nasir J.,
RA Martindale D., Koop B.F., Scherer S.W., Nicholson D.W., Rouleau G.A.,
RA Ikeda J.-E., Hayden M.R.;
RA "Cloning and characterization of three novel genes, ALS2CR1, ALS2CR2,
RT and ALS2CR3, in the juvenile amyotrophic lateral sclerosis (ALS2)
RL critical region at chromosome 2q33-q34: candidate genes for ALS2.";
RL Genomics 71:200-213(2001).
DR EMBL: AB038978; BAB32553.1; -
DR EMBL: AB038973; BAB32553.1; JOINED.
DR EMBL: AB038974; BAB32553.1; JOINED.
DR EMBL: AB038975; BAB32553.1; JOINED.
DR EMBL: AB038977; BAB32553.1; JOINED.
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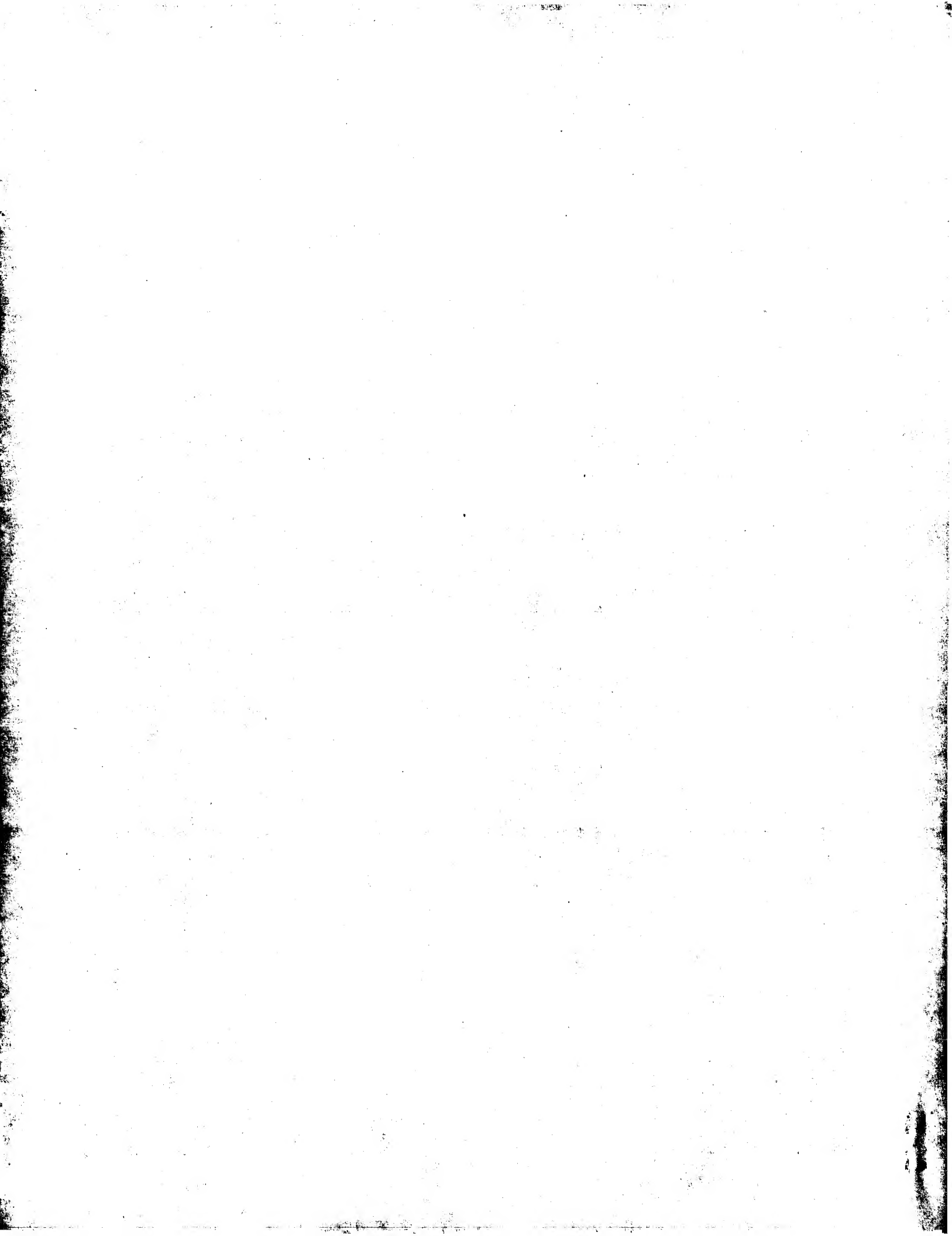
DR	InterPro; IPRO01875; DED.
DR	InterPro; IPRO02398; ICE.
DR	InterPro; IPRO02138; ICE.p10.
DR	InterPro; IPRO01309; ICE.p20.
DR	Pfam; PF01335; DED; 2.
DR	Pfam; PF00655; ICE.p10; 1.
DR	Pfam; PF00656; ICE.p20; 1.
DR	PRINTS; PRO0376; ILICENZYME.
DR	SMART; SMO0115; CASC; 1.
DR	SMART; SMO0031; DED; 2.
DR	PROSITE; PS01122; CASPASE_CYS; 1.
DR	PROSITE; PS01121; CASPASE_HIS; 1.
DR	PROSITE; PS50207; CASPASE_P10; 1.
DR	PROSITE; PS50208; CASPASE_P20; 1.
DR	PROSITE; PS50168; DED; 2.
SQ	SEQUENCE 479 AA; 54565 MW; 1317FD7A4EE03FF CRC64;

Query Match		14.1%; Score 157; DB 4; Length 479;
Best Local Similarity		29.3%; Pred. No. 0.00075;
Matches	60; Conservative	31; Mismatches 86; Indels 28; Gaps 7;

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Db	27	IDSNLGQDVENLKFLC----IGLVNKKLEKSSASADVFEHLAEDLLSEDPFFLAEL 82
Qy	59	LYRVRFDLKRILKMDRKAVEHLLRPHLYSDYRYVMABIGEDLOKSVDSSLIPLMKD 118
Db	83	LYTIQRKQLQH-LNCYKEEVE-RLLPTRQVSLFRNLLEYSGIDSENKDKMIFLTKD 140
Qy	119	YMGRGKISKESFIDLVAVELEKMLNVAPDOLDLLE-----KCLNIHRIDLKTOK 170
Db	141	SLPK-----TEWTSLSFLAFLEKGKQKIDEDNLCTLEDLCKTVVPLLRIEKYKREKAIQI 196
Qy	171	YKOSVGAGTGYRNVLQAATOKSLK 195
Db	197	VTPPVDKAESYQGEELVSQTGVK 221

RESULT 15	
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ID	Q9WRM4
AC	Q9WRM4;
DT	01-NOV-1999 (TrEMBLrel. 12, Created)
DT	01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE	FLIP.
OS	Macaca mulatta rhadinovirus 17577.
OC	Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OX	Gammaherpesvirinae; Rhadinovirus.
NCBI_TaxID	-83534;
RN	[1]
RX	SEQUENCE FROM N.A.
TX	MEDLINE=99174001; Pubmed=10074154;
RA	Searles R.P., Bergquam E.P., Axthelm M.K., Wong S.W.;
RT	"Sequence and genomic analysis of a rhesus macaque rhadinovirus with similarity to Kaposi's sarcoma-associated Herpesvirus/Human herpesvirus 8."
RT	herpesvirus 8."
RU	J. Virol. 73:3040-3053(1999).
RN	[2]
RX	SEQUENCE FROM N.A.
RA	Searles R.P., Bergquam E.P., Axthelm M.K., Wong S.W.;
RT	Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
TX	EMBL: AF083501; AAD21404.1; -
DR	InterPro; IPRO01875; DED.
DR	Pfam; PF01335; DED; 1.
DR	SMART; SMO0031; DED; 1.
DR	PROSITE; PS50168; DED; 1.
SQ	SEQUENCE 174 AA; 19578 MW; 5B9B54A0EAC94CB8 CRC64;

Query Match		12.9%; Score 143.5; DB 12; Length 174;
Best Local Similarity		27.6%; Pred. No. 0.0024;
Matches	42; Conservative	31; Mismatches 78; Indels 1; Gaps 1;



GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 13, 2003, 16:43:55 ; Search time 23.0143 Seconds
(without alignments)
1257.990 Million cell updates/sec

Title: US-09-380-546A-4
Perfect score: 1114
Sequence: 1 MSAEVTHQVEALDTDEKEM.....RMITPYAHCPDLKILGNCSM 221

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 492763 seqs, 131003257 residues

Total number of hits satisfying chosen parameters: 492763

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Published Applications_AA.*
- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pap.*
 - 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pap.*
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 - 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pap.*
 - 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pap.*
 - 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pap.*
 - 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pap.*
 - 14: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pap.*
 - 15: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pap.*
 - 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pap.*
 - 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pap.*
 - 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1114	100.0	221	9	US-09-410-194-15
2	1114	100.0	221	9	US-09-410-194-22
3	1007	90.4	480	9	US-09-861-270-2
4	1007	90.4	480	9	US-09-410-194-11
5	1007	90.4	480	9	US-09-410-194-17
6	1007	90.4	480	11	US-09-009-893-2
7	1007	90.4	480	11	US-09-471-749-1
8	713	64.0	481	9	US-09-410-194-12
9	713	64.0	481	9	US-09-410-194-19
10	701.5	63.0	484	14	US-10-005-921-2
11	532	47.8	391	15	US-10-103-313-318
12	532	47.8	391	15	US-10-115-928-37
13	527	47.3	348	11	US-09-009-893-6
14	465	41.7	93	9	US-09-864-761-36370
15	248	22.3	182	9	US-09-410-194-24

16	239	21.5	171	9	US-09-410-194-4	Sequence 4, Appli
17	234	21.0	169	9	US-09-410-194-2	Sequence 2, Appli
18	234	21.0	188	9	US-09-410-194-23	Sequence 23, Appl
19	198.5	17.8	169	9	US-09-410-194-5	Sequence 5, Appli
20	192.5	17.3	478	11	US-09-009-893-3	Sequence 3, Appli
21	192.5	17.3	479	9	US-09-410-194-20	Sequence 20, Appl
22	185.5	16.7	177	9	US-09-410-194-7	Sequence 7, Appli
23	170.5	15.3	171	9	US-09-410-194-1	Sequence 1, Appli
24	170.5	15.3	171	9	US-09-410-194-13	Sequence 13, Appl
25	170.5	15.3	250	10	US-09-989-903-48	Sequence 48, Appl
26	170.5	15.3	250	15	US-10-068-564-48	Sequence 48, Appl
27	168	15.1	476	10	US-09-954-697-27	Sequence 27, Appl
28	168	15.1	496	9	US-09-952-768-4	Sequence 27, Appl
29	160	14.4	521	9	US-09-962-834A-2	Sequence 2, Appli
30	160	14.4	571	9	US-09-410-194-21	Sequence 21, Appl
31	157	14.1	479	9	US-09-952-768-2	Sequence 2, Appli
32	157	14.1	479	10	US-09-954-697-33	Sequence 33, Appl
33	157	14.1	479	11	US-09-009-893-4	Sequence 4, Appli
34	155	13.9	165	9	US-09-410-194-6	Sequence 6, Appli
35	144	12.9	170	9	US-09-410-194-8	Sequence 8, Appli
36	110	9.9	76	15	US-10-001-254-32	Sequence 32, Appl
37	110	9.9	79	9	US-09-952-768-68	Sequence 2, Appli
38	110	9.9	256	9	US-09-933-814-2	Sequence 2, Appli
39	110	9.9	256	9	US-09-824-134-2	Sequence 3, Appli
40	109.5	9.8	167	9	US-09-410-194-3	Sequence 36543, A
41	107	9.6	110	9	US-09-864-761-36543	Sequence 184, App
42	105	9.4	208	15	US-10-207-655-184	Sequence 190, App
43	105	9.4	208	15	US-10-207-655-190	Sequence 408, App
44	105	9.4	211	15	US-10-207-655-408	Sequence 31, Appl
45	101	9.1	75	15	US-10-001-254-31	

ALIGNMENTS

RESULT 1

US-09-410-194-15
; Sequence 15, Application US/09410194
; Patent No. US20020095030A1
; GENERAL INFORMATION:
; APPLICANT: Tschopp, Jurg
; APPLICANT: Thome, Margot
; APPLICANT: Burns, Kimberly
; APPLICANT: Irmeler, Marten
; APPLICANT: Hahne, Michael
; APPLICANT: Schrotter, Michael
; APPLICANT: Schneider, Pascal
; APPLICANT: Bodmer, Jean- Luc
; APPLICANT: Steiner, Veronique
; APPLICANT: Rimoldi, Donata
; APPLICANT: Hofmann, Kay
; APPLICANT: French, E. Lars
; TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
; FILE REFERENCE: 11141-002001
; CURRENT APPLICATION NUMBER: US/09/410,194
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: PCT/EP98/01857
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-410-194-15

Query Match 100.0%; Score 1114; DB 9; Length 221;
Best Local Similarity 100.0%; Pred. No. 3e-101;
Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSAEVTHQVEALDTDEKEMLLFLCRDVAIDVVPPNVRDLTLRERKLSVGLAEALLY 60

Db 1 MSAEVIHQVEALDTDEKMLFLCRDVAIDVVPNNVRLDILRERKLSVGLAELLY 60
Qy 61 RVRFDLLKRLKMDRAVETHLLRNPHLYSDYRVLMAEIGEDLDKSDVSSLIPLMKDYM 120
Db 61 RVRFDLLKRLKMDRAVETHLLRNPHLYSDYRVLMAEIGEDLDKSDVSSLIPLMKDYM 120
Qy 121 GRGKISKEKSFLLDVLWELEKLNVLAPQDLLEKLNHRIIDLTKTKIYKQSVQAGT 180
Db 121 GRGKISKEKSFLLDVLWELEKLNVLAPQDLLEKLNHRIIDLTKTKIYKQSVQAGT 180
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Db 181 SYRNVLAQAIOKSLKDPNNFRMTTPYAHCPDLKILGNCSM 221

RESULT 2

US-09-410-194-22

; Sequence 22, Application US/09410194

; Patent No. US20020095030A1

; GENERAL INFORMATION:

; APPLICANT: Tschoep, Jurg

; APPLICANT: Thome, Margot

; APPLICANT: Burns, Kimberly

; APPLICANT: Irmeler, Marten

; APPLICANT: Hahne, Michael

; APPLICANT: Schroter, Michael

; APPLICANT: Schneider, Pascal

; APPLICANT: Bodmer, Jean-Luc

; APPLICANT: Steiner, Veronique

; APPLICANT: Rimoldi, Donata

; APPLICANT: Hofmann, Kay

; APPLICANT: French, E. Lars

; TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS

; FILE REFERENCE: 11141-002001

; CURRENT APPLICATION NUMBER: US/09/410.194

; CURRENT FILING DATE: 1999-09-30

; PRIOR FILING DATE: 1998-03-31

; PRIOR FILING DATE: 1997-04-01

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 22

; LENGTH: 221

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-410-194-22

Query Match 100.0%; Score 1114; DB 9; Length 221;
Best Local Similarity 100.0%; Pred. No. 3e-101;
Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSAEVIHQVEALDTDEKMLFLCRDVAIDVVPNNVRLDILRERKLSVGLAELLY 60
Db 1 MSAEVIHQVEALDTDEKMLFLCRDVAIDVVPNNVRLDILRERKLSVGLAELLY 60
Qy 61 RVRFDLLKRLKMDRAVETHLLRNPHLYSDYRVLMAEIGEDLDKSDVSSLIPLMKDYM 120
Db 61 RVRFDLLKRLKMDRAVETHLLRNPHLYSDYRVLMAEIGEDLDKSDVSSLIPLMKDYM 120
Qy 121 GRGKISKEKSFLLDVLWELEKLNVLAPQDLLEKLNHRIIDLTKTKIYKQSVQAGT 180
Db 121 GRGKISKEKSFLLDVLWELEKLNVLAPQDLLEKLNHRIIDLTKTKIYKQSVQAGT 180
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RESULT 3

US-09-861-270-2

; Sequence 2, Application US/09861270

; Patent No. US20020052474A1
; GENERAL INFORMATION:
; APPLICANT: Sul, Hong-Bing
; TITLE OF INVENTION: Regulators of Apoptosis
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Science & Technology Law Group
; STREET: 75 Denise Drive
; CITY: Hillsborough
; STATE: California
; COUNTRY: USA
; ZIP: 94010
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/861.270
; FILING DATE: 18-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/795,088
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 343-4341
; TELEFAX: (650) 343-4342
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 480 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-861-270-2

Query Match 90.4%; Score 1007; DB 9; Length 480;
Best Local Similarity 99.5%; Pred. No. 2.6e-90;
Matches 202; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 RVRFDLLKRLKMDRAVETHLLRNPHLYSDYRVLMAEIGEDLDKSDVSSLIPLMKDYM 120
Db 61 RVRFDLLKRLKMDRAVETHLLRNPHLYSDYRVLMAEIGEDLDKSDVSSLIPLMKDYM 120
Qy 121 GRGKISKEKSFLLDVLWELEKLNVLAPQDLLEKLNHRIIDLTKTKIYKQSVQAGT 180
Db 121 GRGKISKEKSFLLDVLWELEKLNVLAPQDLLEKLNHRIIDLTKTKIYKQSVQAGT 180
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Db 181 SYRNVLAQAIOKSLKDPNNFRM 203

RESULT 4

US-09-410-194-11

; Sequence 11, Application US/09410194

; Patent No. US20020095030A1

; GENERAL INFORMATION:

; APPLICANT: Tschoep, Jurg

; APPLICANT: Thome, Margot

; APPLICANT: Burns, Kimberly

; APPLICANT: Irmeler, Marten

; APPLICANT: Hahne, Michael

```
; APPLICANT: Schroter, Michael
; APPLICANT: Schneider, Pascal
; APPLICANT: Bodmer, Jean- Luc
; APPLICANT: Steiner, Veronique
; APPLICANT: Rimoldi, Donata
; APPLICANT: Hofmann, Kay
; APPLICANT: French, E. Lars
; TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
; FILE REFERENCE: 11141-002001
; CURRENT APPLICATION NUMBER: US/09/410,194
; CURRENT FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: PCT/EP98/01857
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-410-194-11

Query Match          90.4%; Score 1007; DB 9; Length 480;
Best Local Similarity 99.5%; Pred. No. 2.6e-90;
Matches 202; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPNVRDLDTLRGRKLSVGDLAELLY 60
Db 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPNVRDLDTLRGRKLSVGDLAELLY 60
QY 61 RVRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIIFLMKDYM 120
Db 61 RVRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIIFLMKDYM 120
QY 121 GRGKISKEKSFLLDVVELEKLNIVAPDQLDLEKCLKNHRIIDLTKTKIYKQSVGAGT 180
Db 121 GRGKISKEKSFLLDVVELEKLNIVAPDQLDLEKCLKNHRIIDLTKTKIYKQSVGAGT 180
QY 181 SYRNVLQAAAIQKSLKDPSPNNFM 203
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RESULT 6
US-09-009-893-2
; Sequence 2, Application US/09009893
; Publication No. US20030087339A1
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: ROSEN, CRAIG A.
; APPLICANT: DIXIT, VISHVA M.
; APPLICANT: GENTZ, REINER L.
; APPLICANT: KENNY, JOSEPH J.
; TITLE OF INVENTION: I-FLICE, A NOVEL INHIBITOR OF TUMOR
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESS: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: US
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/009,893
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,205
; FILING DATE: 21-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/054,800
; FILING DATE: 05-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0970002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 480 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
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RESULT 9

US-09-410-194-19
; Sequence 19, Application US/09410194
; Patent No. US20020095030A1
; GENERAL INFORMATION:
; APPLICANT: Tschoopp, Jurq
; APPLICANT: Thome, Margot
; APPLICANT: Burns, Kimberly
; APPLICANT: Irmier, Marten
; APPLICANT: Hahne, Michael
; APPLICANT: Schneider, Michael
; APPLICANT: Bodmer, Jean- Luc
; APPLICANT: Steiner, Veronique
; APPLICANT: Rimoldi, Donata
; APPLICANT: Hofmann, Kay
; APPLICANT: French, E. Lars
; TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
; FILE REFERENCE: 11141-002001
; CURRENT APPLICATION NUMBER: US/09/410,194
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: PCT/EP98/01857
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 481
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-410-194-19

Query Match 64.0%; Score 713; DB 9; Length 481;
Best Local Similarity 74.5%; Pred. No. 1.6e-61;
Matches 146; Conservative 19; Mismatches 29; Indels 2; Gaps 2;
QY 1 MSAEVTHQVEEALDTDEKEMMLFLCRDVAIDVVPVPPNVRDLTLRERKLSVGDIAELLY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 6 VSAEVTHQVEECLDEKEMMLFLCRDVTENLAAPNVRDLTLRERKLSVGFATLAELLY 65
QY 61 RVRFDLLKRLKMDKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIPL 120
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 66 RVRFDLLKRLKTDKATVEDHRRNPHLVSDYRVLMEIGESLDQNDVSSLVFLTRDT 125
QY 121 GRGKISKEKSFLLVVELEKLNVAPOQLDLLEKCLKNHRIIDLTKTKIQKYSVQAGT 180
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 126 GRGKIAKSKSFLLVVELEKLNLIASDQLNLEKCLKNHRIIDLTKTKIQKYSVQAGT 184
QY 181 SYRNVLOAAIQK-SLK 195
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 185 SNMNTLOASLPKLSIK 200

RESULT 10

US-10-005-921-2
; Sequence 2, Application US/10005921
; Publication No. US20020174450A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Keith D.
; APPLICANT: Leviten, Michael W.
; TITLE OF INVENTION: TRANSGENIC MICE CONTAINING CASH GENE
; FILE REFERENCE: R-714
; CURRENT APPLICATION NUMBER: US/10/005,921
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: US 60/254,902
; PRIOR FILING DATE: 2000-12-11
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 484
; TYPE: PRT

; ORGANISM: Mus musculus
US-10-005-921-2

Query Match 63.0%; Score 701.5; DB 14; Length 484;
Best Local Similarity 73.4%; Pred. No. 2.2e-60;
Matches 146; Conservative 19; Mismatches 29; Indels 5; Gaps 3;
QY 1 MSAEVTHQVEEALDTDEKEMMLFLCRDVAIDVVPVPPNVRDLTLRERKLSVGDIAELLY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 6 VSAEVTHQVEECLDEKEMMLFLCRDVTENLAAPNVRDLTLRERKLSVGFATLAELLY 65
QY 61 RVRFDLLKRLKMDKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIPL 117
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 66 RVRFDLLKRLKTDKATVEDHRRNPHLVSDYRVLMEIGESLDQNDVSSLVFLTRITR 125
QY 118 DYMGKISKEKSFLLVVELEKLNVAPOQLDLLEKCLKNHRIIDLTKTKIQKYSVQAGT 177
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 126 DYTGRGKIAKSKSFLLVVELEKLNLIASDQLNLEKCLKNHRIIDLTKTKIQKYSVQAGT 185
QY 178 AGTSYRNVLOAAIQK-SLK 195
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 186 A-RSNMNTLOASLPKLSIK 203

RESULT 11

US-10-103-313-318
; Sequence 318, Application US/10103313
; Publication No. US20030082758A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P20707C1
; CURRENT APPLICATION NUMBER: US/10/103,313
; CURRENT FILING DATE: 2002-03-12
; NUMBER OF SEQ ID NOS: 653
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 318
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (97)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
US-10-103-313-318

Query Match 47.8%; Score 532; DB 15; Length 391;
Best Local Similarity 98.2%; Pred. No. 6.4e-44;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 95 VLMAEIGEDLDKSDVSSLIPLMKDYMGKISKEKSFLLVVELEKLNVAPOQLDLLEK 154
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 6 VLMAEIGEDLDKSDVSSLIPLMKDYMGKISKEKSFLLVVELEKLNVAPOQLDLLEK 65
QY 155 CLKNIHRIIDLTKTKIQKYSVQAGTSYRNVLOAAIQKSLKDPNNFRM 203
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 66 CLKNIHRIIDLTKTKIQKYSVQAGTSYRNVLOAAIQKSLKDPNNFRM 114

RESULT 12

US-10-115-928-37
; Sequence 37, Application US/10115928
; Publication No. US20030092615A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT204C1
; CURRENT APPLICATION NUMBER: US/10/115,928
; CURRENT FILING DATE: 2002-04-05
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0

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; SEQ ID NO 37
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (97)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-115-928-37

Query Match      47.8%; Score 532; DB 15; Length 391;
Best Local Similarity 98.2%; Pred. No. 6.4e-44;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 95 VMAEIGEDLDKSDVSSLIIFLMKDYMGKGKISKSEKSFLLDLVVELEKLNVLVAPDQDLLEK 154
Db 6 VMAEIGEDLDKSDVSSLIIFLMKDYMGKGKISKSEKSFLLDLVVELEKLNVLVAPDQDLLEK 65

Qy 155 CLKNHRIIDLTKTKIQKYKQSVQAGTSYRNVLQAAIQKSLKDPSPNNFRM 203
Db 66 CLKNHRIIDLTKTKIQKYKQSVQAGTSYRNVLQAAIQKSLKDPSPNNFR 114

RESULT 13
US-09-009-893-6
; Sequence 6, Application US/09009893
; Publication No. US20030087339A1
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: ROSEN, CRAIG A.
; APPLICANT: DIXIT, VISHVA M.
; APPLICANT: GENTZ, REINER L.
; APPLICANT: KENNY, JOSEPH J.
; TITLE OF INVENTION: I-FLICE, A NOVEL INHIBITOR OF TUMOR
; TITLE OF INVENTION: NECROSIS FACTOR RECEPTOR-1 AND CD-95 INDUCED APOPTOSIS
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 500
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: US
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/009,893
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,205
; FILING DATE: 21-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/054,800
; FILING DATE: 05-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0970002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 348 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-009-893-6
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Query Match      47.3%; Score 527; DB 11; Length 348;
Best Local Similarity 100.0%; Pred. No. 1.7e-43;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 97 MAEIGEDLDKSDVSSLIIFLMKDYMGKGKISKSEKSFLLDLVVELEKLNVLVAPDQDLLEKCL 156
Db 1 MAEIGEDLDKSDVSSLIIFLMKDYMGKGKISKSEKSFLLDLVVELEKLNVLVAPDQDLLEKCL 60

Qy 157 KNIHRIDLTKTKIQKYKQSVQAGTSYRNVLQAAIQKSLKDPSPNNFR 202
Db 61 KNIHRIDLTKTKIQKYKQSVQAGTSYRNVLQAAIQKSLKDPSPNNFR 106

RESULT 14
US-09-864-761-36370
; Sequence 36370, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; FILE REFERENCE: Acomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 36370
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC007272.2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.5
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 8
```


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OM protein - protein search, using sw model

Run on: August 13, 2003, 16:36:59 ; Search time 16.0785 Seconds
(without alignments)
1321.848 Million cell updates/sec

Title: US-09-380-546A-4
Perfect score: 1114
Sequence: 1 MSAEVIHQVEEALDTEREM.....RMITPYAHCPDLKILNGCSM 221

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	218.5	19.6	241	2 T30761	hypothetical prote
2	170.5	15.3	171	2 S55668	hypothetical prote
3	157	14.1	371	2 T30762	hypothetical prote
4	109.5	9.8	167	2 E36813	hypothetical prote
5	105	9.4	208	2 A58912	FADD protein - hum
6	103.5	9.3	422	2 T31008	hypothetical prote
7	103	9.2	1053	2 T09641	DNA-directed RNA p
8	103	9.2	1201	2 AD1107	RNA polymerase (be
9	103	9.2	1201	2 AG1468	RNA polymerase (be
10	99	8.9	2671	2 A49873	inositol 1,4,5-tri
11	98.5	8.8	313	2 S51753	NSP3 protein - por
12	98.5	8.8	389	2 C64876	yclm protein precu
13	98.5	8.8	389	2 E90860	probable heat choc
14	98.5	8.8	389	2 A85759	probable heat choc
15	98	8.8	2670	2 A46719	inositol 1,4,5-tri
16	97	8.7	1199	2 G65998	RNA polymerase (be
17	96	8.6	313	2 S51754	NSP3 protein - por
18	95.5	8.6	310	2 D70328	histidine kinase s
19	95.5	8.6	445	2 E72674	hypothetical prote
20	95	8.5	833	2 H72205	maltoase ABC transp
21	95	8.5	1207	2 A89822	RNA polymerase bet
22	94.5	8.5	313	2 S51730	NSP3 protein - hum
23	94	8.4	1639	1 MMEFB2	laminin gamma-1 ch
24	93.5	8.4	313	2 S51725	NSP3 protein - hum
25	93	8.3	488	2 A37352	myosin heavy chain
26	93	8.3	1055	2 T10432	DNA-directed RNA p
27	93	8.3	1057	2 T10908	DNA-directed RNA p
28	92.5	8.3	1391	2 C82007	DNA-directed RNA p
29	92.5	8.3	1391	2 F81233	DNA-directed RNA p

30	92	8.3	1199	2 T29145	hypothetical prote
31	92	8.3	1837	2 T41023	probable nuclear p
32	91.5	8.2	313	2 S51727	NSP3 protein - hum
33	91.5	8.2	350	2 S20404	casein kinase II (
34	91.5	8.2	384	2 B96919	probable sigma fac
35	91.5	8.2	389	2 AD0655	conserved hypothet
36	91.5	8.2	596	2 B96834	hypothetical prote
37	91	8.2	313	1 MNXRBR	nonstructural prote
38	91	8.2	1400	2 T31555	hypothetical prote
39	91	8.2	3119	2 T18414	protein g377 - mal
40	90.5	8.1	391	2 I49141	casein kinase (EC
41	90	8.1	313	2 S51769	nonstructural prote
42	90	-8.1	350	2 E90347	coenzyme PQ synth
43	90	8.1	1053	2 T09645	DNA-directed RNA p
44	90	8.1	1169	2 H70178	exodeoxyribonuclea
45	90	8.1	1206	2 T44376	DNA-directed RNA p

ALIGNMENTS

RESULT 1

T30761
hypothetical protein 159L - Molluscum contagiosum virus 1
N:Alternate names: MC159L
C:Species: Molluscum contagiosum virus 1
C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 11-May-2000
C:Accession: T30761
R:Senkevich, T.G.; Bugert, J.J.; Sisler, J.R.; Koonin, E.V.; Darai, G.; Moss, B.
Science 273, 813-816, 1996
A:Title: Genome sequence of a human tumorigenic poxvirus: Prediction of specific host
A:Reference number: Z20876; MUID:96325459; PMID:8670425
A:Accession: T30761
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-241 <SEN>
A:Cross-references: EMBL:U60315; PIDN:AAC55287.1
C:Genetics:
A:Note: MC159L

Query Match	19.6%	Score 218.5	DB 2	Length 241
Best Local Similarity	29.9%	Pred. No. 6.2e-09		
Matches	64	Conservative	41	Mismatches 80; Indels 29; Gaps 7;
QY	7	HQVEEALDTEREMLLFLCRDVAIDVVPNPNVRDLILREGRKLSVGDLAELLYRVRRED	66	
Db	15	HLLEE-LDSHEDSLFLFCHDRAAGCT--TVTQALCSLSQQRKLTALALVEMLYLQRM	71	
QY	67	LKRIKMDRKAVETHLLRNPHLVSDYRVMABEIGDLDKSDVSSL-IFL--MKDYMG	123	
Db	72	LLKSRFGLSKEGAEQ--LLGTSTFLTRYRKLWCVGEELDSSELRLRFLACNLNPSL	129	
QY	124	KTSKEKSFLLVVELEKLNIVAPDQDLLEKCLKNTHRIDLTKIKYKQSVQ-----	176	
Db	130	-LSESSRFVELVALENGLVSPSSVSLADMURDLDCQLLVEIQEQEARYRYCY	188	
QY	177	-----GAGTSYRNVLQAAIQKSLKDP	197	
Db	189	AASPSLPVTLRRHGCGASEHEQLCMPVQESSDSP	222	

RESULT 2

S55668
hypothetical protein E8 - equine herpesvirus 2
C:Species: equine herpesvirus 2
C:Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 08-Oct-1999
C:Accession: S55668
R:Telford, E.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.
J. Mol. Biol. 249, 520-528, 1995
A:Title: The DNA sequence of equine herpesvirus 2
A:Reference number: S55594; MUID:95302501; PMID:7783207
A:Accession: S55668
A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA
A;Residues: 1-171 <TEL>
A;Cross-references: GB:U20824; NID:g95172; PIDN:AAC13862.1; PID:g95247
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1995
C;Superfamily: equine herpesvirus 2 hypothetical protein E8

Query Match	15.3%	Score	170.5;	DB	2;	Length	171;
Best Local Similarity	32.7%;	Pred.	No. 1.3e-05;				
Matches	55;	Conservative	22;	Mismatches	72;	Indels	19;
Gaps	5						

QY	12	ALDTBEKEMLLFLCRDAIVDVPNN-----VRDLDLIRERKGLSVGDIAELLVRRVF	65
		: : :	
Db	12	SLDEDETETYLVLCDRLI-----KNKGFEQTRDAFKFLSDYACLSAANQMELLPVGR	66
		: : :	
QY	66	DILKKILKMDRKANVETHLLRNPHLVDSYRVLMIAEIGEDLDKSDVSSLIFL----	MKDYMG 121
		: :	
Db	67	DLIRRFQGTWTPDCSPRYMP-TCSPFRCIALMVNDFLSKDEVEWMYFCAPRLESHE	125
		: :	

Qy	122	RGKISKEKSF	LDLVVELEK	NLVAPQDL	LEKCLKNH	RIDLTKIQ	169
		.	:				:
			:				:
Db	126	PG---	SKKSFLR	ASLEDE	LELLGGDK	LTFLRHLL	TTIGRADLVKNLQ
			:				:
			:				:

RESULT 3
T30762
hypothetical protein 160L - Molluscum contagiosum virus 1
N;Alternate names: MC160L

C:Species: Molluscum contagiosum virus 1
C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 11-May-2000
C:Accession: J30762
R:Senkevitch, T.G.; Bugert, J.J.; Sisler, J.R.; Koonin, E.V.; Darai, G.; Moss, B.
S:Science 273, 813-816, 1996
A:Title: Genome sequence of a human tumorigenic poxvirus: Prediction of specific
A:Reference number: Z20876; MUID:96325459; PMID:8670425

A:Accession: T30762
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-371 <SEN>
A:Cross-references: EMBL:U60315; PIDN:AAC5288.1
C:Genetics:
A:Note: MC160L

Query Match	14.1%	Score 157;	DB 2;	Length 371;
Best Local Similarity	29.9%;	Pred. No. 0.00032;		
Matches 52;	Conservative	25;	Mismatches 81;	Indels 16;
	Gaps			Gaps 5;

Qy	13	LDTDEKEMLFCLRDVAIDWPPNVRDLDILRERCKLSVGDLAELLYRVRRFDLLKRIL	72
		: : :	
Db	18	LDASEHEVLFLCRDVA--PASKTAEDALRALORRLTLTSSMAEELCALREFDLVYRF	75

QY 73 KMDRKAVETHLLRNPHLYSDYRYVLMAEITGEDLDKSDVSLIFLKM DYMRGKI ----SKE 128
| | : | : | : | : | : | :
Dd 76 GMTRECAGR--LLGHGFLSQYRLQVAATINNVGVSEDLRVMC-----LCAGKLAPPSCPT 127

QY

129 KSF~~D~~LVELEKINLVAPDQLDLEKCLKNHRIIDLTKIQ--KKQSVOGAGT 180
: :||| || ::|::| : | : | : :

D6

128 RCLVDLSALEDAGAISODVSVLTVTLHAVCYRDLVSALSAVAGHMTVGVT 181

RESULT 4
E36813
hypothetical protein ORF71 - saimirine herpesvirus 1 (strain 11)
C:Species: saimirine herpesvirus 1
C:Date: 16-Oct-1992 #sequence_revision 16-Oct-1992 #text_change 08-Oct-1999
C:Accession: E36813: A58939

R;Albrecht, J.
submitted to the EMBL Data Library, January 1992
A;Description: Primary structure of the herpesvirus saimiri genome.
A;Reference number: A36806
A;Accession: E36813
A;Molecule type: DNA
A;Residues: 1-167 <A1B>

A;Residues: 1-107 <ADB>
A;Cross-references: GB:X64346; NID:g60320; PIDN:CAA45694.1; PID:g603092

R:Nicholas, J.; Cameron, K.R.; Honess, R.W.
Nature 355, 362-365, 1992
A:Title: Herpesvirus saimiri encodes homologues of G protein-coupled receptors and cy
A:Reference number: S20243; MUID:92115001; PMID:1309943
A:Accession: A58939
A:Molecule type: DNA
A:Residues: 1-61 <NC>
A:Cross-references: GB:576368; NID:g243355; PIDN:AB21118.1; PID:g243355
R:Albrecht, J.C.; Nicholas, J.; Biller, D.; Cameron, K.R.; Biesinger, B.; Newman, C.;
J. Virol. 66, 5047-5058, 1992
A:Title: Primary structure of the herpesvirus saimiri genome.
A:Reference number: A37309; MUID:92333688; PMID:1321287
A:Contents: annotation; protein-coding frames
A:Note: neither protein nor nucleotide sequence is given
C:Genetics:
A:Gene: 71

Query Match 9.8%; Score 109.5; DB 2; Length 167;
Best Local Similarity 24.4%; Pred. No. 0.36;

QY		1 MSAEVIHQVEEALDTDEKEMLLFL---CRDVAIDVPPNVRDLLDLRRGKLVSVD--L 55 : : : : : : : : :
Dd		3 LKTTVLH-LTDSFTDEMYCLLFINGCIPSCNAV--NISDI--IIFTLSKTOWDICL 57 :

Qy 56 AELLYRVRFDDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAETGEDLDKSDVSSLI 115

Dd 58 MQCLYVLRKIGLLNLFQVTEKAVQKSFQTPQL-ETHVLTVNNNNLLAKDEKRLCFI 116

```

QY      116 MKDYMGGRGKISKKEK---SFLDVLVVELEKLNVLVAPQDLDLLEKCLKNIHRIDL 164
Db      117 LDQGFPPRNAAPASVILCVFSLMCEMHVLECLCQ-----LKKCLQIGRSGL 163

```

RESULT 5
A56912
FADD protein - human
N;Alternate names: FAS-associating death domain containing protein FADD; mediator of
C;Species: Homo sapiens (man)
C;Date: 11-Aug-1995 #sequence_revision
C;Accession: A56912; I38041
R;Chinnaiyan, A.M.; O'Rourke, K.; Tewari, M.; Dixit, V.M.
Cell 81, 505-512, 1995
A;Title: FADD, a novel death domain-containing protein, interacts with the death dom
A;Reference number: A56912; MUID:95277837;PWID:7538907

A; Cross-references: GB:U24231; NID:g809486; PID:AAA86517.1; PID:g809487
R; Boldin, M.P.; Varfolomeev, E.E.; Pancer, Z.; Mett, I.L.; Camonis, J.H.; Wallach, D
J. Biol. Chem. 270, 7795-7798, 1995
A; Title: A novel protein that interacts with the death domain of Fas/AP01 contains a
A; Reference number: I38041; MUID:95229578; PMID:7536190

A; Residues: 1-31, 'V', 33-208 <RES>
A; Cross-references: EMBL:X84709; NID:g791037; PIDN:CAA59197.1; PID:g791038
C; Genetics:
A; Gene: GDB:FADD; MORT1
A; Cross-references: GDB:1320394
C; Superfamily: receptor-induced toxicity mediator MORT1
C; Keywords: apoptosis

Query Match	9.4%	Score 105;	DB 2;	Length 208;
Best Local Similarity	25.8%	Pred. No. 1;		
Matches	49;	Conservative	30;	Mismatches 91;
				Indels 20;
				Gaps 7;

QY

5 VIHQVEEALDTDEKEMILFLCRDVA----IDVVPNPVRDLLDIRERGKLSVGDD---LAE 57
 :
 :
 :

Dd

7 LLHSVSSSISSELTTELKFLCGRVKRKKLVQSGL-DLFSLMLEONDIPEGHTELLRE 65
 :
 :
 :

A; Experimental source: strain NCTC 11288

.....

Db

QY 184 -----NVLQAAIQSKLKDPSNNFRMITPYAHCPDLKILGN 218
DB 455 MAVHVPLSAEQAARILMLAAQNIL-NPKDGKPVVTP---SQDM-VLGN 499

RESULT 9
AG1468
RNA polymerase (beta' chain) [imported] - Listeria innocua (strain Clip11262)
C:Species: Listeria innocua
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C:Accession: AG1468
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, J.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kref, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma, O.K.; Schluter, T.; Smoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AG1468
A:Status: preliminary
A:Gene: rpoC
A:Molecule type: DNA
A:Residues: 1-1201 <GLA>
A:Cross-references: PIDN:CAC95519.1; PID:g16412715; GSPDB:GN00178
A:Experimental source: strain Clip11262
C:Genetics:
C:Gene: rpoC
C:Superfamily: Escherichia coli DNA-directed RNA polymerase beta' chain

Query Match 9.2%; Score 103; DB 2; Length 1201;
Best Local Similarity 20.3%; Pred. No. 12;
Matches 59; Conservative 47; Mismatches 62; Indels 122; Gaps 15;

QY 30 IDVPPNVRDLILRERKLSVGDLAELLYRV-RFPDLKRL-----KMD 75
DB 231 LPVTPPEIRPVQL--EGGRATSDLDLYRVNRRNLKRLDLDGAPNIIVNEXRML 288

QY 76 RKAVE-----THLLRNPHLVSDYRVLMAEIGEDLDKSDVSSL 112
DB 289 QEAVALDINGRRGPRVTPGCPNPLKLSHMLKG-----KQGRFQNLGKRVDSGRSVI 344

QY 113 I-----FLMKDYMGKSKISKEKSFDLVLEKLNVLVADQL 149
DB 345 VVGPNLKMVQGLPKEMALELFPVFMKELVGRGLAHNKS-----AKRKIERMAPEIW 398

QY 150 DLLEKCLK-----NIHRDLKTKIQYKQS-VQAG-----TSYR----- 183
DB 399 DVLEEVIREHPVLNRAPTLRLG-----IQAFETLVEGRAIRLHPLVCTAYNADFQDQ 454

QY 184 -----NVLQAAIQSKLKDPSNNFRMITPYAHCPDLKILGN 218
DB 455 MAVHVPLSAEQAARILMLAAQNIL-NPKDGKPVVTP---SQDM-VLGN 499

RESULT 10
A49873
inositol 1,4,5-triphosphate receptor, type 3 - human
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1995 #sequence_revision 30-Jun-1995 #text_change 20-Aug-1999
C:Accession: A49873
R:Maranto, A.R.
J. Biol. Chem. 269, 1222-1230, 1994
A:Title: Primary structure, ligand binding, and localization of the human type 3 inositol
A:Reference number: A49873; MUID:94117432; PMID:8288584
A:Accession: A49873
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-2671 <MAR>
A:Cross-references: GB:U01062; NID:g4533367; PIDN:AAC50064.1; PID:g3939036
C:Genetics:
C:Gene: GDB:ITPR3
A:Cross-references: GDB:127551; OMIM:147267

A:Map position: 6pter-6p21
C:Superfamily: inositol-trisphosphate receptor

Query Match 8.9%; Score 99; DB 2; Length 2671;
Best Local Similarity 20.3%; Pred. No. 62;
Matches 47; Conservative 55; Mismatches 71; Indels 58; Gaps 11;

QY 1 MSAEVIHQVEEA-LDTDEKEMLLFLCRDVAIDV--VPPNVRDLDL-----RERGLK-- 50
DB 451 MLASAVEKLNBEFFISQNDRRFVQLLEDLVFFVDPVPPNGQNVLDIMVTKPNRERQKLMLR 510

QY 51 -----SVGDLAELLYRV-----RFDLLKRLKMDKRAVETH 82
DB 511 EQNLIKQVGLIKVPFFREKGGEGPLVRLLEELSDQKNAPYQHMFRLCYRVL---RYSQEDY 567

QY 83 LLRNPHLVSDYRVLMAEIGEDLDKSD--VSSLIF-----LMKDYMGKGI-----SKE 128
DB 568 RKNQEHAKQFQMQSQIGYDILAEITALLHNRLKLEKHITKTEVETVSVLRKNRE 627

QY 129 KSFLDLVVELEKLNVA-PQOLDLLEKRLKNIHRID--LTKIKIQYKQSVQ 176
DB 628 PRFLDYLSDLCSVNHIALPVTQELICKVCLDPKNSDILIRTELPAVKEMAQ 678

RESULT 11
S51753
NSP3 protein - porcine rotavirus (strain OSU)
N:Alternate names: NS34 protein
C:Species: porcine rotavirus
A:Variety: strain OSU
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Sep-1999
C:Accession: S51753
R: Rao, C.D.; Das, M.; Rao, B.S.; Gowda, K.
submitted to the EMBL Data Library, September 1994
A:Reference number: S51709
A:Accession: S51753
A:Molecule type: genomic RNA
A:Residues: 1-313 <RAO>
A:Cross-references: EMBL:X81431; NID:g607163; PIDN:CAA57190.1; PID:g607164
A:Experimental source: strain OSU
C:Superfamily: rotavirus nonstructural protein
C:Keywords: nonstructural protein

Query Match 8.8%; Score 98.5; DB 2; Length 313;
Best Local Similarity 22.3%; Pred. No. 4.9;
Matches 46; Conservative 37; Mismatches 58; Indels 65; Gaps 9;

QY 54 DLAEILLYRV-RFDLLKRLKMDKRAVETHLL-----RNPHLVSDYR 94
DB 38 DYNEIFTRVSKFDIV-----MDSGVKNLLGKAAITDQALNGKFGSTIRNRWMTDSK 92

QY 95 VLMAEIGEDLDK-----SDVSSLIFLMKDYMGKRGK 124
DB 93 T-VAKLEDDVKNLKMILSSKGIDQKMRVNLNACFSVKRIPGSSSVIKCTRLMKDKIERGE 151

QY 125 ISKEKSFDLVVELEKLNVLVADQLDLEKRLKNIHRIDLTKI-QYKQSVQAGISYR 183
DB 152 VEVDSDSFYDEKMEITDIDWKA--RYDQLEKRFES-----LKQVNEKYNWSVQ--KSKER 202

QY 184 NVLQAAIQSKLKDPSNNFRMITPYAH 209
DB 203 NENMYSLQNVISQQNQNIADLQOYCN 228

RESULT 12
C64876
ycim protein precursor - Escherichia coli (strain K-12)
C:Species: Escherichia coli
C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C:Accession: C64876
R: Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997

A:Title: The complete genome sequence of *Escherichia coli* K-12.

A:Reference number: A64720; MUID:97426617; PMID:9278503

A:Accession: C64876

A>Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-389 <BLAT>

A:Cross-references: GB:AE000226; GB:U00096; NID:92367115; PIDN:ANC74362.1; PID:92367116;

A:Experimental source: strain K-12, substrain MG1655

C:Genetics:

A:Gene: yciM

C:Superfamily: hypothetical protein H11223; tetratricopeptide repeat homology

C:Keywords: DNA binding; zinc finger

F:1-16/Domain: signal sequence #status predicted <SIG>

F:17-389/Product: yciM protein #status predicted <MAT>

F:180-213/Domain: tetratricopeptide repeat homology <TTL>

F:214-247/Domain: tetratricopeptide repeat homology <TTL>

F:357-374/Region: zinc finger CCCC motif

Query Match 8.8%; Score 98.5; DB 2; Length 389;

Best Local Similarity 22.6%; Pred. No. 6.4;

Matches 47; Conservative 44; Mismatches 78; Indels 39; Gaps 11;

QY 6 IHQ--VEEALDTDEKMLF--LCRDVAIDVPPNVRDLIDLRLRERKLSVGLAEILL-- 59

DB 91 IHOTLMSASLTVEQRLLAIQQLGRDYMAGLVDRADMFNQLTDETFRIGALQQLQI 150

QY 60 YRV-----RRFDLLKRLKM--DRKAVE--THL---LRNPHLV---DYRVLMAEIGDLD 105

DB 151 YQATSEWQKAIDVAERLVKLGKQKQVEIAHFAHFCALQALQHMASDDLDLDRAMTLKKGAAAD 210

QY 106 KSDVSSLIFLMKDYMGRGKISKESFLDLVVELEKLNVPADQLDLLEKLNHRIIDLK 165

DB 211 KNSARVSIMGRVFMAGKAYAKAVESLQVRISQDR-ELVS-ETLEMLQTCYQQL----- 262

QY 166 TKIQYKQSVQAGTGYRNVLQAAIQKS 193

DB 263 -----GKTAWEAEFLQRAVEEN 279

Query Match 8.8%; Score 98.5; DB 2; Length 389;

Best Local Similarity 22.6%; Pred. No. 6.4;

Matches 47; Conservative 44; Mismatches 78; Indels 39; Gaps 11;

QY 6 IHQ--VEEALDTDEKMLF--LCRDVAIDVPPNVRDLIDLRLRERKLSVGLAEILL-- 59

DB 91 IHOTLMSASLTVEQRLLAIQQLGRDYMAGLVDRADMFNQLTDETFRIGALQQLQI 150

QY 60 YRV-----RRFDLLKRLKM--DRKAVE--THL---LRNPHLV---DYRVLMAEIGDLD 105

DB 151 YQATSEWQKAIDVAERLVKLGKQKQVEIAHFAHFCALQALQHMASDDLDLDRAMTLKKGAAAD 210

QY 106 KSDVSSLIFLMKDYMGRGKISKESFLDLVVELEKLNVPADQLDLLEKLNHRIIDLK 165

DB 211 KNSARVSIMGRVFMAGKAYAKAVESLQVRISQDR-ELVS-ETLEMLQTCYQQL----- 262

QY 166 TKIQYKQSVQAGTGYRNVLQAAIQKS 193

DB 263 -----GKTAWEAEFLQRAVEEN 279

Query Match 8.8%; Score 98.5; DB 2; Length 389;

Best Local Similarity 22.6%; Pred. No. 6.4;

Matches 47; Conservative 44; Mismatches 78; Indels 39; Gaps 11;

QY 6 IHQ--VEEALDTDEKMLF--LCRDVAIDVPPNVRDLIDLRLRERKLSVGLAEILL-- 59

DB 91 IHOTLMSASLTVEQRLLAIQQLGRDYMAGLVDRADMFNQLTDETFRIGALQQLQI 150

QY 60 YRV-----RRFDLLKRLKM--DRKAVE--THL---LRNPHLV---DYRVLMAEIGDLD 105

DB 151 YQATSEWQKAIDVAERLVKLGKQKQVEIAHFAHFCALQALQHMASDDLDLDRAMTLKKGAAAD 210

QY 106 KSDVSSLIFLMKDYMGRGKISKESFLDLVVELEKLNVPADQLDLLEKLNHRIIDLK 165

DB 211 KNSARVSIMGRVFMAGKAYAKAVESLQVRISQDR-ELVS-ETLEMLQTCYQQL----- 262

QY 166 TKIQYKQSVQAGTGYRNVLQAAIQKS 193

DB 263 -----GKTAWEAEFLQRAVEEN 279

Query Match 8.8%; Score 98.5; DB 2; Length 389;

Best Local Similarity 22.6%; Pred. No. 6.4;

Matches 47; Conservative 44; Mismatches 78; Indels 39; Gaps 11;

QY 6 IHQ--VEEALDTDEKMLF--LCRDVAIDVPPNVRDLIDLRLRERKLSVGLAEILL-- 59

DB 91 IHOTLMSASLTVEQRLLAIQQLGRDYMAGLVDRADMFNQLTDETFRIGALQQLQI 150

QY 60 YRV-----RRFDLLKRLKM--DRKAVE--THL---LRNPHLV---DYRVLMAEIGDLD 105

DB 151 YQATSEWQKAIDVAERLVKLGKQKQVEIAHFAHFCALQALQHMASDDLDLDRAMTLKKGAAAD 210

QY 106 KSDVSSLIFLMKDYMGRGKISKESFLDLVVELEKLNVPADQLDLLEKLNHRIIDLK 165

DB 211 KNSARVSIMGRVFMAGKAYAKAVESLQVRISQDR-ELVS-ETLEMLQTCYQQL----- 262

QY 166 TKIQYKQSVQAGTGYRNVLQAAIQKS 193

DB 263 -----GKTAWEAEFLQRAVEEN 279

A:Title: The complete genome sequence of *Escherichia coli* K-12.

A:Reference number: A64720; MUID:97426617; PMID:9278503

A:Accession: C64876

A>Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-389 <BLAT>

A:Cross-references: GB:AE000226; GB:U00096; NID:92367115; PIDN:ANC74362.1; PID:92367116;

A:Experimental source: strain K-12, substrain MG1655

C:Genetics:

A:Gene: yciM

C:Superfamily: hypothetical protein H11223; tetratricopeptide repeat homology

C:Keywords: DNA binding; zinc finger

F:1-16/Domain: signal sequence #status predicted <SIG>

F:17-389/Product: yciM protein #status predicted <MAT>

F:180-213/Domain: tetratricopeptide repeat homology <TTL>

F:214-247/Domain: tetratricopeptide repeat homology <TTL>

F:357-374/Region: zinc finger CCCC motif

Query Match 8.8%; Score 98.5; DB 2; Length 389;

Best Local Similarity 22.6%; Pred. No. 6.4;

Matches 47; Conservative 44; Mismatches 78; Indels 39; Gaps 11;

QY 6 IHQ--VEEALDTDEKMLF--LCRDVAIDVPPNVRDLIDLRLRERKLSVGLAEILL-- 59

DB 91 IHOTLMSASLTVEQRLLAIQQLGRDYMAGLVDRADMFNQLTDETFRIGALQQLQI 150

QY 60 YRV-----RRFDLLKRLKM--DRKAVE--THL---LRNPHLV---DYRVLMAEIGDLD 105

DB 151 YQATSEWQKAIDVAERLVKLGKQKQVEIAHFAHFCALQALQHMASDDLDLDRAMTLKKGAAAD 210

QY 106 KSDVSSLIFLMKDYMGRGKISKESFLDLVVELEKLNVPADQLDLLEKLNHRIIDLK 165

DB 211 KNSARVSIMGRVFMAGKAYAKAVESLQVRISQDR-ELVS-ETLEMLQTCYQQL----- 262

QY 166 TKIQYKQSVQAGTGYRNVLQAAIQKS 193

DB 263 -----GKTAWEAEFLQRAVEEN 279

Query Match 8.8%; Score 98.5; DB 2; Length 389;

Best Local Similarity 22.6%; Pred. No. 6.4;

Matches 47; Conservative 44; Mismatches 78; Indels 39; Gaps 11;

QY 6 IHQ--VEEALDTDEKMLF--LCRDVAIDVPPNVRDLIDLRLRERKLSVGLAEILL-- 59

DB 91 IHOTLMSASLTVEQRLLAIQQLGRDYMAGLVDRADMFNQLTDETFRIGALQQLQI 150

QY 60 YRV-----RRFDLLKRLKM--DRKAVE--THL---LRNPHLV---DYRVLMAEIGDLD 105

DB 151 YQATSEWQKAIDVAERLVKLGKQKQVEIAHFAHFCALQALQHMASDDLDLDRAMTLKKGAAAD 210

QY 106 KSDVSSLIFLMKDYMGRGKISKESFLDLVVELEKLNVPADQLDLLEKLNHRIIDLK 165

DB 211 KNSARVSIMGRVFMAGKAYAKAVESLQVRISQDR-ELVS-ETLEMLQTCYQQL----- 262

QY 166 TKIQYKQSVQAGTGYRNVLQAAIQKS 193

DB 263 -----GKTAWEAEFLQRAVEEN 279

Query Match 8.8%; Score 98.5; DB 2; Length 389;

Best Local Similarity 22.6%; Pred. No. 6.4;

Matches 47; Conservative 44; Mismatches 78; Indels 39; Gaps 11;

QY 6 IHQ--VEEALDTDEKMLF--LCRDVAIDVPPNVRDLIDLRLRERKLSVGLAEILL-- 59

DB 91 IHOTLMSASLTVEQRLLAIQQLGRDYMAGLVDRADMFNQLTDETFRIGALQQLQI 150

QY 60 YRV-----RRFDLLKRLKM--DRKAVE--THL---LRNPHLV---DYRVLMAEIGDLD 105

DB 151 YQATSEWQKAIDVAERLVKLGKQKQVEIAHFAHFCALQALQHMASDDLDLDRAMTLKKGAAAD 210

QY 106 KSDVSSLIFLMKDYMGRGKISKESFLDLVVELEKLNVPADQLDLLEKLNHRIIDLK 165

DB 211 KNSARVSIMGRVFMAGKAYAKAVESLQVRISQDR-ELVS-ETLEMLQTCYQQL----- 262

QY 166 TKIQYKQSVQAGTGYRNVLQAAIQKS 193

DB 263 -----GKTAWEAEFLQRAVEEN 279

Query Match 8.8%; Score 98.5; DB 2; Length 389;

Best Local Similarity 22.6%; Pred. No. 6.4;

Matches 47; Conservative 44; Mismatches 78; Indels 39; Gaps 11;

QY 6 IHQ--VEEALDTDEKMLF--LCRDVAIDVPPNVRDLIDLRLRERKLSVGLAEILL-- 59

DB 91 IHOTLMSASLTVEQRLLAIQQLGRDYMAGLVDRADMFNQLTDETFRIGALQQLQI 150

QY 60 YRV-----RRFDLLKRLKM--DRKAVE--THL---LRNPHLV---DYRVLMAEIGDLD 105

DB 151 YQATSEWQKAIDVAERLVKLGKQKQVEIAHFAHFCALQALQHMASDDLDLDRAMTLKKGAAAD 210

QY 106 KSDVSSLIFLMKDYMGRGKISKESFLDLVVELEKLNVPADQLDLLEKLNHRIIDLK 165

DB 211 KNSARVSIMGRVFMAGKAYAKAVESLQVRISQDR-ELVS-ETLEMLQTCYQQL----- 262

QY 166 TKIQYKQSVQAGTGYRNVLQAAIQKS 193

DB 263 -----GKTAWEAEFLQRAVEEN 279

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Search completed: August 13, 2003, 16:43:47
Job time : 17.5785 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 13, 2003, 16:21:28 ; Search time 82.8531 Seconds
(without alignments)
919.565 Million cell updates/sec

Title: US-09-380-546A-2
Perfect score: 2473
Sequence: 1 MSAEVIHQVEALDTEKEM.....EKYYVWLQHTLRKILSYT 480

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq.19Jun03.*

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23:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
2473	100.0	480	19	AAW78903	Human G1 protein i
2468	99.8	480	19	AAW76631	Human CFLIP-L prot
2468	99.8	480	19	AAW69715	Human Casper prote
2468	99.8	480	19	AAW69229	I-FLICE-1 protein.
2468	99.8	480	19	AAW58578	Human FIN-1. Homo
2468	99.8	480	20	AAW57454	Human FLICE-like i
2468	99.8	480	20	AAW05787	Human MACH related
2468	99.8	480	21	AAW03960	FLICE-like inhibit
2468	99.8	480	21	AAW67418	Usurpin-alpha poly

10	2468	99.8	480	21	AAW57606	Human apoptosis as
11	2468	99.8	480	23	ABB09294	Human FLIP-c prote
12	2468	99.8	491	21	AAW03964	FLIP with detectab
13	2435.5	98.5	479	19	AAW76625	Human FLIP protein
14	2412	97.5	480	21	AAW59414	Human CLARP protei
15	2265.5	91.6	445	20	AAW90107	Human FLAME-1 prot
16	2265.5	91.6	445	23	AAE26086	Human CLARP-1 prot
17	2224	89.9	462	21	AAW67419	Usurpin-beta polyp
18	1993	80.6	391	22	AAE09601	Human gene 9 encod
19	1993	80.6	391	22	AAU21591	Novel human neopla
20	1993	80.6	391	23	ABG78973	Human apoptosis re
21	1990	80.5	384	20	AAW05791	MRIT alpha 3 polyp
22	1746	70.6	366	20	AAW05788	Human MACH related
23	1630	65.9	348	19	AAW69230	I-FLICE-2 protein.
24	1584	64.1	302	20	AAW05792	MRIT-ND1 polypepti
25	1580	63.9	481	19	AAW76632	Mouse CFLIP-L prot
26	1580	63.9	481	21	AAW03958	FLICE-like inhibit
27	1580	63.9	481	23	ABW09295	Mouse FLIP-c prote
28	1568.5	63.4	484	23	ABB09292	Mouse FLIP-c prote
29	1568.5	63.4	484	24	ABB99383	Amino acid sequenc
30	1560	63.1	483	19	AAW76626	Murine FLIP protei
31	1391	56.2	264	20	AAW05790	Human anti-apoptot
32	1302.5	52.7	291	21	AAW67420	Usurpin-gamma poly
33	1220	49.3	230	20	AAW05793	MRIT-beta 2 polype
34	1131	45.7	227	20	AAW05795	Human FLAME-1b pro
35	1130.5	45.7	270	23	AAE26110	Human CFLIP-S prot
36	1007	40.7	221	19	AAW76630	Human G1 protein i
37	1007	40.7	221	19	AAW78904	Human FLICE-like i
38	1007	40.7	221	20	AAW57455	Human MACH related
39	1007	40.7	221	20	AAW05789	FLICE-like inhibit
40	1007	40.7	221	21	AAW03959	Human MRIT prodoma
41	1007	40.7	221	22	AAW84802	Human MRIT prodoma
42	1007	40.7	221	22	AAW61117	Human MRIT prodoma
43	1007	40.7	221	23	ABB09293	Human MRIT prodoma
44	925	37.4	175	20	AAW05794	MRIT-D/S polypepti
45	701.5	28.4	218	23	ABB09296	Mouse FLIP-c prote

ALIGNMENTS

RESULT 1
AAW78903
ID AAW78903 standard; Protein; 480 AA.
XX AC AAW78903;
XX AC AAW78903;
XX AC AAW78903;
DT 11-JAN-1999 (first entry)
XX Human G1 protein isoform alpha (CASH-alpha).
DE DE Human G1 protein isoform alpha (CASH-alpha).
XX G1 protein; CASH-alpha; human; caspase homologue; Fas receptor;
KW modulator; apoptosis; cell death; inflammation; tumour; HIV;
KW therapy.

XX Homo sapiens.
XX Homo sapiens.
XX Key Location/Qualifiers
FH Key 2..73
FT Domain /note= "death domain/MORT module"
FT Domain 93..142
FT Domain /note= "death domain/MORT module"

XX W09839435-A1.
XX PD 11-SEP-1998.
XX PF 26-FEB-1998; 98WO-IL00098.
XX PR 01-MAY-1997; 97IL-0120759.
XX PR 03-MAR-1997; 97IL-0120367.
XX PA (YEDA) YEDA RES & DEV CO LTD.

XX Brodianski V, Golteev Y, Kovalenko A, Varfolomeev E;
 PI Wallach D;
 XX
 DR WPI; 1998-495842/42.
 DR N-PSDB; AAV52968.
 XX
 XX New DNA encoding isoforms of G1 protein which bind MORT-1 - and
 PT regulate the effects of FAS and tumour necrosis factor receptors,
 PT useful for killing of cells e.g. HIV and cancer cells
 XX
 PS Claim 12; Fig 1B; 132pp; English.
 XX
 CC This is the amino acid sequence of the alpha isoform of novel
 CC human G1 protein. The sequence is deduced from an isolated skin
 CC fibroblast cDNA clone (see AAV52968). G1-alpha (also called CASH
 CC alpha, CASH being caspase homologue) and a shorter isoform, G1-beta
 CC (see AAV78904), represent 2 splice variants of the G1 protein. These
 CC G1 proteins are capable of binding to, or interacting directly or
 CC indirectly, via their N-terminal MORT modules, with MORT-1 or with
 CC MORT-binding proteins such as Mch4 (CASP-10) and MACH (CASP-8), and
 CC thereby of binding to the intracellular domain of the FAS-R
 CC receptor, to which MORT-1 binds, or of binding to the intracellular
 CC domain of the p55 tumour necrosis factor (TNF) receptor, to which
 CC TRADD binds and to which TRADD protein MORT-1 binds. Hence, they
 CC are considered as mediators or modulators of FAS-R having a role in
 CC e.g. the signalling process that is initiated by the binding of FAS
 CC ligand to FAS-R, and also having a role in the signalling process
 CC initiated by the binding of TNF to p55-R. The longer isoform also
 CC has a C-terminal caspase activity region involved in cytotoxic
 CC activity. G1 DNA (I) and polypeptide (II), vectors and fragments
 CC are used to regulate cell death or inflammatory processes. (II) is
 CC used to inhibit cell death, and its inhibitors augment/enhance the
 CC processes. (I) and (II) regulate the FAS-R ligand or TNF effect on
 CC cells carrying an FAS-R or p55-R. Tumour, HIV-infected or other
 CC diseased cells can be treated using a viral vector encoding a viral
 CC surface protein, which binds a specific cell surface receptor and a
 CC sequence encoding (II), which kills the cell. Antisense
 CC oligonucleotides, introduced using the above vector, block the
 CC expression of (II) and can also regulate the above effects. These
 CC effects can also be regulated using a vector encoding a ribozyme
 CC that interacts with a cellular mRNA encoding (II), and allows (II)
 CC expression.
 XX
 SQ Sequence 480 AA;

Query Match 100.0%; Score 2473; DB 19; Length 480;
 Best Local Similarity 100.0%; Pred. No. 4.8e-217;
 Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSAEVIHQVEALDTDEKMLFLCRDVAIDVPPNVRDLIDLRLRGKLSVGLAEALLY 60
 DB 1 MSAEVIHQVEALDTDEKMLFLCRDVAIDVPPNVRDLIDLRLRGKLSVGLAEALLY 60
 QY 61 RVRRFDLLKRLKMDRAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSLIFLMKDYM 120
 DB 61 RVRRFDLLKRLKMDRAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSLIFLMKDYM 120
 QY 121 GRGKISKEKSPDLVWELEKLNVLAPQDLLEKLNHRIIDLTKIYKQSVQAGT 180
 DB 121 GRGKISKEKSPDLVWELEKLNVLAPQDLLEKLNHRIIDLTKIYKQSVQAGT 180
 QY 181 SYRNVLAQAQSKLDPSNNFRLNHRGSKRQRLKEQLGAQOEPVKKIQSEAEFLPOSIP 240
 DB 181 SYRNVLAQAQSKLDPSNNFRLNHRGSKRQRLKEQLGAQOEPVKKIQSEAEFLPOSIP 240
 QY 241 EERYKMKSPKIGICLLIDCIGNETELLRLDTFTSGYEVQKFLHSMHGISOILGQFACMP 300
 DB 241 EERYKMKSPKIGICLLIDCIGNETELLRLDTFTSGYEVQKFLHSMHGISOILGQFACMP 300
 QY 301 EHRDYSFVCVLRGGSSQSVYGVDTQTHSLGPLHRIHRRMFMDGSCPYLAGKPKMFFIQNY 360
 DB 301 EHRDYSFVCVLRGGSSQSVYGVDTQTHSLGPLHRIHRRMFMDGSCPYLAGKPKMFFIQNY 360

QY 361 VVSEGOLENSLLEVDGPAKKNVEFKAQKRGCLCTVHREADFFWSLCTADMSLLEQSHSP 420
 DB 361 VVSEGOLENSLLEVDGPAKKNVEFKAQKRGCLCTVHREADFFWSLCTADMSLLEQSHSP 420
 QY 421 SLVLOCLSQKLRQERKRPDLDLHTELNGYMDNRSRYSAKEYYVWLOHTLRKKLILSYT 480
 DB 421 SLVLOCLSQKLRQERKRPDLDLHTELNGYMDNRSRYSAKEYYVWLOHTLRKKLILSYT 480
 RESULT 2
 AAW76631
 ID AAW76631 standard; Protein; 480 AA.
 XX
 AC AAW76631;
 XX
 DT 12-JUL-1999 (first entry)
 XX
 DE Human CFLIP-L protein.
 XX
 KW Death effector domain; human; murine; anti-apoptotic; treatment;
 KW HIV infection; autoimmune disease; FLIP protein.
 XX
 OS Homo sapiens.
 XX
 PN DE19713393-AL.
 XX
 PD 08-OCT-1998.
 XX
 PF 01-APR-1997; 97DE-1013393.
 XX
 PR 01-APR-1997; 97DE-1013393.
 XX
 PA (TSCH/) TSCHOPE J.
 PA (APOT-) APOTECH SA.
 XX
 PI Bodmer J, Burns K, French EL, Hahne M, Hoffmann K;
 PI Irmler M, Rimoldi D, Schneider P, Schroeter M, Steiner V;
 PI Thome M, Tschoepe J, Hofmann K;
 XX
 DR WPI; 1998-532710/46.
 DR N-PSDB; AAV61937.
 XX
 PT New DNA encoding for anti-apoptotic gene product - used to treat HIV
 PT infections and autoimmune diseases
 XX
 PS Claim 20; Fig 4B; 45pp; German.
 CC
 CC This invention describes novel human and mouse anti-apoptotic gene
 CC products which contain at least one death effector domain. The products
 CC of the invention are used in the treatment of HIV infections and
 CC autoimmune diseases.
 XX
 SQ Sequence 480 AA;

Query Match 99.8%; Score 2468; DB 19; Length 480;
 Best Local Similarity 99.8%; Pred. No. 1.4e-216;
 Matches 479; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSAEVIHQVEALDTDEKMLFLCRDVAIDVPPNVRDLIDLRLRGKLSVGLAEALLY 60
 DB 1 MSAEVIHQVEALDTDEKMLFLCRDVAIDVPPNVRDLIDLRLRGKLSVGLAEALLY 60
 QY 61 RVRRFDLLKRLKMDRAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSLIFLMKDYM 120
 DB 61 RVRRFDLLKRLKMDRAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSLIFLMKDYM 120
 QY 121 GRGKISKEKSPDLVWELEKLNVLAPQDLLEKLNHRIIDLTKIYKQSVQAGT 180
 DB 121 GRGKISKEKSPDLVWELEKLNVLAPQDLLEKLNHRIIDLTKIYKQSVQAGT 180
 QY 181 SYRNVLAQAQSKLDPSNNFRLNHRGSKRQRLKEQLGAQOEPVKKIQSEAEFLPOSIP 240
 DB 181 SYRNVLAQAQSKLDPSNNFRLNHRGSKRQRLKEQLGAQOEPVKKIQSEAEFLPOSIP 240

Db 181 SYRNVLAIAIQLKSDPSNNFRLHNGRSKEQRLKEQLGAQQEPYKKSIOESEAFILPQSIP 240
 QY 241 EERYKMKSPKLGICILIIIDICIGNETELLRTDTFTSLGYEVQKFLHLSMHGISOILGQFACMP 300
 Db 241 EERYKMKSPKLGICILIIIDICIGNETELLRTDTFTSLGYEVQKFLHLSMHGISOILGQFACMP 300
 QY 301 EHRDYDSFVCLVSRGGSSQSYGVQDTHSGPLPHHIRMFWMGDSCPYLAGPKMFFIIONY 360
 Db 301 EHRDYDSFVCLVSRGGSSQSYGVQDTHSGPLPHHIRMFWMGDSCPYLAGPKMFFIIONY 360
 QY 361 VYSEGQLENSLLEVDGPPAMKNVEFKAKRGKGLCTVHREADPFWSLCTADMSLLEQSHSP 420
 Db 361 VYSEGQLENSLLEVDGPPAMKNVEFKAKRGKGLCTVHREADPFWSLCTADMSLLEQSHSP 420
 QY 421 SLYLQCLSKLROERKRPLLDLHIELNGYMYDWNRSVSAKEKYVYWLQHTLRKKLILSYT 480
 Db 421 SLYLQCLSKLROERKRPLLDLHIELNGYMYDWNRSVSAKEKYVYWLQHTLRKKLILSYT 480

RESULT 3

AAW69715
 ID AAW69715 standard; Protein; 480 AA.

AC AAW69715;

DT 24-NOV-1998 (first entry)

XX Human Casper protein.

DE Casper; caspase-eight-related protein; human; apoptosis.

XX Homo sapiens.

OS WO9833883-A1.

PN 06-AUG-1998.

PD 05-FEB-1998; 98WO-US02117.

PF 05-FEB-1997; 97US-0795088.

PR (TULA-) TULARIK INC.

PI Goeddel DV, Shu H;

DR WPI; 1998-437440/37.

DR N-PSDB; AAV50436.

XX New Casper protein involved in regulation of apoptosis - used, e.g.
 PT to identify specific modulators, identify or isolate similar
 PT sequences and in gene therapy

XX Claim 1; Page 22-23; 29pp; English.

XX This is the amino acid sequence of a novel human protein,
 CC designated Casper (for caspase-eight-related protein), that is
 CC involved in regulation of apoptosis. The sequence is deduced from
 CC an isolated cDNA clone (see AAV50436). Casper protein interacts with
 CC FADD and is recruited to Fas. It also interacts with caspase-8
 CC and caspase-3, and with TRAF1 and TRAF2. A claimed isolated
 CC polypeptide comprises the full-length Casper amino acid sequence,
 CC or a fragment of at least 6 consecutive amino acid residues
 CC including at least one of residues 1-96, 1-202, 1-435, 78-480,
 CC 192-480, 390-480 or residue 360. The isolated protein, or
 CC cells that express the protein, can be used to screen for agents,
 CC e.g. antibodies or T-cell receptors, that specifically modify the
 CC binding of Casper to a target, and thus its function.

XX Sequence 480 AA;

Query Match

Best Local Similarity 99.8%; Score 2468; DB 19; Length 480;

Matches 479; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSAEVIHVEBALDTDEKEMLLFLCRDVAIDVVPNVRDLIDLIRERKLSVGDIAELLY 60
 Db 1 MSAEVIHVEBALDTDEKEMLLFLCRDVAIDVVPNVRDLIDLIRERKLSVGDIAELLY 60
 QY 61 RVRRDILKRLILKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIFLMKDYM 120
 Db 61 RVRRDILKRLILKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIFLMKDYM 120
 QY 121 GRGKISKEKSFLLDVVELEKLNIVAPDQDLLEKLNHRIIDLTKTOKYKQSVQAGT 180
 Db 121 GRGKISKEKSFLLDVVELEKLNIVAPDQDLLEKLNHRIIDLTKTOKYKQSVQAGT 180
 QY 181 SYRNVLAIAIQLKSDPSNNFRLHNGRSKEQRLKEQLGAQQEPYKKSIOESEAFILPQSIP 240
 Db 181 SYRNVLAIAIQLKSDPSNNFRLHNGRSKEQRLKEQLGAQQEPYKKSIOESEAFILPQSIP 240
 QY 241 EERYKMKSPKLGICILIIIDICIGNETELLRTDTFTSLGYEVQKFLHLSMHGISOILGQFACMP 300
 Db 241 EERYKMKSPKLGICILIIIDICIGNETELLRTDTFTSLGYEVQKFLHLSMHGISOILGQFACMP 300
 QY 301 EHRDYDSFVCLVSRGGSSQSYGVQDTHSGPLPHHIRMFWMGDSCPYLAGPKMFFIIONY 360
 Db 301 EHRDYDSFVCLVSRGGSSQSYGVQDTHSGPLPHHIRMFWMGDSCPYLAGPKMFFIIONY 360
 QY 361 VYSEGQLENSLLEVDGPPAMKNVEFKAKRGKGLCTVHREADPFWSLCTADMSLLEQSHSP 420
 Db 361 VYSEGQLENSLLEVDGPPAMKNVEFKAKRGKGLCTVHREADPFWSLCTADMSLLEQSHSP 420
 QY 421 SLYLQCLSKLROERKRPLLDLHIELNGYMYDWNRSVSAKEKYVYWLQHTLRKKLILSYT 480
 Db 421 SLYLQCLSKLROERKRPLLDLHIELNGYMYDWNRSVSAKEKYVYWLQHTLRKKLILSYT 480

RESULT 4

AAW69229
 ID AAW69229 standard; Protein; 480 AA.

AC AAW69229;

DT 16-OCT-1998 (first entry)

DE I-FLICE-1 protein.

XX I-FLICE-1; FADD like ICE protein; inhibitor; TNFR-1; Alzheimer's disease;
 KW CD-95 induced apoptosis; Parkinson's disease; rheumatoid arthritis;
 KW CNS inflammation; osteoporosis; ischaemia; polycystic kidney disease;
 KW multiple sclerosis; head injury; cancer; autoimmune disorder; therapy;
 KW viral infection; graft versus host disease; graft rejection.

OS Homo sapiens.

PN WO9831801-A1.

PD 23-JUL-1998.

PF 21-JAN-1998; 98WO-US00969.

PR 05-AUG-1997; 97US-0054800.

PR 21-JAN-1997; 97US-0034205.

XX (HUMA-) HUMAN GENOME SCI INC.

PA (UNMI) UNIV MICHIGAN.

PI Dixit VM, Gentz RL, Kenny JJ, Ni J, Rosen CA;

XX WPI; 1998-414100/35.

DR N-PSDB; AAV44806.

XX New inhibitory polypeptides of FLICE - used to develop products for
 PT treating e.g. Alzheimer's disease, sepsis, stroke, osteoporosis,
 PT cancers, autoimmune disorders, viral infection or graft rejection
 XX

PS Claim 9; Fig 1; 118pp; English.

XX This sequence is an inhibitor of Fas-ligand associated with death
 CC domain (FADD) like ICE (I-FLICE) protein, designated I-FLICE-1. The
 CC proteins can inhibit both TNFR-1 and CD-95 induced apoptosis. These are
 CC the first examples of a naturally occurring catalytically inactive
 CC caspase that can act as a dominant negative inhibitor of apoptosis. The
 CC polypeptides and agonists can be used for treating e.g. Alzheimer's
 CC disease, Parkinson's disease, rheumatoid arthritis, septic shock, sepsis,
 CC stroke, CNS inflammation, osteoporosis, ischaemia, reperfusion injury,
 CC cell death associated with cardiovascular disease, polycystic kidney
 CC disease, apoptosis of endothelial cells in cardiovascular disease,
 CC degenerative liver disease, multiple sclerosis (MS) and head injury
 CC damage. Antagonists of the polypeptides can be used for treating cancers
 CC (e.g. follicular lymphomas, carcinomas with p53 mutations,
 CC hormone-dependent tumours, and cancers of the breast, ovary, prostate,
 CC bone, liver, lung, pancreas, and spleen), autoimmune disorders
 CC (e.g. systemic lupus erythematosus, immune-related glomerulonephritis,
 CC rheumatoid arthritis), and viral infections (e.g. herpes viruses, pox
 CC viruses and adenoviruses), graft versus host disease, acute disease,
 CC acute graft rejection, and chronic graft rejection. The products can also
 CC be used for detection, diagnosis and drug screening.

XX Sequence 480 AA;

Query Match 99.8%; Score 2468; DB 19; Length 480;
 Best Local Similarity 99.8%; Pred. No. 1.4e-216;
 Matches 479; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSAEVTHQVEALDTEKEMLLFLCRDVAIDVPPNVRDLILRERKLSVGDLAELLY 60
 DB 1 MSAEVTHQVEALDTEKEMLLFLCRDVAIDVPPNVRDLILRERKLSVGDLAELLY 60
 QY 61 RVRFDLLKRLKMDRAKAVETHLLRNPHLYSDYRVLMAEIGEDLDKSDVSSLIPLMKDYM 120
 DB 61 RVRFDLLKRLKMDRAKAVETHLLRNPHLYSDYRVLMAEIGEDLDKSDVSSLIPLMKDYM 120
 QY 121 GRGKISKEKSFLLDVLVELEKLNIVAPQDLLEKLNHRIIDLTKYKIQKOSVQAGT 180
 DB 121 GRGKISKEKSFLLDVLVELEKLNIVAPQDLLEKLNHRIIDLTKYKIQKOSVQAGT 180
 QY 181 SYRNVLOAAIQSKLDPNNFRLHNGSKQRLEKQLGAQOEPVKKSIQSEAFLOPISIP 240
 DB 181 SYRNVLOAAIQSKLDPNNFRLHNGSKQRLEKQLGAQOEPVKKSIQSEAFLOPISIP 240
 QY 241 EERYKMKSKPLGICLIIDICIGNETELLRDFTFTSLGYEVQKFLHLSMHGISQILGQACMP 300
 DB 241 EERYKMKSKPLGICLIIDICIGNETELLRDFTFTSLGYEVQKFLHLSMHGISQILGQACMP 300
 QY 301 EHRDYSFVCLVSRGGSQSVYGVQDTHSGPLPLHHIRRMFMGSDCPLYLACKPKMFFIQNY 360
 DB 301 EHRDYSFVCLVSRGGSQSVYGVQDTHSGPLPLHHIRRMFMGSDCPLYLACKPKMFFIQNY 360
 QY 361 VSEGLQENSLLEVDGPAKNNVEFFKAQRGLCTVHREADFVWLSLCTADMSLLEQSHSP 420
 DB 361 VSEGLQENSLLEVDGPAKNNVEFFKAQRGLCTVHREADFVWLSLCTADMSLLEQSHSP 420
 QY 421 SLVLIQCLSQKLRQERKRLPLDLHIELNGYMYDWNRSYSAKEKYVWLQHTLRKKLILSYT 480
 DB 421 SLVLIQCLSQKLRQERKRLPLDLHIELNGYMYDWNRSYSAKEKYVWLQHTLRKKLILSYT 480

RESULT 5

AAW58578

ID AAW58578 standard; Protein: 480 AA.

XX AAW58578;

AC AAW58578;

DT 07-SEP-1998 (first entry)

XX Human FIN-1.

DE Human; FIN-1; FLICE inhibitor-1; ICE-LAP7; death effector domain; DED;

XX Human; FIN-1; FLICE inhibitor-1; ICE-LAP7; death effector domain; DED;

KW apoptosis-related protein; caspase; viral infection; cancer; tumour;
 KW diagnosis; ischaemic injury; neuro-degenerative disorder.

OS Homo sapiens.

XX EP841399-A2.

XX 13-MAY-1998.

XX 10-NOV-1997; 97EP-0309003.

XX 12-NOV-1996; 96US-0748086.

XX (SMIK) SMITHKLINE BEECHAM CORP.

XX Emery JG, Kikly K;

XX WPI; 1998-252943/23.

XX N-PSDB; AAV31375.

XX New nucleic acid encoding human apoptosis-related protein - used for
 PT diagnosis and treatment of e.g. viral infections, tumour, ischaemic
 PT injury and neuro-degenerative disorders

XX Claim 11; Page 25-27; 48pp; English.

XX The present sequence represents human FIN-1 (FLICE inhibitor-1), which is
 CC a caspase. FLICE (ICE-LAP7) is a protease of the interleukin-converting
 CC enzyme family, a protein involved in the regulation of cell death. A
 CC host cell, comprising a vector containing FIN-1 encoding DNA, can be
 CC used to produce FIN-1. The vector containing the DNA can be used for
 CC producing a cell which expresses a polypeptide by transforming or
 CC transfecting the cell with it so that the cell expresses the polypeptide
 CC encoded the human cDNA contained in the vector. The polypeptide or its
 CC antagonist can be used in the treatment of patients needing FIN-1 by
 CC in-vivo administration. Conditions which may be treated include viral
 CC infection, tumours (especially solid tumours), ischaemic injury (e.g.
 CC stroke or myocardial infarction), neurodegenerative disorders (e.g.
 CC Alzheimer's or Parkinson's disease), osteoporosis, osteoarthritis,
 CC polycystic kidney disease, chronic degenerative liver disease, acquired
 CC immunodeficiency syndrome (AIDS) and aplastic anaemia. The
 CC polynucleotides may also be used for chromosome identification.

XX Sequence 480 AA;

Query Match 99.8%; Score 2468; DB 19; Length 480;

Best Local Similarity 99.8%; Pred. No. 1.4e-216;

Matches 479; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSAEVTHQVEALDTEKEMLLFLCRDVAIDVPPNVRDLILRERKLSVGDLAELLY 60
 DB 1 MSAEVTHQVEALDTEKEMLLFLCRDVAIDVPPNVRDLILRERKLSVGDLAELLY 60
 QY 61 RVRFDLLKRLKMDRAKAVETHLLRNPHLYSDYRVLMAEIGEDLDKSDVSSLIPLMKDYM 120
 DB 61 RVRFDLLKRLKMDRAKAVETHLLRNPHLYSDYRVLMAEIGEDLDKSDVSSLIPLMKDYM 120
 QY 121 GRGKISKEKSFLLDVLVELEKLNIVAPQDLLEKLNHRIIDLTKYKIQKOSVQAGT 180
 DB 121 GRGKISKEKSFLLDVLVELEKLNIVAPQDLLEKLNHRIIDLTKYKIQKOSVQAGT 180
 QY 181 SYRNVLOAAIQSKLDPNNFRLHNGSKQRLEKQLGAQOEPVKKSIQSEAFLOPISIP 240
 DB 181 SYRNVLOAAIQSKLDPNNFRLHNGSKQRLEKQLGAQOEPVKKSIQSEAFLOPISIP 240
 QY 241 EERYKMKSKPLGICLIIDICIGNETELLRDFTFTSLGYEVQKFLHLSMHGISQILGQACMP 300
 DB 241 EERYKMKSKPLGICLIIDICIGNETELLRDFTFTSLGYEVQKFLHLSMHGISQILGQACMP 300
 QY 301 EHRDYSFVCLVSRGGSQSVYGVQDTHSGPLPLHHIRRMFMGSDCPLYLACKPKMFFIQNY 360
 DB 301 EHRDYSFVCLVSRGGSQSVYGVQDTHSGPLPLHHIRRMFMGSDCPLYLACKPKMFFIQNY 360


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OY 361 VVSEGOLENSLLEVDGPAKKNVEFKAQKRGGLCTVHREADFWLSLCTADMSLLEQSHSSP 420
DB 361 VVSEGOLENSLLEVDGPAKKNVEFKAQKRGGLCTVHREADFWLSLCTADMSLLEQSHSSP 420
OY 421 SLYLOCLSQKLRQERRRPLDLHLIELNGYMDWNSRVSAKEYVYVWLOHTLRKKLLISYT 480
DB 421 SLYLOCLSQKLRQERRRPLDLHLIELNGYMDWNSRVSAKEYVYVWLOHTLRKKLLISYT 480

RESULT 6
AAY57454
ID AAY57454 standard; Protein; 480 AA.
XX
AC AAY57454;
XX
DT 25-FEB-2000 (first entry)
XX
DE Human FLICE-like inhibitory protein long form protein sequence.
XX
KW Human; FLICE-like inhibitory protein long form; FLIP-L; FLIP-S;
KW FLICE-like inhibitory protein short form; apoptosis inhibitor;
KW arteriosclerosis; vascular wall inflammation; vascular injury;
KW Fas ligand-mediated apoptosis; atherosclerosis; transplant.
XX
OS Homo sapiens.
XX
PN W09942570-A1.
XX
PD 26-AUG-1999.
XX
PF 19-FEB-1999; 99WO-US03558.
XX
PR 20-FEB-1998; 98US-0075471.
XX
PA (SELI-) ST ELIZABETH'S MEDICAL CENT BOSTON INC.
XX
PI Walsh K;
XX
DR WPI; 1999-527469/44.
XX
DR N-PSDB; AA239040.
XX
PT Treating conditions characterized by vascular wall inflammation
XX
PS Claim 5; Page 69-71; 105pp; English.
XX
CC The present sequence represents human FLICE-like inhibitory protein long
CC form, designated FLIP-L. The present invention describes a new treatment
CC of a condition characterised by vascular wall inflammation in a subject
CC comprising administering a FLIP molecule to inhibit Fas ligand-mediated
CC apoptosis of vascular endothelial cells in the subject. The method can
CC be used to treat atherosclerosis, transplant arteriosclerosis and
CC vascular injury.
XX
SQ Sequence 480 AA;

Query Match 99.8%; Score 2468; DB 20; Length 480;
Best Local Similarity 99.8%; Pred. No. 1.4e-216;
Matches 479; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 MSAEVIHQVEEALDTDEKEMLLFLCHRDVAIDVVPVPPNRDLILRGRKLSVGDIAELLY 60
DB 1 MSAEVIHQVEEALDTDEKEMLLFLCHRDVAIDVVPVPPNRDLILRGRKLSVGDIAELLY 60
OY 61 RYRRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIFLMKDYM 120
DB 61 RYRRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIFLMKDYM 120
OY 121 GRGKISKEKSFLLDVVVELEKLNVLVAPDQLDLEKCLKNTHRIDLTKIKYKQSVQAGT 180
DB 121 GRGKISKEKSFLLDVVVELEKLNVLVAPDQLDLEKCLKNTHRIDLTKIKYKQSVQAGT 180
OY 181 SYRNVLOAAIQKSLKDPSSNFRHLNGRSKEQRLKEQGAQQEPVKKSIOESEAFLPQSIP 240
DB 181 SYRNVLOAAIQKSLKDPSSNFRHLNGRSKEQRLKEQGAQQEPVKKSIOESEAFLPQSIP 240
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DB 181 SYRNVLOAAIQKSLKDPSSNFRHLNGRSKEQRLKEQGAQQEPVKKSIOESEAFLPQSIP 240
OY 241 EERYKMKSKPLGICLIIDICIGNETELLRTDFTSLGYEVOKFLHLSMHGISOILGQFACMP 300
DB 241 EERYKMKSKPLGICLIIDICIGNETELLRTDFTSLGYEVOKFLHLSMHGISOILGQFACMP 300
OY 301 EHRDYDSFVCLVSRGSGSVYGVQDTHSGLPJHHIRRMFPMGSDSCPYLAGKPKMFFTONY 360
DB 301 EHRDYDSFVCLVSRGSGSVYGVQDTHSGLPJHHIRRMFPMGSDSCPYLAGKPKMFFTONY 360
OY 361 VVSEGOLENSLLEVDGPAKKNVEFKAQKRGGLCTVHREADFWLSLCTADMSLLEQSHSSP 420
DB 361 VVSEGOLENSLLEVDGPAKKNVEFKAQKRGGLCTVHREADFWLSLCTADMSLLEQSHSSP 420
OY 421 SLYLOCLSQKLRQERRRPLDLHLIELNGYMDWNSRVSAKEYVYVWLOHTLRKKLLISYT 480
DB 421 SLYLOCLSQKLRQERRRPLDLHLIELNGYMDWNSRVSAKEYVYVWLOHTLRKKLLISYT 480

RESULT 7
AAY05787
ID AAY05787 standard; Protein; 480 AA.
XX
AC AAY05787;
XX
DT 02-AUG-1999 (first entry)
XX
DE Human MACH related inducer of toxicity MRIT alpha 1.
XX
KW MRIT alpha 1; MACH related inducer of toxicity; human; apoptosis;
KW pro-apoptotic; cancer; autoimmune disease; infection; angiogenesis;
KW atherosclerosis; neurodegenerative disease; Alzheimer's disease;
KW Parkinson's disease; retinitis pigmentosa; stroke; AIDS;
KW aplastic anaemia; myocardial infarction; therapy.
XX
OS Homo sapiens.
XX
FH Key
FT Region 1..165
FT /note= "death effector domain homology region"
FT Region 301..480
FT /note= "caspase homology region"
FT Active-site 358..362
FT Region 140..178
FT /note= "Bcl-2 homology region"
FT Region 196..228
FT /note= "Bcl-2 homology region"
FT Region 258..289
FT /note= "Bcl-2 homology region"
FT Region 299..350
FT /note= "Bcl-2 homology region"
FT Region 356..397
FT /note= "Bcl-2 homology region"
XX
PN W09918230-A2.
XX
PD 15-APR-1999.
XX
PF 07-OCT-1998; 98WO-US21132.
XX
PR 07-OCT-1997; 97US-0946226.
XX
PA (UNIW ) UNIV WASHINGTON.
XX
PI Chaudhary PM;
XX
DR WPI; 1999-277275/23.
DR N-PSDB; AA235508.
XX
PT Identifying regulators of MACH-related inducer of toxicity
XX
XX Example 1; Fig 1F; 78pp; English.
XX
```

CC The present sequence represents novel human MACH-related inducer
CC of toxicity (MRIT) isoform MRIT alpha 1, a CED-4 homologue that
CC interacts simultaneously with caspases and Bcl-2 family
CC polypeptides, and which has pro-apoptotic activity. Multiple
CC isoforms of MRIT have been identified, some of which function
CC to induce caspase dependent apoptosis in mammalian cells, e.g.
CC MRIT alpha 1 and MRIT beta 1 (see AY05789), while others have
CC anti-apoptotic activity, e.g. MRIT alpha 2 (see AY05788). MRIT
CC alpha 1 includes an N-terminal death effector domain and a
CC C-terminal caspase homology domain, but is not a cysteine protease.
CC Selective enhancers and inhibitors of MRIT apoptotic activity can
CC be identified and used to treat diseases mediated by the dysfunction
CC of programmed cell death or proliferation. A cell accumulation
CC disorder such as cancer, autoimmune disease, viral infection,
CC angiogenesis or atherosclerosis is treated by administering an agent
CC that selectively enhances MRIT apoptotic activity, thereby inducing
CC apoptosis in a subject. A disorder of cell loss, such as a
CC neurodegenerative disorder, including Alzheimer's disease,
CC Parkinson's disease, retinitis pigmentosa, stroke, aplastic
CC anaemia, myocardial infarction or AIDS can be treated by
CC administering an agent that selectively inhibits MRIT apoptotic
CC activity.
XX
XX
SQ Sequence 480 AA;

Query Match 99.8%; Score 2468; DB 20; Length 480;
Best Local Similarity 99.8%; Pred. No. 1.4e-216;
Matches 479; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSAEVIHQVEALDTDEKEMLLFLCRDVAIDVPPNVRDLDDLRLRERKLSVGLDAELLY 60
Db 1 MSAEVIHQVEALDTDEKEMLLFLCRDVAIDVPPNVRDLDDLRLRERKLSVGLDAELLY 60
QY 61 RVRRFDLLKRLTKMDRAKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSLIFLMKDYM 120
Db 61 RVRRFDLLKRLTKMDRAKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSLIFLMKDYM 120
QY 121 GRGKISREKSFLLDWVELEKLNLYAPDQLDLLEKLNHRLDKTKIQYKQSVQAGT 180
Db 121 GRGKISREKSFLLDWVELEKLNLYAPDQLDLLEKLNHRLDKTKIQYKQSVQAGT 180
QY 181 SYRNVLAQAIQKSLKDPNSNFRNLHNGRSKEORLEQGAQEPVKKSIOESEAFLPQISIP 240
Db 181 SYRNVLAQAIQKSLKDPNSNFRNLHNGRSKEORLEQGAQEPVKKSIOESEAFLPQISIP 240
QY 241 EERYKMKSKPLGICLIIDICIGNETELLRLDTFTSLGYEVQKFLHLSMHGISQILGQFACMP 300
Db 241 EERYKMKSKPLGICLIIDICIGNETELLRLDTFTSLGYEVQKFLHLSMHGISQILGQFACMP 300
QY 301 EHRDYDSPCVLVSRRGGSQVYGVDOHSGPLHHRMFMDGSDCPYLAKGPKMFFIQNY 360
Db 301 EHRDYDSPCVLVSRRGGSQVYGVDOHSGPLHHRMFMDGSDCPYLAKGPKMFFIQNY 360
QY 361 VYSEGLSNSLLEVDGPKMKNVEFKAKRGICLVTHREADFWSICTADMSLLQSHSP 420
Db 361 VYSEGLSNSLLEVDGPKMKNVEFKAKRGICLVTHREADFWSICTADMSLLQSHSP 420
QY 421 SLYLQCLSQKLRQERKRLPLDLHIELNGYMYDWSNRVSAKEKYVWQLHTLRKKLLISYT 480
Db 421 SLYLQCLSQKLRQERKRLPLDLHIELNGYMYDWSNRVSAKEKYVWQLHTLRKKLLISYT 480

RESULT 8
AAB03960
ID AAB03960 standard; Protein; 480 AA.
XX
AC AAB03960;
XX
DT 26-FEB-2001 (first entry)
XX
DE FLICE-like inhibitor protein (Genbank Accession No. 2253679).
XX
KW Chimeric protein; fusion protein; FLICE like inhibitor protein;

KW FLIP; Fas; TNF; apoptosis; caspase-8; ligand; T cell; thymocyte;
KW tumour specific antigen; immune response; therapy; prophylaxis;
KW diagnosis; HIV; human immunodeficiency syndrome; AIDS;
KW acquired immune deficiency syndrome; human.
OS Homo sapiens.
OS Synthetic.
XX W0200059935-A1.
XX 12-OCT-2000.
XX 05-APR-2000; 2000WO-US09002.
XX 05-APR-1999; 99US-0127867.
XX 06-APR-1999; 99US-0128021.
XX (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
XX (PAYA/) PAYA C.
XX (ALGE/) ALGECIRAS-SCHMINICH A.
XX Paya C, Algeciras-schminich A;
XX WPI; 2000-664988/64.
XX Fusion polypeptide useful for inhibiting ligand-induced apoptosis,
XX comprises portion of anti-apoptotic polypeptide linked to a transport
XX group
XX Disclosure; Page 79-81; 89pp; English.
XX A chimeric group or fusion peptide which comprises a portion of an
XX anti-apoptotic polypeptide which inhibits apoptosis of lymphocytes in
XX combination with a transport group is described. The transport group
XX is capable of transporting the chimeric group or fusion peptide
XX across the cell membrane. The anti-apoptotic polypeptide is FLICE-like
XX inhibitor protein (FLIP) which inhibits Fas and TNF mediated apoptosis
XX by inhibiting binding of caspase-8 to the Fas receptor complex, thus
XX shutting off the downstream Fas signalling pathway. The chimeric group
XX and fusion peptide are useful for inhibiting ligand-induced apoptosis
XX by bringing them into contact with T cells. The chimeric group is
XX useful for expanding T cells in vitro e.g. T cells specific for
XX particular antigens such as tumour-specific antigen, for enhancing
XX immune response and to inhibit the apoptosis of chronically activated
XX T cells e.g. activated CD4⁺ T cells in HIV infected patients. The
XX chimeric group is also useful for therapeutic, prophylactic or
XX diagnosis of intracellular delivery of small molecules and
XX macromolecules such as anti-apoptotic polypeptides and nucleic
XX acids encoding such polypeptides.
SQ Sequence 480 AA;

Query Match 99.8%; Score 2468; DB 21; Length 480;
Best Local Similarity 99.8%; Pred. No. 1.4e-216;
Matches 479; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSAEVIHQVEALDTDEKEMLLFLCRDVAIDVPPNVRDLDDLRLRERKLSVGLDAELLY 60
Db 1 MSAEVIHQVEALDTDEKEMLLFLCRDVAIDVPPNVRDLDDLRLRERKLSVGLDAELLY 60
QY 61 RVRRFDLLKRLTKMDRAKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSLIFLMKDYM 120
Db 61 RVRRFDLLKRLTKMDRAKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSLIFLMKDYM 120
QY 121 GRGKISREKSFLLDWVELEKLNLYAPDQLDLLEKLNHRLDKTKIQYKQSVQAGT 180
Db 121 GRGKISREKSFLLDWVELEKLNLYAPDQLDLLEKLNHRLDKTKIQYKQSVQAGT 180
QY 181 SYRNVLAQAIQKSLKDPNSNFRNLHNGRSKEORLEQGAQEPVKKSIOESEAFLPQISIP 240
Db 181 SYRNVLAQAIQKSLKDPNSNFRNLHNGRSKEORLEQGAQEPVKKSIOESEAFLPQISIP 240
QY 241 EERYKMKSKPLGICLIIDICIGNETELLRLDTFTSLGYEVQKFLHLSMHGISQILGQFACMP 300

|||||
241 EERYKMSKPLGICLLIICIGNETELLRTFTSLGYEVQKFLHLSMHGSIQLGQACMP 300
301 EHRDYSFVCLVLSRGGSSQSVYGVDTQTHSGLPLHHRMFMGDSQPCYLAGKPKMFFIQNY 360
301 EHRDYSFVCLVLSRGGSSQSVYGVDTQTHSGLPLHHRMFMGDSQPCYLAGKPKMFFIQNY 360
361 VVSEGOLENSLLEVDGPAKKNVEFKAKRGLCTVHREADFWLSLCTADMSLLEQSHSP 420
361 VVSEGOLENSLLEVDGPAKKNVEFKAKRGLCTVHREADFWLSLCTADMSLLEQSHSP 420
421 SLYLQCLSKLROERKRPDLHLIELNGYMDNSRVSAREKYYVWLQHTLRKKLLSYT 480
421 SLYLQCLSKLROERKRPDLHLIELNGYMDNSRVSAREKYYVWLQHTLRKKLLSYT 480

RESULT 9
AAY67418
ID AAY67418 standard; Protein; 480 AA.
AC AAY67418;
XX
DT 12-MAY-2000 (first entry)
XX
DE Usurin-alpha polypeptide.
XX
KW Usurin-alpha; death effector domain; DED; prodomain; usurin-beta;
KW usurin-gamma; procaspase-8; CD95; apoptosis; cancer; immunosuppressive;
KW caspase; cytostatic; antiParkinsonian; antidiabetic.
XX
OS Homo sapiens.
XX
PN WO200003023-A1.
XX
PD 20-JAN-2000.
XX
PF 07-JUL-1999; 99WO-CA00615.
XX
PR 08-JUL-1998; 98US-0092005.
XX
PA (MERI) MERCK FROSST CANADA INC.
XX
PI Nicholson DW, Rasper DM, Xanthoudakis S, Roy S;
XX
PS WPI; 2000-160929/14.
XX
DR N-PSDB; AAZ56987.
XX
PT Novel recombinant DNA molecules and polypeptides for treating apoptosis
PT mediated diseases e.g. autoimmune diabetes, cancer and Parkinson's
XX disease
PS Claim 6; Fig 9B; 69pp; English.
XX
XX
XX The invention provides recombinant nucleic acid molecules encoding
CC usurin-alpha (lacking the first death effector domain (DED) or its
CC prodomain), usurin-beta or usurin-gamma. Usurin polypeptides are
CC useful for in vitro and in vivo identification of usurin-procaspase-8
CC interaction inhibitor. Usurin is useful as modulator of the sensitivity
CC of cells to CD95(Fas/Apo-1) mediated apoptosis. Modulation of apoptosis
CC is useful for treating diseases like autoimmune diabetes, cancer and
CC Parkinson's disease. Activators and inhibitors of usurin-procaspase-8
CC interaction are also useful for treating various diseases mediated by
CC apoptosis. Usurin provides an attractive model for modulating caspase
CC activation. Sensitivity of cells bearing CD95(Fas/Apo-1) receptor can
CC be regulated at several levels in the presence of usurin, conferring
CC resistance to Fas-ligand cell death. The present sequence represents
CC the usurin-alpha polypeptide.
XX
SQ Sequence 480 AA;
Query Match 99.8%; Score 2468; DB 21; Length 480;
Best Local Similarity 99.8%; Pred. No. 1.4e-216;
Matches 479; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSAEVIHQVEEALDTDEKEMLLFLCRDAIDVVPVPPNVRDLDTLRERKLSVGDLAELLY 60
Db |||||
1 MSAEVIHQVEEALDTDEKEMLLFLCRDAIDVVPVPPNVRDLDTLRERKLSVGDLAELLY 60
QY 61 RYRFDLLKRIILKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIFLMKDYM 120
Db |||||
61 RYRFDLLKRIILKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIFLMKDYM 120
QY 121 GRGKTSKESKSFIDLVDVVELEKLNVPDQDLLEKCLKNTHRIDLTKTKIKYKOSVOGAGT 180
Db |||||
121 GRGKTSKESKSFIDLVDVVELEKLNVPDQDLLEKCLKNTHRIDLTKTKIKYKOSVOGAGT 180
QY 181 SYRNVLQAAIQKSLKDPSSNFRLNHNGRSKEQRLKEQLGAQOQEPVKKSIQSEAFLOPSIP 240
Db |||||
181 SYRNVLQAAIQKSLKDPSSNFRLNHNGRSKEQRLKEQLGAQOQEPVKKSIQSEAFLOPSIP 240
QY 241 EERYKMSKPLGICLLIICIGNETELLRTFTSLGYEVQKFLHLSMHGSIQLGQACMP 300
Db |||||
241 EERYKMSKPLGICLLIICIGNETELLRTFTSLGYEVQKFLHLSMHGSIQLGQACMP 300
QY 301 EHRDYSFVCLVLSRGGSSQSVYGVDTQTHSGLPLHHRMFMGDSQPCYLAGKPKMFFIQNY 360
Db |||||
301 EHRDYSFVCLVLSRGGSSQSVYGVDTQTHSGLPLHHRMFMGDSQPCYLAGKPKMFFIQNY 360
QY 361 VVSEGOLENSLLEVDGPAKKNVEFKAKRGLCTVHREADFWLSLCTADMSLLEQSHSP 420
Db |||||
361 VVSEGOLENSLLEVDGPAKKNVEFKAKRGLCTVHREADFWLSLCTADMSLLEQSHSP 420
QY 421 SLYLQCLSKLROERKRPDLHLIELNGYMDNSRVSAREKYYVWLQHTLRKKLLSYT 480
Db |||||
421 SLYLQCLSKLROERKRPDLHLIELNGYMDNSRVSAREKYYVWLQHTLRKKLLSYT 480

RESULT 10
AAY57606
ID AAY57606 standard; Protein; 480 AA.
AC AAY57606;
XX
DT 10-MAR-2000 (first entry)
XX
DE Human apoptosis associated protein HAPOP-1.
XX
KW Human; apoptosis associated protein; HAPOP; diagnosis; cytostatic;
KW antiarteriosclerotic; antiarthritic; hepatotropic; apoptosis regulator;
KW cell proliferative disorder; atherosclerosis; arteriosclerosis; cancer;
KW immune disorder; rheumatoid arthritis; systemic lupus erythematosus;
KW reproductive disorder; tumour; gastrointestinal disorder; cirrhosis;
KW colitis; hepatitis; pancreatitis.
XX
OS Homo sapiens.
XX
PN WO958692-A2.
XX
PD 18-NOV-1999.
XX
PF 11-MAY-1999; 99WO-US10386.
XX
PR 13-MAY-1998; 98US-0078402.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Hillman JL, Corley NC, Guegler KJ, Patterson C, Baughn M;
XX WPI; 2000-062303/05.
XX N-PSDB; AAZ47926.
XX
XX New protein for diagnosing, treating or preventing disorders associated
PT with increased or decreased apoptosis
XX
PS Claim 1; Page 70-71; 81pp; English.
XX

CC The present sequence represents a human apoptosis associated protein
 CC designated HAPOP-1. HAPOP proteins are apoptosis regulators which have
 CC antiarteriosclerotic, cytostatic, antiarthritic and hepatotropic
 CC activity. A pharmaceutical composition comprising HAPOP in conjunction
 CC with a carrier, a purified antagonist of HAPOP, vectors and agonists of
 CC HAPOP, are administered for diagnosing, treating or preventing disorders
 CC associated with increased or decreased apoptosis, e.g. cell proliferative
 CC disorders such as arteriosclerosis, arteriosclerosis and cancers; immune
 CC disorders such as rheumatoid arthritis, systemic lupus erythematosus;
 CC reproductive disorders such as prostate cancer, endometrial and ovarian
 CC tumours; and gastrointestinal disorders such as cirrhosis, colitis,
 CC hepatitis and pancreatitis. The polynucleotides encoding HAPOP proteins
 CC may be useful to detect and quantitate expression of HAPOP genes which
 CC are correlated with diseases and are also useful to detect differences
 CC in the chromosomal location due to translocation, inversion etc., among
 CC normal, carrier, or affected individuals. The combination of the
 CC therapeutic agents may act synergistically to effect the treatment or
 CC prevention of various disorders providing improved efficacy with lower
 CC dosages of each agent and thus reducing the potential for adverse side
 CC effects.

xx Sequence 480 AA;

Query Match 99.8%; Score 2468; DB 21; Length 480;
 Best Local Similarity 99.8%; Pred. No. 1.4e-216;
 Matches 479; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSAEVIHQVEALDTDEKEMLLFLCRDVAIDVPPNVRDLDDLRLRERKLSVGLDAELLY 60
 Db 1 MSAEVIHQVEALDTDEKEMLLFLCRDVAIDVPPNVRDLDDLRLRERKLSVGLDAELLY 60
 Qy 61 RVRFDLLKRLTKMDRAVETHLRNPHLVSDYRVLMAEIGEDLDKSDVSLIFLMDY 120
 Db 61 RVRFDLLKRLTKMDRAVETHLRNPHLVSDYRVLMAEIGEDLDKSDVSLIFLMDY 120
 Qy 121 GRGKISKEKSFLLDVLWELEKLNVLAPDQLDLLEKLNHRLDKTKIQKQSVQAGT 180
 Db 121 GRGKISKEKSFLLDVLWELEKLNVLAPDQLDLLEKLNHRLDKTKIQKQSVQAGT 180
 Qy 181 SYRNVLAQAIQKSLKDPNNPRLNHRGSKRQRLKEQLGAQOEPVKKSTQSEAFLPQ 240
 Db 181 SYRNVLAQAIQKSLKDPNNPRLNHRGSKRQRLKEQLGAQOEPVKKSTQSEAFLPQ 240
 Qy 241 EERYKMSKPLGICLLIDICIGNETELLRLDTFTSLGYEVQKFLHSLMHGISOILQFAC 300
 Db 241 EERYKMSKPLGICLLIDICIGNETELLRLDTFTSLGYEVQKFLHSLMHGISOILQFAC 300
 Qy 301 EHRDYDSFVCLVSRGGSQSVYVDQTHSGPLHHRMFMDGSCPYLAGPKPMFFIQNY 360
 Db 301 EHRDYDSFVCLVSRGGSQSVYVDQTHSGPLHHRMFMDGSCPYLAGPKPMFFIQNY 360
 Qy 361 VVSEGLSENSLLEVDGPMKNNVEFKAKRGKLCVTHREADFWLSLCTADMSLLBQSHSP 420
 Db 361 VVSEGLSENSLLEVDGPMKNNVEFKAKRGKLCVTHREADFWLSLCTADMSLLBQSHSP 420
 Qy 421 SLYLQCLISQKLRQERKPLDLHLIELNGYMDWNSRVSACEKYVWLQHTLRKKLLISYT 480
 Db 421 SLYLQCLISQKLRQERKPLDLHLIELNGYMDWNSRVSACEKYVWLQHTLRKKLLISYT 480

RESULT 11

ABB09294

ID ABB09294 standard; Protein; 480 AA.

AC ABB09294;

DT 15-JUL-2002 (first entry)

DE Human FLIP-c protein SEQ ID NO:11.

KW Human; FLIP-c; caspase 8 dominant negative regulator; antiinflammatory;
 KW anti-tumour; FLIP-c inhibitor; apoptosis; antisense gene therapy;
 KW phosphorothioate; antisense modulation; infection; inflammation;

KW tumour.

OS Homo sapiens.

PN WO200224717-A1.

XX 28-MAR-2002.

XX 14-SEP-2001; 2001WO-US28732.

XX 20-SEP-2000; 2000US-0666269.

(ISIS-) ISIS PHARM INC.

XX Ackermann EJ, Bennett CF, Zhang H, Watt AT, Ricketts W, Dean NM;
 WPI: 2002-401983/43.

DR N-PSDB: ABL52333.

XX Novel antisense compound that hybridizes and inhibits nucleic acid
 encoding a natural dominant negative regulator of caspase 8, FLIP-c,
 useful for preventing or delaying infection, inflammation or tumor
 formation

XX Example 13; Page 118-120; 154pp; English.

CC The present invention describes a compound (I) 8-50 nucleobases in length
 targeted to a nucleic acid molecule (II) encoding a natural dominant
 negative regulator of caspase 8, FLIP-c, where (I) specifically
 hybridises with and inhibits expression of the protein, or specifically
 hybridises with at least an 8-nucleobase portion of an active site on
 (II). (I) has antiinflammatory and anti-tumour activities. (I) is an
 inhibitor of FLIP-c expression, a modulator of apoptosis and can be used
 in antisense gene therapy. (I) is useful for inhibiting the expression of
 FLIP-c in cells or tissues, and for treating an animal having a disease
 or condition associated with FLIP-c. (I) is also useful for modulating
 apoptosis in a cell, where a caspase such as caspase 8, caspase 3 or
 caspase 7 is activated, and the FLIP-c is the long form of FLIP-c. (I) is
 also useful for diagnostics, therapeutics, prophylaxis, as research
 reagents and kits, for distinguishing functions of various members of a
 biological pathway, and in antisense gene therapy. (I) is also useful
 prophylactically, e.g., to prevent or delay infection, inflammation or
 tumour formation. The present sequence represents human FLIP-c as given
 in an example from the present invention.

xx Sequence 480 AA;

Query Match 99.8%; Score 2468; DB 23; Length 480;
 Best Local Similarity 99.8%; Pred. No. 1.4e-216;
 Matches 479; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSAEVIHQVEALDTDEKEMLLFLCRDVAIDVPPNVRDLDDLRLRERKLSVGLDAELLY 60
 Db 1 MSAEVIHQVEALDTDEKEMLLFLCRDVAIDVPPNVRDLDDLRLRERKLSVGLDAELLY 60
 Qy 61 RVRFDLLKRLTKMDRAVETHLRNPHLVSDYRVLMAEIGEDLDKSDVSLIFLMDY 120
 Db 61 RVRFDLLKRLTKMDRAVETHLRNPHLVSDYRVLMAEIGEDLDKSDVSLIFLMDY 120
 Qy 121 GRGKISKEKSFLLDVLWELEKLNVLAPDQLDLLEKLNHRLDKTKIQKQSVQAGT 180
 Db 121 GRGKISKEKSFLLDVLWELEKLNVLAPDQLDLLEKLNHRLDKTKIQKQSVQAGT 180
 Qy 181 SYRNVLAQAIQKSLKDPNNPRLNHRGSKRQRLKEQLGAQOEPVKKSTQSEAFLPQ 240
 Db 181 SYRNVLAQAIQKSLKDPNNPRLNHRGSKRQRLKEQLGAQOEPVKKSTQSEAFLPQ 240
 Qy 241 EERYKMSKPLGICLLIDICIGNETELLRLDTFTSLGYEVQKFLHSLMHGISOILQFAC 300
 Db 241 EERYKMSKPLGICLLIDICIGNETELLRLDTFTSLGYEVQKFLHSLMHGISOILQFAC 300
 Qy 301 EHRDYDSFVCLVSRGGSQSVYVDQTHSGPLHHRMFMDGSCPYLAGPKPMFFIQNY 360
 Db 301 EHRDYDSFVCLVSRGGSQSVYVDQTHSGPLHHRMFMDGSCPYLAGPKPMFFIQNY 360

Db 301 EHRDYDSFVCLVSRGSGSVYGVDTQTHSGLPLHHIRRMFMGDCSPYLAGKPKMFFIQNY 360
QY 361 VVSEGOLESLSLEVDGPAKKNVEFKAQKRGCTVHREADFFWSLCTADMSLLEQSHSSP 420
Db 361 VVSEGOLESLSLEVDGPAKKNVEFKAQKRGCTVHREADFFWSLCTADMSLLEQSHSSP 420
QY 421 SLYLQCLSQKLRQERKRPDLHLHIELNGYMYDWSRVSAREKYYVWLQHTLRKKLILSYT 480
Db 421 SLYLQCLSQKLRQERKRPDLHLHIELNGYMYDWSRVSAREKYYVWLQHTLRKKLILSYT 480

RESULT 12

AA03964
ID AAB03964 standard; Protein; 491 AA.

XX AAB03964;
XX
DT 26-FEB-2001 (first entry)
XX

DE FLIP with detectable peptide tag.

XX Chimeric protein; fusion protein; FLICE like inhibitor protein;
KW FLIP; Fas; TNF; apoptosis; caspase-8; ligand; T cell; thymocyte;
KW tumour specific antigen; immune response; therapy; prophylaxis;
KW diagnosis; HIV; human immunodeficiency syndrome; AIDS;
XX acquired immune deficiency syndrome; human.

XX Homo sapiens.
OS Synthetic.
XX
PN WO200059935-A1.

XX 12-OCT-2000.

PF 05-APR-2000; 2000WO-US09002.

PR 05-APR-1999; 99US-0127867.

PR 06-APR-1999; 99US-0128021.

XX (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.

PA (PAYA/) PAYA C.

PA (ALGE/) ALGECIRAS-SCHMINICH A.

XX Paya C, Algeclras-schminich A;

XX WPI; 2000-664988/64.

XX N-PSDB; AAA54301.

XX Fusion polypeptide useful for inhibiting ligand-induced apoptosis,
PT comprises portion of anti-apoptotic polypeptide linked to a transport
PT group

PS Disclosure; Page 84-85; 89pp; English.

XX A chimeric group or fusion peptide which comprises a portion of an
CC anti-apoptotic polypeptide which inhibits apoptosis of lymphocytes in
CC combination with a transport group is described. The transport group
CC is capable of transporting the chimeric group or fusion peptide
CC across the cell membrane. The anti-apoptotic polypeptide is FLICE-like
CC inhibitor protein (FLIP) which inhibits Fas and TNF mediated apoptosis
CC by inhibiting binding of Caspase-8 to the Fas receptor complex, thus
CC shutting off the downstream Fas signalling pathway. The chimeric group
CC and fusion peptide are useful for inhibiting ligand-induced apoptosis
CC by bringing them into contact with T cells. The chimeric group is
CC useful for expanding T cells in vitro e.g. T cells specific for
CC particular antigens such as tumour-specific antigen, for enhancing
CC immune response and to inhibit the apoptosis of chronically activated
CC T cells e.g. activated CD4+ T cells in HIV infected patients. The
CC chimeric group is also useful for therapeutic, prophylactic or
CC diagnosis of intracellular delivery of small molecules and
CC macromolecules such as anti-apoptotic polypeptides and nucleic
CC acids encoding such polypeptides.

XX

SQ Sequence 491 AA;

Query Match 99.8%; Score 2468; DB 21; Length 491;
Best Local Similarity 99.8%; Pred. No. 1.4e-216;
Matches 479; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSAEVIHQVEEALDTEDEKMLFLCRDVAIDVVPVPPNVDLTLRERGLSVGDLAELLY 60
Db 12 MSAEVIHQVEEALDTEDEKMLFLCRDVAIDVVPVPPNVDLTLRERGLSVGDLAELLY 71

QY 61 RYRRFDLLKRIKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLLFLMKDYM 120
Db 72 RYRRFDLLKRIKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLLFLMKDYM 131

QY 121 GRGKISKEKSFLLDVVELEKLNIVAPDQLDLLEKCLKNHRIHIDKTKIOKYKQSVGAGT 180
Db 132 GRGKISKEKSFLLDVVELEKLNIVAPDQLDLLEKCLKNHRIHIDKTKIOKYKQSVGAGT 191

QY 181 SYRNVLQAAIQKSLKDPNSNFRHLNGRSKEQRLKEQLGAQOEVPVKSIQSEAFLPQSIP 240
Db 192 SYRNVLQAAIQKSLKDPNSNFRHLNGRSKEQRLKEQLGAQOEVPVKSIQSEAFLPQSIP 251

QY 241 EERYKMKSPGLGICLIIDICIGNETELLRTFTSLGYEVQKFLHLSMHGISOILGQACMP 300
Db 252 EERYKMKSPGLGICLIIDICIGNETELLRTFTSLGYEVQKFLHLSMHGISOILGQACMP 311

QY 301 EHRDYDSFVCLVSRGSGSVYGVDTQTHSGLPLHHIRRMFMGDCSPYLAGKPKMFFIQNY 360
Db 312 EHRDYDSFVCLVSRGSGSVYGVDTQTHSGLPLHHIRRMFMGDCSPYLAGKPKMFFIQNY 371

QY 361 VVSEGOLESLSLEVDGPAKKNVEFKAQKRGCTVHREADFFWSLCTADMSLLEQSHSSP 420
Db 372 VVSEGOLESLSLEVDGPAKKNVEFKAQKRGCTVHREADFFWSLCTADMSLLEQSHSSP 431

QY 421 SLYLQCLSQKLRQERKRPDLHLHIELNGYMYDWSRVSAREKYYVWLQHTLRKKLILSYT 480
Db 432 SLYLQCLSQKLRQERKRPDLHLHIELNGYMYDWSRVSAREKYYVWLQHTLRKKLILSYT 491

RESULT 13

AAW76625

ID AAW76625 standard; protein; 479 AA.

XX AAW76625;

XX 12-JUL-1999 (first entry)

DE Human FLIP protein fragment containing death effector domain.

XX Death effector domain; human; murine; anti-apoptotic; treatment;
KW HIV infection; autoimmune disease; FLIP protein.

XX Homo sapiens.

XX DE19713393-A1.

XX 08-OCT-1998.

XX 01-APR-1997; 97DE-1013393.

XX 01-APR-1997; 97DE-1013393.

XX (TSCCH/) TSCCHOPP J.

XX (APOI-) APOTECH SA.

XX Bodmer J, Burns K, French EL, Hahne M, Hoffmann K;

PI Irmiler M, Rimoldi D, Schneider P, Schroeter M, Steiner V;

XX Thome M, Tschoep J, Hofmann K;

DR WPI; 1998-532710/46.

XX New DNA encoding for anti-apoptotic gene product - used to treat HIV
PT infections and autoimmune diseases

XX PS Disclosure; Fig 3; 45pp; German.

XX CC This invention describes novel human and mouse anti-apoptotic gene

XX CC products which contain at least one death effector domain. The products

XX CC of the invention are used in the treatment of HIV infections and

XX CC autoimmune diseases.

XX SQ Sequence 479 AA;

Query Match 98.5%; Score 2435.5; DB 19; Length 479;

Best Local Similarity 99.08; Pred. No. 1.3e-213; Indels 1; Gaps 1;

Matches 475; Conservative 1; Mismatches 3;

Qy 1 MSAEVIHQVEALDTDEKEMLLFLCRDVAIDVPPNVRDLIDLRLERKLSVGLAEALLY 60

Db 1 MSAEVIHQVEALDTDEKEMLLFLCRDVAIDVPPNVRDLIDLRLERKLSVGLAEALLY 59

Qy 61 RVRFRDILLKRLKMDRAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIPLMKDYM 120

Db 60 RVRFRDILLKRLKMDRAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIPLMKDYM 119

Qy 121 GRGKISKEKSFLLVVELEKLNVLAPDQLDLLEKLNHRIIDLTKTIQYKQSVQAGT 180

Db 120 GRGKISKEKSFLLVVELEKLNVLAPDQLDLLEKLNHRIIDLTKTIQYKQSVQAGT 179

Qy 181 SYRNVLAQAIOKSLKDPNSNFRNLHNGRSKEQRLKEQLGAQOEPVKKSIQSEAFLPQISIP 240

Db 180 SYRNVLAQAIOKSLKDPNSNFRNLHNGRSKEQRLKEQLGAQOEPVKKSIQSEAFLPQISIP 239

Qy 241 EERYKMSKPIGICLLIDCIGNETELLRLDTFTSLGYEVQKFLHLSMHGISOILGOFACMP 300

Db 240 EERYKMSKPIGICLLIDCIGNETELLRLDTFTSLGYEVQKFLHLSMHGISOILGOFACMP 299

Qy 301 EHRDYDSFVCLVSRGGSQSVYGVQDQTHSGPLHRIHRRMFMDGSCPYLAGKPKMFFIIONY 360

Db 300 EHRDYDSFVCLVSRGGSQSVYGVQDQTHSGPLHRIHRRMFMDGSCPYLAGKPKMFFIIONY 359

Qy 361 VVSEGLQENSLLEVDGPKMKNVEFKAQKRGCLCTVHREADPFWSLCTADMSLLBQSHSSP 420

Db 360 VVSEGLQENSLLEVDGPKMKNVEFKAQKRGCLCTVHREADPFWSLCTADMSLLBQSHSSP 419

Qy 421 SLYLQCLSQKLRQERKRPDLIDLHTELNGYMDNRSVSAKEYVWVWQHTLRKKLILSYT 480

Db 420 SLYLQCLSQKLRQERKRPDLIDLHTELNGYMDNRSVSAKEYVWVWQHTLRKKLILSYT 479

RESULT 14

AAY59414

ID AAY59414 standard; Protein; 480 AA.

XX AC AAY59414;

XX DT 21-MAR-2000 (first entry)

XX DE Human CLARP protein sequence.

XX KW RICK; human; RIP-like interacting CLARP kinase; apoptosis regulator; ARC;

XX KW caspase-8; caspase-10; CD95 signalling; apoptosis signalling pathway;

XX KW CIDE-A; CIDE-B; DREP-1; diagnosis; cell growth; apoptosis dysregulation;

XX KW gene therapy; cardiac disorder; cancer; neurodegenerative disorder; AIDS;

XX KW aplastic anaemia; ischaemic injury; toxin-induced liver disease;

XX KW CLARP.

XX OS Homo sapiens.

XX PN WO9955134-A2.

XX PD 04-NOV-1999.

XX PF 27-APR-1999; 99WO-US09183.

XX PR 27-APR-1998; 98US-0069023.

XX FA (UNMI) UNIV MICHIGAN.

XX PI Nunez G, Inohara N, Koseki T;

XX DR WPI; 2000-072163/06.

XX DR N-PSDB; AAZ48769.

XX PT Compositions for identifying apoptosis signalling pathway inhibitors

XX PS useful for treating diseases

XX Example 10; Fig 21b; 93pp; English.

XX This sequence is the human CLARP protein. The invention relates to

CC the human RICK (RIP-like interacting CLARP kinase) protein. The RICK

CC protein acts as a positive regulator of apoptosis, potentiating apoptosis

CC induced by caspase-8 and caspase-10 during CD95 signalling. The invention

CC provides methods for identifying apoptosis signalling pathway inhibitors

CC and activators, and methods and compositions for screening compounds

CC which will modulate the interactions of the various compositions

CC identified: ARC, RICK, and the CIDE family of activators (CIDE-A, CIDE-B

CC and DREP-1). RICK is useful in screening assays for agents, useful in the

CC diagnosis, prognosis or treatment of disease associated with excess cell

CC growth and dysregulation of apoptosis. Complexes containing RICK and

CC CLARP can be used in drug screening assays to identify inhibitor

CC molecules blocking CD95-mediated apoptosis. Overexpression of ARC in an

CC in vitro cell system can be used to identify inhibitors of the enzymatic

CC activity of caspase-8. Identification of ARC-like inhibitory compounds

CC may be useful for gene therapy treatment of disease with increased cell

CC death in muscle tissue and cardiac disorders. Therapeutic compositions of

CC CIDEs can be used to treat e.g. cancer, AIDS, neurodegenerative

CC disorders, aplastic anaemia, ischaemic injury, and toxin-induced liver

CC disease. Anti-RICK antibodies can be used as reagents for the preparation

CC or affinity chromatography media, and for diagnostically measuring RICK

CC levels. A specific inhibitor of an essential step in the biochemistry of

CC apoptosis is needed. RICK interaction with intracellular factors such as

CC CLARP and FADD appears to be essential for apoptosis, inhibitors of RICK

CC binding to intracellular apoptosis factors are potential drug candidates.

XX SQ Sequence 480 AA;

Query Match 97.5%; Score 2412; DB 21; Length 480;

Best Local Similarity 97.7%; Pred. No. 1.8e-211;

Matches 469; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MSAEVIHQVEALDTDEKEMLLFLCRDVAIDVPPNVRDLIDLRLERKLSVGLAEALLY 60

Db 1 MSAEVIHQVEALDTDEKEMLLFLCRDVAIDVPPNVRDLIDLRLERKLSVGLAEALLY 60

Qy 61 RVRFRDILLKRLKMDRAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIPLMKDYM 120

Db 61 RVRFRDILLKRLKMDRAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIPLMKDYM 120

Qy 121 GRGKISKEKSFLLVVELEKLNVLAPDQLDLLEKLNHRIIDLTKTIQYKQSVQAGT 180

Db 121 GRGKISKEKSFLLVVELEKLNVLAPDQLDLLEKLNHRIIDLTKTIQYKQSVQAGT 180

Qy 181 SYRNVLAQAIOKSLKDPNSNFRNLHNGRSKEQRLKEQLGAQOEPVKKSIQSEAFLPQISIP 240

Db 181 SYRNVLAQAIOKSLKDPNSNFRNLHNGRSKEQRLKEQLGAQOEPVKKSIQSEAFLPQISIP 240

Qy 241 EERYKMSKPIGICLLIDCIGNETELLRLDTFTSLGYEVQKFLHLSMHGISOILGOFACMP 300

Db 241 EERYKMSKPIGICLLIDCIGNETELLRLDTFTSLGYEVQKFLHLSMHGISOILGOFACMP 300

Qy 301 EHRDYDSFVCLVSRGGSQSVYGVQDQTHSGPLHRIHRRMFMDGSCPYLAGKPKMFFIIONY 360

Db 301 EHRDYDSFVCLVSRGGSQSVYGVQDQTHSGPLHRIHRRMFMDGSCPYLAGKPKMFFIIONY 360

Qy 361 VVSEGLQENSLLEVDGPKMKNVEFKAQKRGCLCTVHREADPFWSLCTADMSLLBQSHSSP 420

Db 361 VVSEGLQENSLLEVDGPKMKNVEFKAQKRGCLCTVHREADPFWSLCTADMSLLBQSHSSP 420

QY 421 SLYLQCLSQKLRQERKRPDLHLIELNGYMYDWSRVSAKEKYVWVWLTQTLRKLILSYT 480
Db 421 SLYLQCLSQKLRQERKRPDLHLIELNGYMYDWSRVSAKEKYVWVWLTQTLRKLILSYT 480

RESULT 15

AAW90107
ID AAW90107 standard; Protein; 445 AA.

XX AC AAW90107;

XX DT 12-APR-1999 (first entry)

XX DE Human FLAME-1 protein.

XX KW FLAME-1; FADD-like apoptotic/anti-apoptotic molecule; human;

XX KW apoptosis; HIV; infection; Alzheimer's disease; cancer; therapy.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Domain 1..341

FT /note= "p39 subunit, specifically claimed in Claim 3"

FT Domain 342..445

FT /note= "p12 subunit, specifically claimed in Claim 4"

FT Region 5..71

FT /note= "FADD-DED homology A"

FT Region 90..168

FT /note= "FADD-DED homology B"

FT Region 197..445

FT /note= "caspase-domain homology region"

FT Active-site 322..327

FT /note= "active site motif"

FT Cleavage-site 338..342

FT /note= "caspase cleavage site, generating p39 and p12"

XX W09852963-A1.

XX 26-NOV-1998.

XX 20-MAY-1998; 98WO-US10200.

XX 20-MAY-1997; 97US-0859167.

XX (UYJE-) UNIV JEFFERSON THOMAS.

XX Alnemri ES;

XX WPI; 1999-045296/04.

XX N-PSDB; AAV74136.

XX New isolated FADD-like anti-apoptotic molecules - used to develop
XX apoptotic and anti-apoptotic agents for treating, e.g. HIV
XX infection, Alzheimer's disease or neoplastic conditions
XX Claim 2; Page 39-40; 68pp; English.
XX This is the amino acid sequence of human FLAME-1, or FADD-like
XX apoptotic/anti-apoptotic molecule 1. FLAME-1 is a novel
XX anti-apoptotic protein that interacts specifically with FADD, Mch4,
XX Mch5 and FLAME-2. It is recruited to the Fas receptor complex and
XX can abrogate Fas/TNF-induced apoptosis upon expression in
XX Fas/TNF-sensitive MCF-7 cells. Despite having a caspase domain-like
XX region, it does not have caspase activity. The amino acid sequence
XX of FLAME-1 was deduced from the nucleotide sequence (see AAV74136) of
XX a Jurkat cell-derived cDNA clone. Host cells, recombinant vectors,
XX and methods of using FLAME-1 to identify substrates, activators or
XX inhibitors of FLAME-1 are provided. FLAME-1, FLAME-2 (see AAW90108)
XX and agonists can be used to inhibit apoptosis, e.g. for treating
XX HIV infection or Alzheimer's disease. Inhibitors can be used as

CC apoptotic agents.

XX Sequence 445 AA;

Query Match 91.6%; Score 2265.5; DB 20; Length 445;
Best Local Similarity 92.5%; Pred. No. 3.9e-198;
Matches 444; Conservative 1; Mismatches 0; Indels 35; Gaps 1;

QY 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPNPVNRDLTLRERKLSVGDIAELLY 60

Db 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPNPVNRDLTLRERKLSVGDIAELLY 60

QY 61 RVRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVYVMAETGEDLDKSDVSSLIFLMKDYM 120

Db 61 RVRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVYVMAETGEDLDKSDVSSLIFLMKDYM 120

QY 121 GRGKISKEKSFLLVVELEKLNLVAPDQLDLEKLNHRIHRIIDLTKIYKQSVQAGT 180

Db 121 GRGKISKEKSFLLVVELEKLNLVAPDQLDLEKLNHRIHRIIDLTKIYKQSVQAGT 180

QY 181 SYRNVLQAAIQKSLKDPSPNNFRLHNGRSKEQLKEQLGAQQEPVKKSIQSEAFLOPSIP 240

Db 181 SYRNVLQAAIQKSLKDPSPNNFRLHNGRSKEQLKEQLGAQQEPVKKSIQSEAFLOPSIP 240

QY 241 EERYKMKSPGLGICLIIDICIGNETELLRLDTFTSLGYEVQKFLHLSMHGISOILGQFACMP 300

Db 206 EERYKMKSPGLGICLIIDICIGNETELLRLDTFTSLGYEVQKFLHLSMHGISOILGQFACMP 265

QY 301 EHRDYDSFVCLVSRGSGSVYGVDTQTHSGPLPHHIRMFMGSDSCPYLAGKPKMFFTONY 360

Db 266 EHRDYDSFVCLVSRGSGSVYGVDTQTHSGPLPHHIRMFMGSDSCPYLAGKPKMFFTONY 325

QY 361 VVSEGOLENSLLEVDGPAKKNVEFKAQKRGCTVHREADFFWSLCTADMSLLEQSHSP 420

Db 326 VVSEGOLENSLLEVDGPAKKNVEFKAQKRGCTVHREADFFWSLCTADMSLLEQSHSP 385

QY 421 SLYLQCLSQKLRQERKRPDLHLIELNGYMYDWSRVSAKEKYVWVWLTQTLRKLILSYT 480

Db 386 SLYLQCLSQKLRQERKRPDLHLIELNGYMYDWSRVSAKEKYVWVWLTQTLRKLILSYT 445

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Job time : 84.8531 secs

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OM protein - protein search, using sw model

Run on: August 13, 2003, 16:43:55 ; Search time 49.9857 Seconds
(without alignments)
1257.990 Million cell updates/sec

Title: US-09-380-546A-2
Perfect score: 2473
Sequence: 1 MSAAVHQVEALDTEREM.....EKYYVLQTLKKLILSYT 480

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 492763 seqs, 131003257 residues

Total number of hits satisfying chosen parameters: 492763

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications AA.*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2468	99.8	480	9 US-09-861-270-2	Sequence 2, Appli
2	2468	99.8	480	9 US-09-410-194-11	Sequence 11, Appl
3	2468	99.8	480	9 US-09-410-194-17	Sequence 17, Appl
4	2468	99.8	480	11 US-09-009-893-2	Sequence 2, Appli
5	2468	99.8	480	11 US-09-471-749-1	Sequence 1, Appli
6	1993	80.6	391	15 US-10-103-313-318	Sequence 318, App
7	1993	80.6	391	15 US-10-115-928-37	Sequence 37, Appl
8	1630	65.9	348	11 US-09-009-893-6	Sequence 6, Appli
9	1580	63.9	481	9 US-09-410-194-12	Sequence 12, Appl
10	1580	63.9	481	9 US-09-410-194-19	Sequence 19, Appl
11	1568.5	63.4	484	14 US-10-005-921-2	Sequence 2, Appli
12	1007	40.7	221	9 US-09-410-194-15	Sequence 15, Appl
13	1007	40.7	221	9 US-09-410-194-22	Sequence 22, Appl
14	465	18.8	93	9 US-09-864-761-36370	Sequence 36370, A
15	410	16.6	479	9 US-09-410-194-20	Sequence 20, Appl

Sequence 3, Appli
Sequence 35073, A
Sequence 4, Appli
Sequence 27, Appl
Sequence 2, Appli
Sequence 21, Appli
Sequence 2, Appli
Sequence 33, Appli
Sequence 4, Appli
Sequence 24, Appli
Sequence 1, Appli
Sequence 4, Appli
Sequence 2, Appli
Sequence 23, Appli
Sequence 48, Appl
Sequence 48, Appl
Sequence 5, Appli
Sequence 21, Appl
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Sequence 48728, A
Sequence 7, Appli
Sequence 4, Appli
Sequence 108, App
Sequence 202, App
Sequence 3, Appli
Sequence 3, Appli
Sequence 12, Appl
Sequence 36, Appl
Sequence 52, Appl
Sequence 28, Appl

16 408.5 16.5 478 11 US-09-009-893-3
17 389 15.7 76 9 US-09-864-761-35073
18 381.5 15.4 496 9 US-09-952-768-4
19 370.5 15.0 476 10 US-09-954-697-27
20 323.5 13.0 521 9 US-09-962-834A-2
21 323.5 13.1 571 9 US-09-410-194-21
22 318.5 12.9 479 9 US-09-952-768-2
23 318.5 12.9 479 10 US-09-954-697-33
24 318.5 12.9 479 11 US-09-009-893-4
25 248 10.0 182 9 US-09-410-194-24
26 246.5 10.0 286 9 US-09-862-915-1
27 239 9.7 171 9 US-09-410-194-4
28 234 9.5 169 9 US-09-410-194-2
29 234 9.5 188 9 US-09-410-194-23
30 204 8.2 250 10 US-09-989-903-48
31 204 8.2 250 15 US-10-068-564-48
32 198.5 8.0 169 9 US-09-410-194-5
33 192 7.8 293 10 US-09-954-697-21
34 192 7.8 293 15 US-10-171-077-5
35 191.5 7.7 167 9 US-09-864-761-48728
36 185.5 7.5 177 9 US-09-410-194-7
37 184 7.4 277 9 US-09-895-263-4
38 184 7.4 277 15 US-10-214-932-108
39 184 7.4 277 15 US-10-207-655-202
40 181 7.3 264 14 US-10-103-448-3
41 181 7.3 264 14 US-10-108-929-3
42 181 7.3 277 10 US-09-954-697-12
43 180 7.3 300 10 US-09-954-697-36
44 177.5 7.2 452 12 US-10-205-219-52
45 177 7.2 451 10 US-09-888-243-28

ALIGNMENTS

RESULT 1

US-09-861-270-2
; Sequence 2, Application US/09861270
; Patent No. US20020052474A1
; GENERAL INFORMATION:
; APPLICANT: Sul, Hong-Bing
; TITLE OF INVENTION: Regulators of Apoptosis
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Science & Technology Law Group
; STREET: 75 Denise Drive
; CITY: Hillsborough
; STATE: California
; COUNTRY: USA
; ZIP: 94010
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/861,270
; FILING DATE: 18-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/795,088
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 343-4341
; TELEFAX: (650) 343-4342
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 480 amino acids

; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-861-270-2

Query Match 99.8%; Score 2468; DB 9; Length 480;
Best Local Similarity 99.8%; Pred. No. 1.4e-218;
Matches 479; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSAEVHQVERALDTDEKEMLLFLCRDVAIDVVPNNVRDLDDLRLRERKLSVGDLAELLY 60
DB 1 MSAEVHQVERALDTDEKEMLLFLCRDVAIDVVPNNVRDLDDLRLRERKLSVGDLAELLY 60
QY 61 RVRFDLLKRLKMDRAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIPLMKDYM 120
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QY 121 GRGKISKEKSFLLDVELEKLNVLAPQDLLEKLNHRIHIDLTCTKIYKQSVQAGT 180
DB 121 GRGKISKEKSFLLDVELEKLNVLAPQDLLEKLNHRIHIDLTCTKIYKQSVQAGT 180
QY 181 SYRNVLAQAIOKSLKDPNNFRLHNGRSKEORLKEQLGAQOEPVKYSIOSEAFLOPISIP 240
DB 181 SYRNVLAQAIOKSLKDPNNFRLHNGRSKEORLKEQLGAQOEPVKYSIOSEAFLOPISIP 240
QY 241 EERYKMKSPKLGICLIIDICIGNETELLRTDTFTSLGYEVQKPLHLSMHGISOILGQFACMP 300
DB 241 EERYKMKSPKLGICLIIDICIGNETELLRTDTFTSLGYEVQKPLHLSMHGISOILGQFACMP 300
QY 301 EHRDYDFVCVLSVRSQSQSVYGVDTQTHSGPLHRIHRRMFMDGSCPYLAGPKMFFIYQNY 360
DB 301 EHRDYDFVCVLSVRSQSQSVYGVDTQTHSGPLHRIHRRMFMDGSCPYLAGPKMFFIYQNY 360
QY 361 VVSEGOLENSLLEVDGPKMKNVEFKAKRGCLCTVHREADFFWSLCTADMSLLEQSHSSP 420
DB 361 VVSEGOLENSLLEVDGPKMKNVEFKAKRGCLCTVHREADFFWSLCTADMSLLEQSHSSP 420
QY 421 SLYLQCLSQKLRQERKRPDLDLHIELNGYMDWNSRVSAREKYYVWLQHTLRKKLLISYT 480
DB 421 SLYLQCLSQKLRQERKRPDLDLHIELNGYMDWNSRVSAREKYYVWLQHTLRKKLLISYT 480

RESULT 2
US-09-410-194-11
; Sequence 11, Application US/09410194
; Patent No. US20020095030A1
; GENERAL INFORMATION:
; APPLICANT: Tschopp, Jurg
; APPLICANT: Thome, Margot
; APPLICANT: Burns, Kimberly
; APPLICANT: Irmeler, Marten
; APPLICANT: Hahne, Michael
; APPLICANT: Schroter, Michael
; APPLICANT: Schneider, Pascal
; APPLICANT: Bodmer, Jean-Luc
; APPLICANT: Hofmann, Kay
; APPLICANT: French, E. Lars
; APPLICANT: Rimoldi, Donata
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
; FILE REFERENCE: 11141-002001
; CURRENT APPLICATION NUMBER: US/09/410,194
; CURRENT FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: PCT/EP98/01857
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 480

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-410-194-11
Query Match 99.8%; Score 2468; DB 9; Length 480;
Best Local Similarity 99.8%; Pred. No. 1.4e-218;
Matches 479; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSAEVHQVERALDTDEKEMLLFLCRDVAIDVVPNNVRDLDDLRLRERKLSVGDLAELLY 60
DB 1 MSAEVHQVERALDTDEKEMLLFLCRDVAIDVVPNNVRDLDDLRLRERKLSVGDLAELLY 60
QY 61 RVRFDLLKRLKMDRAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIPLMKDYM 120
DB 61 RVRFDLLKRLKMDRAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIPLMKDYM 120
QY 121 GRGKISKEKSFLLDVELEKLNVLAPQDLLEKLNHRIHIDLTCTKIYKQSVQAGT 180
DB 121 GRGKISKEKSFLLDVELEKLNVLAPQDLLEKLNHRIHIDLTCTKIYKQSVQAGT 180
QY 181 SYRNVLAQAIOKSLKDPNNFRLHNGRSKEORLKEQLGAQOEPVKYSIOSEAFLOPISIP 240
DB 181 SYRNVLAQAIOKSLKDPNNFRLHNGRSKEORLKEQLGAQOEPVKYSIOSEAFLOPISIP 240
QY 241 EERYKMKSPKLGICLIIDICIGNETELLRTDTFTSLGYEVQKPLHLSMHGISOILGQFACMP 300
DB 241 EERYKMKSPKLGICLIIDICIGNETELLRTDTFTSLGYEVQKPLHLSMHGISOILGQFACMP 300
QY 301 EHRDYDFVCVLSVRSQSQSVYGVDTQTHSGPLHRIHRRMFMDGSCPYLAGPKMFFIYQNY 360
DB 301 EHRDYDFVCVLSVRSQSQSVYGVDTQTHSGPLHRIHRRMFMDGSCPYLAGPKMFFIYQNY 360
QY 361 VVSEGOLENSLLEVDGPKMKNVEFKAKRGCLCTVHREADFFWSLCTADMSLLEQSHSSP 420
DB 361 VVSEGOLENSLLEVDGPKMKNVEFKAKRGCLCTVHREADFFWSLCTADMSLLEQSHSSP 420
QY 421 SLYLQCLSQKLRQERKRPDLDLHIELNGYMDWNSRVSAREKYYVWLQHTLRKKLLISYT 480
DB 421 SLYLQCLSQKLRQERKRPDLDLHIELNGYMDWNSRVSAREKYYVWLQHTLRKKLLISYT 480

RESULT 3
US-09-410-194-17
; Sequence 17, Application US/09410194
; Patent No. US20020095030A1
; GENERAL INFORMATION:
; APPLICANT: Tschopp, Jurg
; APPLICANT: Thome, Margot
; APPLICANT: Burns, Kimberly
; APPLICANT: Irmeler, Marten
; APPLICANT: Hahne, Michael
; APPLICANT: Schroter, Michael
; APPLICANT: Schneider, Pascal
; APPLICANT: Bodmer, Jean-Luc
; APPLICANT: Steiner, Veronique
; APPLICANT: Rimoldi, Donata
; APPLICANT: Hofmann, Kay
; APPLICANT: French, E. Lars
; TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
; FILE REFERENCE: 11141-002001
; CURRENT APPLICATION NUMBER: US/09/410,194
; CURRENT FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: PCT/EP98/01857
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-410-194-17

Query Match 99.8%; Score 2468; DB 9; Length 480;
Best Local Similarity 99.8%; Pred. No. 1.4e-218;
Matches 479; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLDIRRERKLSVGDIAELLY 60
DB 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLDIRRERKLSVGDIAELLY 60
QY 61 RVRREFLLKRIILKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIIFLMKDYM 120
DB 61 RVRREFLLKRIILKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIIFLMKDYM 120
QY 121 GRGKISKESFSLDVLVVELEKLNVAPODLDLLEKLNHRIIDLTCTVHREADFWSLCTADMSLLEQSHSSP 420
DB 121 GRGKISKESFSLDVLVVELEKLNVAPODLDLLEKLNHRIIDLTCTVHREADFWSLCTADMSLLEQSHSSP 420
QY 181 SYRNVLQAAIQSLKDPNSNFRHLNGRSKEQRLKEQLGAQOQEPVKKSIOESEAFLPQSIP 240
DB 181 SYRNVLQAAIQSLKDPNSNFRHLNGRSKEQRLKEQLGAQOQEPVKKSIOESEAFLPQSIP 240
QY 241 EERYKMSKPLGICLIIDICIGNETELLRTFTSLGYEVOKFLHLSMHGISOILGQFACMP 300
DB 241 EERYKMSKPLGICLIIDICIGNETELLRTFTSLGYEVOKFLHLSMHGISOILGQFACMP 300
QY 301 EHRDYSFVCLVSRGSGSVYGVQDTHSGLPLHHIRRMFMGDSQPYLAGPKMFFIQNY 360
DB 301 EHRDYSFVCLVSRGSGSVYGVQDTHSGLPLHHIRRMFMGDSQPYLAGPKMFFIQNY 360
QY 361 VVSEGOLESLSLEVDGPAMKNVEFKAQKRGCTVHREADFWSLCTADMSLLEQSHSSP 420
DB 361 VVSEGOLESLSLEVDGPAMKNVEFKAQKRGCTVHREADFWSLCTADMSLLEQSHSSP 420
QY 421 SLYLQCLSKLQKRRRPLDLHLIELNGYMDWNSRVSAREKYYVWLQHTLRKKLILSYT 480
DB 421 SLYLQCLSKLQKRRRPLDLHLIELNGYMDWNSRVSAREKYYVWLQHTLRKKLILSYT 480

RESULT 4
US-09-009-893-2
Sequence 2, Application US/09009893
Publication No. US20030087339A1
GENERAL INFORMATION:
APPLICANT: NI, JIAN
APPLICANT: ROSEN, CRAIG A.
APPLICANT: DIXIT, VISHVA M.
APPLICANT: GENTZ, REINER L.
APPLICANT: KENNY, JOSEPH J.
TITLE OF INVENTION: I-FLICE, A NOVEL INHIBITOR OF TUMOR.
TITLE OF INVENTION: NECROSIS FACTOR RECEPTOR-1 AND CD-95 INDUCED APOPTOSIS
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: US
ZIP: 20005
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,893
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,205
FILING DATE: 21-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/054,800
FILING DATE: 03-AUG-1997

ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0970002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 480 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-009-893-2

Query Match 99.8%; Score 2468; DB 11; Length 480;
Best Local Similarity 99.8%; Pred. No. 1.4e-218;
Matches 479; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLDIRRERKLSVGDIAELLY 60
DB 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLDIRRERKLSVGDIAELLY 60
QY 61 RVRREFLLKRIILKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIIFLMKDYM 120
DB 61 RVRREFLLKRIILKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIIFLMKDYM 120
QY 121 GRGKISKESFSLDVLVVELEKLNVAPODLDLLEKLNHRIIDLTCTVHREADFWSLCTADMSLLEQSHSSP 420
DB 121 GRGKISKESFSLDVLVVELEKLNVAPODLDLLEKLNHRIIDLTCTVHREADFWSLCTADMSLLEQSHSSP 420
QY 181 SYRNVLQAAIQSLKDPNSNFRHLNGRSKEQRLKEQLGAQOQEPVKKSIOESEAFLPQSIP 240
DB 181 SYRNVLQAAIQSLKDPNSNFRHLNGRSKEQRLKEQLGAQOQEPVKKSIOESEAFLPQSIP 240
QY 241 EERYKMSKPLGICLIIDICIGNETELLRTFTSLGYEVOKFLHLSMHGISOILGQFACMP 300
DB 241 EERYKMSKPLGICLIIDICIGNETELLRTFTSLGYEVOKFLHLSMHGISOILGQFACMP 300
QY 301 EHRDYSFVCLVSRGSGSVYGVQDTHSGLPLHHIRRMFMGDSQPYLAGPKMFFIQNY 360
DB 301 EHRDYSFVCLVSRGSGSVYGVQDTHSGLPLHHIRRMFMGDSQPYLAGPKMFFIQNY 360
QY 361 VVSEGOLESLSLEVDGPAMKNVEFKAQKRGCTVHREADFWSLCTADMSLLEQSHSSP 420
DB 361 VVSEGOLESLSLEVDGPAMKNVEFKAQKRGCTVHREADFWSLCTADMSLLEQSHSSP 420
QY 421 SLYLQCLSKLQKRRRPLDLHLIELNGYMDWNSRVSAREKYYVWLQHTLRKKLILSYT 480
DB 421 SLYLQCLSKLQKRRRPLDLHLIELNGYMDWNSRVSAREKYYVWLQHTLRKKLILSYT 480

RESULT 5
US-09-471-749-1
Sequence 1, Application US/09471749
Publication No. US20030124113A1
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Patterson, Chandra
APPLICANT: Baughn, Mariah
TITLE OF INVENTION: HUMAN APOPTOSIS ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette

QY 95 VLMABIGEDLDKSDVSSLIIFLMKDYMGKISKEKSFIDLVLVVELEKLNLVAPDQDLLEK 154
Db 6 VLMABIGEDLDKSDVSSLIIFLMKDYMGKISKEKSFIDLVLVVELEKLNLVAPDQDLLEK 65
QY 155 CLKNIHRIDLTKIQKYKOSVQAGTSYRNVLQAAIOKSLKDPNSNFRHLNGRSKEQRLK 214
Db 66 CLKNIHRIDLTKIQKYKOSVQAGTSYRNVLQAAIOKSLKDPNSNFRHLNGRSKEQRLK 125
QY 215 EQLGAQOQPVKKSIOSEAFIPQSIPEERYKMKSPGLGICLIIDICIGNETELLRTFTSL 274
Db 126 EQLGAQOQPVKKSIOSEAFIPQSIPEERYKMKSPGLGICLIIDICIGNETELLRTFTSL 185
QY 275 GVEVOKFHLMSHGISQILGOFACMPHEDYDSFVCLVSRGGSQSVGYVDQTHSGPLPH 334
Db 186 GVEVOKFHLMSHGISQILGOFACMPHEDYDSFVCLVSRGGSQSVGYVDQTHSGPLPH 245
QY 335 HIRRMFGDSCPYLAGKPKMFIQNYVSEGOLENSLLEVDGPAKNVFEKAKRGGLCT 394
Db 246 HIRRMFGDSCPYLAGKPKMFIQNYVSEGOLENSLLEVDGPAKNVFEKAKRGGLCT 305
QY 395 VHRADFFWSLCTADMSLLEQSHSSPSLYLQCLSQKLRQERKRLPLDLHLIELNGYMDWN 454
Db 306 VHRADFFWSLCTADMSLLEQSHSSPSLYLQCLSQKLRQERKRLPLDLHLIELNGYMDWN 365
QY 455 SRVSAKERYWLOHTLRKKLILSYT 480
Db 366 SRVSAKERYWLOHTLRKKLILSYT 391

RESULT 8

US-09-009-893-6
; Sequence 6, Application US/09009893
; Publication No. US20030087339A1
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: ROSEN, CRAIG A.
; APPLICANT: DIXIT, VISHVA M.
; APPLICANT: GENTZ, REINER L.
; APPLICANT: KENNY, JOSEPH J.
; TITLE OF INVENTION: I-FLICE, A NOVEL INHIBITOR OF TUMOR
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: US
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/009,893
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,205
; FILING DATE: 21-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/054,800
; FILING DATE: 05-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0970002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 348 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-009-893-6
Query Match 65.9%; Score 1630; DB 11; Length 348;
Best Local Similarity 93.8%; Pred. No. 1.2e-141;
Matches 318; Conservative 3; Mismatches 0; Indels 18; Gaps 1;
QY 97 MABIGEDLDKSDVSSLIIFLMKDYMGKISKEKSFIDLVLVVELEKLNLVAPDQDLLEKCL 156
Db 1 MAEIGEDLDKSDVSSLIIFLMKDYMGKISKEKSFIDLVLVVELEKLNLVAPDQDLLEKCL 60
QY 157 KNIHRIDLTKIQKYKOSVQAGTSYRNVLQAAIOKSLKDPNSNFRHLNGRSKEQRLKEQ 216
Db 61 KNIHRIDLTKIQKYKOSVQAGTSYRNVLQAAIOKSLKDPNSNFR----- 106
QY 217 LGAQOQPVKKSIOSEAFIPQSIPEERYKMKSPGLGICLIIDICIGNETELLRTFTSLGY 276
Db 107 ----EPPYKKSIOSEAFIPQSIPEERYKMKSPGLGICLIIDICIGNETELLRTFTSLGY 162
QY 277 EVOKFHLMSHGISQILGOFACMPHEDYDSFVCLVSRGGSQSVGYVDQTHSGPLPHHI 336
Db 163 EVOKFHLMSHGISQILGOFACMPHEDYDSFVCLVSRGGSQSVGYVDQTHSGPLPHHI 222
QY 337 RRMFGDSCPYLAGKPKMFIQNYVSEGOLENSLLEVDGPAKNVFEKAKRGGLCTVH 396
Db 223 RRMFGDSCPYLAGKPKMFIQNYVSDGQLEDSLLEVDGPAKNVFEKAKRGGLCTVH 321
QY 397 READFFWSLCTADMSLLEQSHSSPSLYLQCLSQKLRQER 435
Db 283 READFFWSLCTADMSLLEQSHSSPSLYLQCLSQKLRQER 321

RESULT 9

US-09-410-194-12
; Sequence 12, Application US/09410194
; Patent No. US20020095030A1
; GENERAL INFORMATION:
; APPLICANT: Tschopp, Jurg
; APPLICANT: Thome, Margot
; APPLICANT: Burns, Kimberly
; APPLICANT: Immler, Marten
; APPLICANT: Hahne, Michael
; APPLICANT: Schroter, Michael
; APPLICANT: Schneider, Pascal
; APPLICANT: Bodmer, Jean- Luc
; APPLICANT: Steiner, Veronique
; APPLICANT: Rimoldi, Donata
; APPLICANT: Hofmann, Ray
; APPLICANT: French, E. Lars
; TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
; FILE REFERENCE: 11141-002001
; CURRENT APPLICATION NUMBER: US/09/410,194
; CURRENT FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: PCT/EP98/01857
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 481
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-410-194-12

Query Match 63.9%; Score 1580; DB 9; Length 481;
Best Local Similarity 66.9%; Pred. No. 8e-137;
Matches 322; Conservative 56; Mismatches 97; Indels 6; Gaps 4;

Db 126 DTGKTKAKDSFLLVVELEKLNLDVAPDQDLLEKLNHRIDLTNKTIOKYQSSOG 185
QY 178 ACTSYRNVLQAAIQK-SLKDPNNFRLHNGRSKEQRLKEQLGAQOEPVKKTSQESAEFLP 236
Db 186 A-RSNMNTLQASLPKLSIK---YNSRLQNGRSKEPFEYRDSQRTLVTKTSIQESGAFLP 241
QY 237 QSIPEPYKMKSKPLGICLIIDICIGNETELLRDFTTSLGVEYQKFLHLSMHGSIQLQOF 296
Db 242 PHIREETRMQSKPLGICLIIDICIGNTKYLOETFTSLGYHIQLFLPKSHDITQIVRY 301
QY 297 ACMPEHRDYDFVCLVSRGSGSVYGVDOETHSLPLHHIRRMFMGDCPYLAGPKMFF 356
Db 302 ASMAHQDYDFACVLSVSGSQSMGRDQVHSGFSLDHVKNNFTGDCPCSLRGPKLFF 361
QY 357 IQNYVYSEGLENSLLEVDGPKMKNVEFKAKRGKLCVTHREADPFWISCTADMSSLEQS 416
Db 362 IQNYESLSQLEDSS-LEVDPGSIKNVDSKPLQPRCHTTHPEADIFWISCTADVSHLEKP 420
QY 417 HSPSLYQLCSLQKLRQERKRLDLDHIELNGYMTDWSRVSAKYYVWLQHTLRKKLI 476
Db 421 SSSSVYLQKLSQQLKGRRRPLVDLHVLMQVYAWNSGVSSKEKYSLSLQHTLRKKLI 480
QY 477 LSYT 480
Db 481 LAPT 484

RESULT 12
US-09-410-194-15
; Sequence 15, Application US/09410194
; Patent No. US20020095030A1

; GENERAL INFORMATION:
; APPLICANT: Tschopp, Jurg
; APPLICANT: Thome, Margot
; APPLICANT: Burns, Kimberly
; APPLICANT: Irmier, Marten
; APPLICANT: Hahne, Michael
; APPLICANT: Schroter, Michael
; APPLICANT: Schneider, Pascal
; APPLICANT: Bodmer, Jean- Luc
; APPLICANT: Steiner, Veronique
; APPLICANT: Rimoldi, Donata
; APPLICANT: Hofmann, Kay
; APPLICANT: French, E. Lars

; TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
; FILE REFERENCE: 11141-002001
; CURRENT APPLICATION NUMBER: US/09/410,194
; CURRENT FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: PCT/EP98/01857
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-410-194-15

Query Match 40.7%; Score 1007; DB 9; Length 221;
Best Local Similarity 99.5%; Pred. No. 1.4e-84;
Matches 202; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSAEVIHVEEALDTDEKEMLLFLCRDVAIDVVPNNVRDLDIRERKLSVGDLAELLY 60
Db 1 MSAEVIHVEEALDTDEKEMLLFLCRDVAIDVVPNNVRDLDIRERKLSVGDLAELLY 60
QY 61 RYRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIFLMKDYM 120
Db 61 RYRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIFLMKDYM 120

QY 121 GRGKISKEKSFLLVVELEKLNLDVAPDQDLLEKLNHRIDLTNKTIOKYKOSVOGACT 180
Db 121 GRGKISKEKSFLLVVELEKLNLDVAPDQDLLEKLNHRIDLTNKTIOKYKOSVOGACT 180
QY 181 SYRNVLQAAIQKSLKDPSSNNFRL 203
Db 181 SYRNVLQAAIQKSLKDPSSNNFRL 203

RESULT 13
US-09-410-194-22
; Sequence 22, Application US/09410194
; Patent No. US20020095030A1

; GENERAL INFORMATION:
; APPLICANT: Tschopp, Jurg
; APPLICANT: Thome, Margot
; APPLICANT: Burns, Kimberly
; APPLICANT: Irmier, Marten
; APPLICANT: Hahne, Michael
; APPLICANT: Schroter, Michael
; APPLICANT: Schneider, Pascal
; APPLICANT: Bodmer, Jean- Luc
; APPLICANT: Steiner, Veronique
; APPLICANT: Rimoldi, Donata
; APPLICANT: Hofmann, Kay
; APPLICANT: French, E. Lars

; TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
; FILE REFERENCE: 11141-002001
; CURRENT APPLICATION NUMBER: US/09/410,194
; CURRENT FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: PCT/EP98/01857
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-410-194-22

Query Match 40.7%; Score 1007; DB 9; Length 221;
Best Local Similarity 99.5%; Pred. No. 1.4e-84;
Matches 202; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSAEVIHVEEALDTDEKEMLLFLCRDVAIDVVPNNVRDLDIRERKLSVGDLAELLY 60
Db 1 MSAEVIHVEEALDTDEKEMLLFLCRDVAIDVVPNNVRDLDIRERKLSVGDLAELLY 60
QY 61 RYRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIFLMKDYM 120
Db 61 RYRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIFLMKDYM 120
QY 121 GRGKISKEKSFLLVVELEKLNLDVAPDQDLLEKLNHRIDLTNKTIOKYKOSVOGACT 180
Db 121 GRGKISKEKSFLLVVELEKLNLDVAPDQDLLEKLNHRIDLTNKTIOKYKOSVOGACT 180
QY 181 SYRNVLQAAIQKSLKDPSSNNFRL 203
Db 181 SYRNVLQAAIQKSLKDPSSNNFRL 203

RESULT 14
US-09-864-761-36370
; Sequence 36370, Application US/09864761
; Patent No. US20020048763A1

; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO

;; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
;; FILE REFERENCE: Aecomica-X-1
;; CURRENT APPLICATION NUMBER: US/09/864,761
;; CURRENT FILING DATE: 2001-05-23
;; PRIOR APPLICATION NUMBER: US 60/180,312
;; PRIOR FILING DATE: 2000-02-04
;; PRIOR APPLICATION NUMBER: US 60/207,456
;; PRIOR FILING DATE: 2000-05-26
;; PRIOR APPLICATION NUMBER: US 09/632,366
;; PRIOR FILING DATE: 2000-08-03
;; PRIOR APPLICATION NUMBER: GB 24263.6
;; PRIOR FILING DATE: 2000-10-04
;; PRIOR APPLICATION NUMBER: US 60/236,359
;; PRIOR FILING DATE: 2000-09-27
;; PRIOR APPLICATION NUMBER: PCT/US01/00666
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00667
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00664
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00669
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00665
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00668
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00663
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00662
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00661
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00670
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: US 60/234,687
;; PRIOR FILING DATE: 2000-09-21
;; PRIOR APPLICATION NUMBER: US 09/608,408
;; PRIOR FILING DATE: 2000-06-30
;; PRIOR APPLICATION NUMBER: US 09/774,203
;; PRIOR FILING DATE: 2001-01-29
;; NUMBER OF SEQ ID NOS: 49117
;; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
;; SEQ ID NO 36370
;; LENGTH: 93
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: MAP TO AC007272.2
;; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.5
;; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 8
;; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2
;; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.1
;; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.9
;; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.3
;; OTHER INFORMATION: EXPRESSED IN HEAT, SIGNAL = 3.5
;; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.6
;; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.5
;; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2
;; OTHER INFORMATION: SWISSPROT HIT: Q66674, EVALUE 3.00e-04
;; OTHER INFORMATION: EST_HUMAN HIT: W23795.1, EVALUE 2.00e-46
US-09-864-761-36370

Query Match 18.8%; Score 465; DB 9; Length 93;
Best Local Similarity 100.0%; Pred. No. 3e-35;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MSAEVIHOVEALDTDEKMLFLCRDVAIDVPPNVRDLDIRRERKLSVGLAELLY 60
Db 1 MSAEVIHOVEALDTDEKMLFLCRDVAIDVPPNVRDLDIRRERKLSVGLAELLY 60
Qy 61 RVRFDLKRLIKMDRKAVETHLLRNPHLYSDY 93
Db 61 RVRFDLKRLIKMDRKAVETHLLRNPHLYSDY 93

RESULT 15

US-09-410-194-20
; Sequence 20, Application US/09410194
; Patent No. US20020095030A1
; GENERAL INFORMATION:
; APPLICANT: Tschopp, Jurg
; APPLICANT: Thome, Margot
; APPLICANT: Burns, Kimberly
; APPLICANT: Irmeler, Marten
; APPLICANT: Hahne, Michael
; APPLICANT: Schrotter, Michael
; APPLICANT: Schneider, Pascal
; APPLICANT: Bodmer, Jean-Luc
; APPLICANT: Steiner, Veronique
; APPLICANT: Rimoldi, Donata
; APPLICANT: Hofmann, Kay
; APPLICANT: French, E. Lars
; TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
; FILE REFERENCE: 11141-002001
; CURRENT APPLICATION NUMBER: US/09/410,194
; CURRENT FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: PCT/EP98/01857
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-410-194-20

Query Match 16.6%; Score 410; DB 9; Length 479;
Best Local Similarity 26.1%; Pred. No. 4.1e-29;
Matches 137; Conservative 106; Mismatches 172; Indels 110; Gaps 22;
Qy 6 IQHVEEALDTDEKMLFLCRDVAIDVPPN---VRDLDI---LRERKLSVGLA-- 56
Db 7 LYDIGEQDSEDLASLFL---SLDIYQKQEPKIDALMLFORLEKRMLESNSFL 62
Qy 57 -ELLYRVRRFDLLKRLIKMDRKAVETHLLRNPN---HLVSDYRVLMAEIGEDLDKSDVSSLI 113
Db 63 KELLFRINRLDLITYLNTKREEMERE-LQTPGQAQISAYRVMLYQISEVSRSELSFK 121
Qy 114 FLKMDYMGKGIKSKESFLDLVVELEKLNIVAPDQDLLEKLNIRHIDLTKIKYKQ 173
Db 122 FLQEEISKCKLDDMNLDDIFIEWRVILGEGKLDILKRVCAQIKNSLLKI-INDYEE 180
Qy 174 -----SVQAGTSYRNVLQAAIQSKLQPSNNFRLHNGRSKQRLKQLGAQOEPVK 226
Db 181 FSKERSSLEGPDEFSGELCGVMTISDSPRE----- 214
Qy 227 SIQSEAFPLQSPPEERYKMKSKPLGLICLIDIG-----NETEL--- 266
Db 215 --QDSSES---QTL-DKYIQMKSKPRGYCLINNNHFAKAREKVPKLSIRDRNGTHLDAG 268
Qy 267 -LRDTFTSLGYEVOKFLHLSMHGISQILGOFACMPEDRDYDFVCLVSRGSGSVYGVQ 325
Db 269 ALTTTFEELHFEIKPHDDCTVEQIYEILKIYQLM-DHSNMDCFICCLSHGDKGIIYGT 327
Qy 326 QTHSGPLHHRIRFMFGDSCPYLAGKPKMFFIQ-----NY---YVSEGLENSLLEVD- 376
Db 328 GQEA--PIYELTSQTLGKCPFLAGKPKVFFIQACQDNYQKQIPVETDSEQPYLEMDL 385
Qy 377 -GPAMKNVFEKAQRGLCTVHREADFWSLCTADMSLLEQSHSPSYLQCLSKLQOE- 434
Db 386 SSPQTRIP-----DEADFLGMATVNCVSYRNPAEGTWYIQSLCOSLRERC 433
Qy 435 -RKRPLDLHLTLNGYMYDWNRSVSAKE--KYYVWLQHTLRKKLI 476

Db 434 PRGDDILTILTEVN---YEVSNKDDKKNMGKOMPQPTFTLRKKLV 475

Search completed: August 13, 2003, 16:56:02
Job time : 51.9857 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: August 13, 2003, 16:33:14 ; Search time 20.5421 Seconds
(without alignments)
1098.857 Million cell updates/sec

Title: US-09-380-546a-2

Perfect score: 2473

Sequence: 1 MSAEVIHQVEALDTERK.....EKYYVWLQTLRKKLILSYT 480

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2468	99.8	480	1	CFLA_HUMAN
2	1568.5	63.4	484	1	CFLA_MOUSE
3	420	17.0	480	1	ICB8_MOUSE
4	410	16.6	479	1	ICB8_HUMAN
5	323.5	13.1	521	1	ICFA_HUMAN
6	231.5	9.4	241	1	CFLA_MCV1
7	192	7.8	293	1	ICB6_HUMAN
8	191.5	7.7	282	1	ICB3_XENLA
9	190.5	7.7	386	1	ICBA_XENLA
10	189	7.6	424	1	ICB2_CHICK
11	181	7.3	277	1	ICB3_HUMAN
12	180.5	7.3	277	1	ICB3_MOUSE
13	178.5	7.2	277	1	ICB3_CRILO
14	178.5	7.2	277	1	ICB3_RAT
15	176.5	7.1	435	1	ICB2_MOUSE
16	175.5	7.1	435	1	ICB2_HUMAN
17	171.5	6.9	276	1	ICB6_MOUSE
18	170.5	6.9	171	1	CFLA_HSV2
19	168	6.8	303	1	ICB7_HUMAN
20	167	6.8	303	1	ICB7_MESAU
21	166	6.7	312	1	ICB2_RAT
22	163	6.6	303	1	ICB7_MOUSE
23	160	6.5	382	1	ICB6_XENLA
24	152	6.1	323	1	ICEL_DROME
25	148	6.0	416	1	ICB9_HUMAN
26	144.5	5.8	339	1	ICE_DROME
27	142	5.7	405	1	ILBC_HORSE
28	139.5	5.6	299	1	ICEL_SPOFR
29	133.5	5.4	418	1	ICB5_HUMAN
30	132.5	5.4	402	1	ILBC_RAT
31	132.5	5.4	419	1	ICB3_MOUSE
32	131.5	5.3	404	1	ILBC_PIG
33	129	5.2	404	1	ILBC_CANFA

RESULT 1

ID	CFLA_HUMAN	STANDARD;	PRT;	480 AA.
AC	O15519; O14673; O14674; O15137; O15138; O15356; O15510;			
AC	O43618; O43619; O43620; O60458; O60459; Q5UEW1;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	CASP8 and FADD-like apoptosis regulator precursor (Cellular FLICE-like inhibitory protein) (c-FLIP) (Caspase-eight-related protein) (Casper)			
DE	(Caspase-like apoptosis regulatory protein) (CLARP) (MACH-related inducer of toxicity) (MRIT) (Caspase homolog) (CASH) (Inhibitor of FLICE) (I-FLICE) (FADD-like antiapoptotic molecule 1) (Flame-1) (Usurpin).			
GN	CFLAR OR CLARP OR MRIT OR CASH.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORMS 1; 13 AND 14), AND MUTAGENESIS OF TYR-360.			
RC	TISSUE=Embryonic kidney, and Umbilical vein endothelial cells;			
RX	MEDLINE=97352452; PubMed=9208847;			
RA	Shu H.-B., Halpin D.R., Goeddel D.V.;			
RL	"Casper is a FADD- and caspase-related inducer of apoptosis.";			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).			
RX	MEDLINE=97470967; PubMed=9326610;			
RA	Han D.K.M., Chaudhary P.M., Wright M.E., Friedman C., Trask B.J., Riedel R.T., Baskin D.G., Schwartz S.M., Hood L.;			
RT	"MRIT, a novel death-effector domain-containing protein, interacts with caspases and BclXL and initiates cell death.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 94:11333-11338(1997).			
RN	[3]			
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).			
RC	TISSUE=Peripheral blood lymphocytes;			
RX	MEDLINE=97360133; PubMed=9217161;			
RA	Irmiler M., Thome M., Hahne M., Schneider P., Hofmann K., Steiner V., Bodmer J.-L., Schroeder M., Burns K., Mattmann C., Rimoldi D., French L.E., Tschoep J.;			
RT	"Inhibition of death receptor signals by cellular FLIP.";			
RL	Nature 388:190-193(1997).			
RN	[4]			
RP	SEQUENCE FROM N.A. (ISOFORMS 1; 8; 9 AND 10), AND MUTAGENESIS OF ASP-376.			
RC	TISSUE=T-cell;			
RX	MEDLINE=97373543; PubMed=9228018;			
RA	Srinivasula S.M., Ahmad M., Oltalie S., Bullrich F., Banks S., Wang Y., Fernandes-Alnemri T., Croce C.M., Litwack G., Tomaselli K.J., Armstrong R.C., Alnemri E.S.;			
RT	"FLAME-1, a novel FADD-like anti-apoptotic molecule that regulates Fas/TNFR1-induced apoptosis.";			
RL	J. Biol. Chem. 272:18542-18545(1997).			
RN	[5]			

P70343 mus musculus
P29466 homo sapien
O14248 schizosacch
Q8wxh0 homo sapien
P29452 mus musculus
P42573 caenorhabdi
P58301 arabidopsis
Q07970 pyrodictus
O14573 homo sapien
O63269 rattus norv
O75601 bos taurus
O14157 schizosacch

34 128 5.2 373 1 ICEB_MOUSE
35 126.5 5.1 404 1 ILBC_HUMAN
36 126 5.1 1125 1 YE62_SCHPO
37 126 5.1 6885 1 SNE2_HUMAN
38 125.5 5.1 402 1 ILBC_MOUSE
39 125 5.1 503 1 CED3_CAEEL
40 121.5 4.9 793 1 ATKL_ARATH
41 121 4.9 882 1 RASO_PYRFU
42 121 4.9 2671 1 IP3T_HUMAN
43 120 4.9 2670 1 IP3T_RAT
44 119 4.8 377 1 ICED_BOVIN
45 116.5 4.7 2104 1 MYS3_SCHPO

ALIGNMENTS

RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE-Umbilical vein endothelial cells;
 RX MEDLINE=97362203; PubMed=9211860;
 RA Hu S., Vincenz C., Ni J., Gentz R., Dixit V.M.;
 RT "I-FLICE, a novel inhibitor of tumor necrosis factor receptor-1- and
 RL CD-95-induced apoptosis.";
 RN J. Biol. Chem. 272:17255-17257(1997).
 [6]
 RP SEQUENCE FROM N.A. (ISOFORMS 4; 5; 6 AND 7).
 RA Hu S., Dixit V.M.;
 RT Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 [7]
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 11 AND 12).
 RC TISSUE-Kidney;
 RX MEDLINE=99218584; PubMed=10200473;
 RA Rasper D.M., Vaillancourt J.P., Hadano S., Houtzager V.M., Seiden I.,
 RA Keen S.L.C., Tawa P., Xanthoudakis S., Nasir J., Martindale D.,
 RA Koop B.F., Peterson E.P., Thornberry N.A., Huang J., MacPherson D.P.,
 RA Black S.C., Hornung F., Lenardo M.J., Hayden M.R., Roy S.,
 RA Nicholson D.W.;
 RT "Cell death attenuation by 'Usurpin', a mammalian DED-caspase
 RT homologue that precludes caspase-8 recruitment and activation by the
 RT CD-95 (Fas, APO-1) receptor complex.";
 RL Cell Death Differ. 5:271-288(1998).
 [8]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC TISSUE-Skin fibroblast;
 RX MEDLINE=97426025; PubMed=9289491;
 RA Goltsev Y.V., Kovalenko A.V., Arnold E., Varfolomeev E.E.,
 RA Brodianskii V.M., Wallach D.;
 RT "CASH, a novel caspase homologue with death effector domains.";
 RL J. Biol. Chem. 272:19641-19644(1997).
 [9]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC TISSUE-Colon carcinoma;
 RX MEDLINE=98021435; PubMed=9380701;
 RA Inohara N., Koseki T., Hu Y., Chen S., Nunez G.;
 RT "CLARP, a death effector domain-containing protein interacts with
 RT caspase-8 and regulates apoptosis.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:10717-10722(1997).
 [10]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Lymph;
 RX MEDLINE=92388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raba S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Borak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Wozney K.C., Hale S., Garcia A.M., Gay L.J., Huily S.W.,
 RA Villalón D.K., Morley D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Heiton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shvchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzyzinski M.I., Skalska U., Smalls D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RL human and mouse cDNA sequences.";
 RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [11]
 RP FUNCTION.
 RX MEDLINE=99098897; PubMed=9889531;
 RA Scalfidi C., Schmitz I., Krammer P.H., Peter M.E.;
 RT "The role of c-FLIP in modulation of CD95-induced apoptosis.";
 RL J. Biol. Chem. 274:1541-1548(1999).
 [12]
 RP INDUCTION.
 RX MEDLINE=99244884; PubMed=10227994;

RA Algeciras-Schimmich A., Griffith T.S., Lynch D.H., Paya C.V.;
 RT "Cell cycle-dependent regulation of FLIP levels and susceptibility to
 RT Fas-mediated apoptosis.";
 RL J. Immunol. 162:5205-5211(1999).
 CC -1- FUNCTION: APOPTOSIS REGULATOR PROTEIN WHICH MAY FUNCTION AS A
 CC CRUCIAL LINK BETWEEN CELL SURVIVAL AND CELL DEATH PATHWAYS IN
 CC MAMMALIAN CELLS. ACTS AS AN INHIBITOR OF TNFRSF6 MEDIATED
 CC APOPTOSIS. A PROTEOLYTIC FRAGMENT (P43) IS LIKELY RETAINED IN THE
 CC DEATH-INDUCING SIGNALING COMPLEX (DISC) THEREBY BLOCKING FURTHER
 CC RECRUITMENT AND PROCESSING OF CASPASE-8 AT THE COMPLEX. FULL
 CC LENGTH AND SHORTER ISOFORMS HAVE BEEN SHOWN EITHER TO INDUCE
 CC APOPTOSIS OR TO REDUCE TNFRSF-TRIGGERED APOPTOSIS. LACKS ENZYMATIC
 CC (CASPASE) ACTIVITY.
 CC -1- SUBUNIT: TNFRSF6 STIMULATION TRIGGERS RECRUITMENT TO THE DEATH-
 CC INDUCING SIGNALING COMPLEX (DISC) FORMED BY TNFRSF6, FADD AND
 CC CASPASE-8. A PROTEOLYTIC FRAGMENT (P43) STAYS ASSOCIATED WITH THE
 CC DISC. ALSO INTERACTS WITH CASPASE-10, CASPASE-3, TRAF1, TRAF2 AND
 CC BCL-X(L) (IN VITRO).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms-14;
 CC Name-1; Synonyms=FLIP-L, CLARP1, MRIT alpha-1, CASH alpha, I-FLICE
 CC 1, FLAME-1 gamma, Usurpin alpha;
 CC IsoId=015519-1; Sequence=Displayed;
 CC Name-2; Synonyms=FLIP-S, CLARP2, MRIT beta-1, CASH beta;
 CC IsoId=015519-2; Sequence=VSP_000828, VSP_000829;
 CC Name-3; Synonyms=MRIT alpha-2;
 CC IsoId=015519-3; Sequence=VSP_000824, VSP_000838;
 CC Name-4; Synonyms=I-FLICE 2;
 CC IsoId=015519-4; Sequence=VSP_000825;
 CC Name-5; Synonyms=I-FLICE 3;
 CC IsoId=015519-5; Sequence=VSP_000840;
 CC Name-6; Synonyms=I-FLICE 4;
 CC IsoId=015519-6; Sequence=VSP_000826, VSP_000841;
 CC Name-7; Synonyms=I-FLICE 5;
 CC IsoId=015519-7; Sequence=VSP_000824, VSP_000827, VSP_000838;
 CC Name-8; Synonyms=Flame-1 alpha;
 CC IsoId=015519-8; Sequence=VSP_000830;
 CC Name-9; Synonyms=Flame-1 beta;
 CC IsoId=015519-9; Sequence=VSP_000830, VSP_000836, VSP_000837;
 CC Name-10; Synonyms=Flame-1 delta;
 CC IsoId=015519-10; Sequence=VSP_000834, VSP_000835;
 CC Name-11; Synonyms=Usurpin beta;
 CC IsoId=015519-11; Sequence=VSP_000838;
 CC Name-12; Synonyms=Usurpin gamma;
 CC IsoId=015519-12; Sequence=VSP_000832, VSP_000833;
 CC Name-13;
 CC IsoId=015519-13; Sequence=VSP_000831;
 CC Name-14;
 CC IsoId=015519-14; Sequence=VSP_000839;
 CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED. HIGHER EXPRESSION IN
 CC SKELETAL MUSCLE, PANCREAS, HEART, KIDNEY, PLACENTA, AND PERIPHERAL
 CC BLOOD LEUKOCYTES. ALSO DETECTED IN DIVERSE CELL LINES. ISOFORM 8
 CC IS PREDOMINANTLY EXPRESSED IN TESTIS AND SKELETAL MUSCLE.
 CC -1- INDUCTION: REPRESSION BY IL-2 AFTER TCR STIMULATION, DURING
 CC PROGRESSION TO THE S-PHASE OF THE CELL CYCLE.
 CC -1- DOMAIN: THE CASPASE DOMAIN LACKS THE ACTIVE SITES RESIDUES
 CC INVOLVED IN CATALYSIS.
 CC -1- PTM: PROTEOLYTICALLY PROCESSED; PROBABLY BY CASPASE-8. PROCESSING
 CC LIKELY OCCURS AT THE DISC, GENERATES SUBUNIT P43 AND P12.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
 CC -1- SIMILARITY: Contains 2 death effector (DED) domains.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AF010127; AAB64110.1; -
 DR EMBL; U85059; AAB82648.1; -
 DR EMBL; U97074; AAC51622.1; -

Query Match	99.8%;	Score 2468;	DB 1;	Length 480;
Best Local Similarity	99.8%;	Pred. No. 7.5e-146;		
Matches 479;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MSAEVTHVVEEALDDEKEMLLFLCRDVAIDVVPNNVRDLDDLILRGRKLSVGDIAELLY	60	
DB	1	MSAEVTHVVEEALDDEKEMLLFLCRDVAIDVVPNNVRDLDDLILRGRKLSVGDIAELLY	60	
QY	61	RYRREDLKRILKMDRKAVETHLLRNPHLVSYRVLMAEIGEDLQKSDVSSLIIFLMKQYM	120	
DB	61	RYRREDLKRILKMDRKAVETHLLRNPHLVSYRVLMAEIGEDLQKSDVSSLIIFLMKQYM	120	
QY	121	GRGKISKESFIDLVLVELEKLNVPADQDLLEKLNTHIRDLTKIKYKOSVOGAGT	180	
DB	121	GRGKISKESFIDLVLVELEKLNVPADQDLLEKLNTHIRDLTKIKYKOSVOGAGT	180	
QY	181	SYRNVLOAIAOKSLKDPNSNFRHNGRSKEORLKEOLGAQOQPVKKSIOESAFLOPST	240	
DB	181	SYRNVLOAIAOKSLKDPNSNFRHNGRSKEORLKEOLGAQOQPVKKSIOESAFLOPST	240	
QY	241	ERYKMKSPGLICILIDICIGNETELLRTFTSLGYEVOKFLHLSMHGISOILGOFACMP	300	
DB	241	ERYKMKSPGLICILIDICIGNETELLRTFTSLGYEVOKFLHLSMHGISOILGOFACMP	300	
QY	301	EHRDYDSFVCLVSRGSGSVYGVQDTHSGLPLHHRMFMGDCSPYLAGKPKMFFIQNY	360	
DB	301	EHRDYDSFVCLVSRGSGSVYGVQDTHSGLPLHHRMFMGDCSPYLAGKPKMFFIQNY	360	
QY	361	VYSEGOLENSLLEVDGPAKMKVPEKAKRGGLCTVHREADFWSLCTADMSLLEQSHSP	420	
DB	361	VYSEGOLENSLLEVDGPAKMKVPEKAKRGGLCTVHREADFWSLCTADMSLLEQSHSP	420	
QY	421	SLYLQCSLQKLRQERKRPILLDHLIELNGYMYDWNRSVSAKERYVWLOHTLRKKLLSYT	480	
DB	421	SLYLQCSLQKLRQERKRPILLDHLIELNGYMYDWNRSVSAKERYVWLOHTLRKKLLSYT	480	
RESULT 2				
CFLA_MOUSE STANDARD; PRT; 484 AA.				
AC	O35732:	O35733;		
DT	16-OCT-2001	(Rel. 40, Created)		
DT	16-OCT-2001	(Rel. 40, Last sequence update)		
DE	15-SEP-2003	(Rel. 42, Last annotation update)		
DE	CASP8 and FADD-like apoptosis regulator precursor	(Cellular FLICE-like		
DE	Inhibitory protein) (c-FLIP)	(Caspase-eight-related protein) (Casper)		
DE	(Caspase-like apoptosis regulatory protein) (CLARP)	(WACH-related		
DE	inducer of toxicity) (MRT)	(Caspase homolog) (CASH) (inhibitor of		
DE	FLICE) (i-FLICE) (FADD-like antiapoptotic molecule 1) (Flame-1)			
DE	(Usurpin)			
GN	CFLAR OR CASH.			
OS	Mus musculus			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
OX	NCBI_TaxID=10090;			
QY	1	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).		
RP	TISSUE=Liver;			
RX	MEDLINE=97426025;	PubMed=9289491;		
RA	Coltsev Y.V., Kovalenko A.V., Arnold E., Varfolomeev E.E.,			
RA	Brodianskii V.M., Wallach D.;			
RT	"CASH, a novel caspase homologue with death effector domains."			
RL	J. Biol. Chem. 272:19641-19644(1997).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RC	TISSUE=Heart;			
RX	MEDLINE=97360133;	PubMed=9217161;		
RA	Irmier M., Thome M., Hahne M., Schneider P., Hofmann K., Steiner V.,			
RA	Bodmer J.-L., Schroeter M., Burns K., Mattmann C., Rimoldi D.,			
RA	French L.E., Tschoop J.;			
RT	"Inhibition of death receptor signals by cellular FLIP."			
RL	Nature 388:190-195(1997).			

RN	FUNCTION.
RP	MEDLINE=20350661; PubMed=10894163;
RX	Yeh W.-C., Itle A., Elia A.J., Ng M., Shu H.-B., Wakeham A.,
RA	Mirtsos C., Suzuki N., Bonnard M., Goeddel D.V., Mak T.W.;
RT	"Requirement for Casper (c-FLIP) in regulation of death
RL	receptor-induced apoptosis and embryonic development."
RL	Immunity 12:633-642(2000).
RN	[4]
RP	FUNCTION.
RX	MEDLINE=20069388; PubMed=10602037;
RA	Wang J., Lobito A.A., Shen F., Hornung F., Winoto A., Lenardo M.J.;
RT	"Inhibition of Fas-mediated apoptosis by the B cell antigen receptor
RL	through c-FLIP."
RL	Eur. J. Immunol. 30:155-163(2000).
CC	-1- FUNCTION: APOPTOSIS REGULATOR PROTEIN WHICH MAY FUNCTION AS A
CC	CRUCIAL LINK BETWEEN CELL SURVIVAL AND CELL DEATH PATHWAYS IN
CC	MAMMALIAN CELLS. ACTS AS AN INHIBITOR OF TNFRSF6 MEDIATED
CC	APOPTOSIS. A PROTEOLYTIC FRAGMENT (P43) IS LIKELY RETAINED IN THE
CC	DEATH-INDUCING SIGNALING COMPLEX (DISC) THEREBY BLOCKING FURTHER
CC	RECRUITMENT AND PROCESSING OF CASPASE-8 AT THE COMPLEX. FULL
CC	LENGTH AND SHORTER ISOFORMS HAVE BEEN SHOWN EITHER TO INDUCE
CC	APOPTOSIS OR TO REDUCE TNFRSF-TRIGGERED APOPTOSIS. LACKS ENZYMIC
CC	(CASPASE) ACTIVITY (BY SIMILARITY).
CC	-1- SUBUNIT: TNFRSF6 STIMULATION TRIGGERS RECRUITMENT TO THE DEATH-
CC	INDUCING SIGNALING COMPLEX (DISC) FORMED BY TNFRSF6, FADD AND
CC	CASPASE-8. A PROTEOLYTIC FRAGMENT (P43) STAYS ASSOCIATED WITH THE
CC	DISC (BY SIMILARITY).
CC	-1- ALTERNATIVE PRODUCTS:
CC	Event-Alternative splicing; Named isoforms=2;
CC	Name=1; Synonyms=FLIP-L, CASH alpha;
CC	isoId=O35732-1; Sequence=Displayed;
CC	Name=2; Synonyms=FLIP-S, CASH beta;
CC	isoId=O35732-2; Sequence=VSP_000842, VSP_000843;
CC	-1- TISSUE SPECIFICITY: Highly expressed in heart.
CC	-1- DEVELOPMENTAL STAGE: AT EMBRYONIC DAYS E9.5 AND E10.5 HIGHEST
CC	EXPRESSION IN DEVELOPPING HEART.
CC	-1- INDUCTION: ISOFORM 1 BUT NOT ISOFORM 2 IS ACTIVATED BY BCR CROSS-
CC	LINKING IN PRIMARY B-CELLS.
CC	-1- DOMAIN: THE CASPASE DOMAIN LACKS THE ACTIVE SITES RESIDUES
CC	INVOLVED IN CATALYSIS.
CC	-1- PTM: PROTEOLYTICALLY PROCESSED; PROBABLY BY CASPASE-8. PROCESSING
CC	LIKELY OCCURS AT THE DISC, GENERATES SUBUNIT P43 AND P12 (BY
CC	SIMILARITY).
CC	-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
CC	-1- SIMILARITY: Contains 2 death effector (DED) domains.
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC	or send an email to license@isb-sib.ch).
CC	-----
DR	EMBL; Y14041; CAA74368.1; -
DR	EMBL; Y14042; CAA74369.1; -
DR	EMBL; U97076; AAC53281.1; -
DR	HSSP; Q15806; IQDU.
DR	MEROPS; C14.974; -
DR	MGD; MGI:1336166; CfIar.
DR	InterPro; IPR001875; DED.
DR	InterPro; IPR002398; ICE.
DR	InferPro; IPR001309; ICE_p20.
DR	Pfam; PF01335; DED; 2.
DR	Pfam; PF00656; Peptidase_C14; 1.
DR	SMART; SM00115; CASC; 1.
DR	SMART; SM00031; DED; 2.
DR	PROSITE; PS0208; CASPASE_P20; 1.
DR	PROSITE; PS0168; DED; 2.
KW	Apoptosis; Repeat; Alternative splicing.
FT	CASP8 AND FADD-LIKE APOPTOSIS REGULATOR
FT	SUBUNIT P43 (BY SIMILARITY).
FT	CHAIN 1 380

RA Armstrong R.C., Alnemri E.S.;
RT "FLAME-1, a novel FADD-like anti-apoptotic molecule that regulates Fas/TNFR1-induced apoptosis";
RL J. Biol. Chem. 272:18542-18545(1997).
[6]
RP SEQUENCE FROM N.A.
RX MEDLINE-21100893; PubMed-11161814;
RA Hadano S., Yanagisawa Y., Skauf J., Fichter K., Nasir J.,
RA Martindale D., Koop B.F., Scherer S.W., Nicholson D.W., Rouleau G.A.,
RA Ikeda J.-E., Hayden M.R.;
RT "Cloning and characterization of three novel genes, ALS2CR1, ALS2CR2,
RT and ALS2CR3, in the juvenile amyotrophic lateral sclerosis (ALS2);
RT critical region at chromosome 2q33-q34: Candidate genes for ALS2";
RL Genomics 71:200-213(2001).
[7]
RN SEQUENCE FROM N.A. (ISOFORM 7), AND FUNCTION OF ISOFORM 7.
RP TISSUE=Leukocyte;
RC MEDLINE-22005982; PubMed-12010809;
RA Himeji D., Horiuchi T., Tsukamoto H., Hayashi K., Watanabe T.,
RA Harada M.;
RT "Characterization of caspase-8L: a novel isoform of caspase-8 that
RT behaves as an inhibitor of the caspase cascade";
RL Blood 99:4070-4078(2002).
[8]
RN SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 9), AND INTERACTION OF ISOFORM 9
RP WITH BCL2 AT THE ENDOPLASMIC RETICULUM.
RX MEDLINE-21927603; PubMed-11917123;
RA Breckenridge D.G., Nguyen M., Kuppig S., Reth M., Shore G.C.;
RT "The procaspase-8 isoform, procaspase-8L, recruited to the BAP31
RT complex at the endoplasmic reticulum";
RL Proc. Natl. Acad. Sci. U.S.A. 99:4331-4336(2002).
[9]
RN SEQUENCE FROM N.A. (ISOFORM 7).
RP TISSUE=Leukocyte;
RX MEDLINE-22386257; PubMed-12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Heiton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinstead J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krawinski M.I., Skalska U., Smalhus D.B.,
RA Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[10]
RN PARTIAL SEQUENCE, AND PROCESSING.
RX MEDLINE-97121412; PubMed-8962078;
RA Srinivasula S.M., Ahmad M., Fernandes-Alnemri T., Litwack G.,
RA Alnemri E.S.;
RT "Molecular ordering of the Fas-apoptotic pathway: the Fas/APO-1
RT protease Mch5 is a crmA-inhibitable protease that activates multiple
RT Ced-3/ICE-like cysteine proteases";
RL Proc. Natl. Acad. Sci. U.S.A. 93:14486-14491(1996).
[11]
RN FUNCTION.
RX MEDLINE-97160607; PubMed-9006941;
RA Muzio M., Salvesen G.S., Dixit V.M.;
RT "FLICE induced apoptosis in a cell-free system. Cleavage of caspase
RT zymogens";
RL J. Biol. Chem. 272:2952-2956(1997).
[12]
RN PROCESSING.

RX MEDLINE-97327557; PubMed-9184224;
RA Medema J.P., Scaffidi C., Kischkel F.C., Shevchenko A., Mann M.,
RA Krammer P.H., Peter M.E.;
RT "FLICE is activated by association with the CD95 death-inducing
RT signaling complex (DISC)";
RL EMBO J. 16:2794-2804(1997).
[13]
RN CHARACTERIZATION OF ISOFORM 7.
RX MEDLINE-20318377; PubMed-10860845;
RA Horiuchi T., Himeji D., Tsukamoto H., Harashima S., Hashimura C.,
RA Hayashi K.;
RT "Dominant expression of a novel splice variant of caspase-8 in human
RT peripheral blood lymphocytes";
RL Biochem. Biophys. Res. Commun. 272:877-881(2000).
[14]
RN INTERACTION WITH BCL2; BCL2L1 AND BCAP31.
RX MEDLINE-97477382; PubMed-9334338;
RA Ng F.W.H., Nguyen M., Kwan T., Branton P.E., Nicholson D.W.,
RA Cronin J.A., Shore G.C.;
RT "p28 Bap31, a Bcl-2/Bcl-XL- and procaspase-8-associated protein in the
RT endoplasmic reticulum";
RL J. Cell Biol. 139:327-338(1997).
[15]
RN X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
RX MEDLINE-99451259; PubMed-10508784;
RA Blanchard H., Kodandapani L., Mittl P.R.E., Di Marco S., Krebs J.F.,
RA Wu J.C., Tomaselli K.J., Gruetter M.G.;
RT "The three-dimensional structure of caspase-8: an initiator enzyme in
RT apoptosis";
RL Structure 7:1125-1133(1999).
[16]
RN VARIANT CASP8 TRP-248.
RX MEDLINE-22239940; PubMed-12353035;
RA Chun H.J., Zheng L., Ahmad M., Wang J., Speirs C.K., Siegel R.M.,
RA Dale J.K., Puck J., Davis J., Hall C.G., Skoda-Smith S.,
RA Atkinson T.P., Straus S.E., Lenardo M.J.;
RT "Pleiotropic defects in lymphocyte activation caused by caspase-8
RT mutations lead to human immunodeficiency";
RL Nature 419:395-399(2002).
-!- FUNCTION: Most upstream protease of the activation cascade of
caspases responsible for the TNFRSF6/FAS mediated and TNFRSF1A
induced cell death. Binding to the adapter molecule FADD recruits
it to either receptor. The resulting aggregate called death-
inducing signaling complex (DISC) performs CASP8 proteolytic
activation. The active dimeric enzyme is then liberated from the
DISC and free to activate downstream apoptotic proteases.
Proteolytic fragments of the N-terminal propeptide (termed CAP3,
CAP5 and CAP6) are likely retained in the DISC. Cleaves and
activates CASP3, CASP4, CASP6, CASP7, CASP9 and CASP10. May
participate in the G2MB apoptotic pathways. Cleaves ADPRT.
Hydrolyzes the small-molecule substrate, Ac-Asp-Glu-Val-Asp-|-AMC.
Likely target for the cowpox virus CRMA death inhibitory protein.
Isoforms 5, 6, 7 and 8 lack the catalytic site and may interfere
with the pro-apoptotic activity of the complex.
-!- SUBUNIT: Heterodimer of a 18 kDa (p18) and a 10 kDa (p10) subunit.
Interacts with FADD and CFLAR. Isoform 9 interacts at the
endoplasmic reticulum with a complex containing BCAP31, BAP29,
BCL2 and/or BCL2L1.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- ALTERNATIVE PRODUCTS:
Event-Alternative splicing; Named isoforms-9;
Name-1; Synonyms=Alpha-1;
IsoId=Q14790-1; Sequence=Displayed;
Name=2; Synonyms=Alpha-2, MCH5-beta;
IsoId=Q14790-2; Sequence=VSP_000810;
Name=3; Synonyms=Alpha-3;
IsoId=Q14790-3; Sequence=VSP_000813;
Name=4; Synonyms=Alpha-4;
IsoId=Q14790-4; Sequence=VSP_000809, VSP_000810;
Name=5; Synonyms=Beta-1;
IsoId=Q14790-5; Sequence=VSP_000814, VSP_000815;
Name=6; Synonyms=Beta-2;
IsoId=Q14790-6; Sequence=VSP_000811, VSP_000812;


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CC EMBL; U20536; AAC50168.1; -
DR EMBL; U20537; AAC50169.1; -
DR EMBL; BC000305; AAH00305.1; -
DR EMBL; BC004460; AAH04460.1; -
DR HSSP; P42574; 1PAU.
DR MEROPS; C14.005; -
DR Genew; HGNC:1507; CASP6.
DR MIM; 601532; -
DR GO; GO:0008234; F:cysteine-type peptidase activity; TAS.
DR GO; GO:0006917; P:induction of apoptosis; TAS.
DR GO; GO:0006508; P:proteolysis and peptidolysis; TAS.
DR InterPro; IPR002398; ICE.
DR InterPro; IPR002138; ICE_p10.
DR Pfam; PF00655; ICE_p10; 1.
DR Pfam; PF00656; ICE_p20; 1.
DR PRINTS; PR00376; IL1BCENZYME.
DR SMART; SM00115; CASG; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
KW Hydrolase; Thiol protease; Apoptosis; Zymogen; Alternative splicing.
FT CHAIN 1 23
FT PROPEP 24 179 CASPASE-6 SUBUNIT P18.
FT PROPEP 180 193
FT CHAIN 194 293 CASPASE-6 SUBUNIT P11.
FT ACT_SITE 121 121 BY SIMILARITY.
FT ACT_SITE 163 163 BY SIMILARITY.
FT VARSPIC 14 102 Missing (in isoform Beta).
FT CONFLICT 66 66 /FTID=VSP_000805.
FT SEQUENCE 293 AA; 33310 MW; 0738AE4F9791EBD7 CRC64;
Query Match 7.8%; Score 192; DB 1; Length 293;
Best Local Similarity 25.9%; Pred. No. 3.5e-05;
Matches 65; Conservative 38; Mismatches 74; Indels 74; Gaps 9;
QY 225 KKSQSEAFAPQSI--PEERYKMKRPLGLICLIID-----CIGNTEL 266
DB 16 ENNTETDAFYKREMFDPKRYKMDHRRRGIALIFNHERFPWHLTLPERRGTCADRDN-- 73
QY 267 LRDFTSLGYEVQKF-----LHLSMHGISQILGQFACMPHEHSDYDFVCLVSRGSG 319
DB 74 LTRFSDLGFEVCKFNDLKAEEELKTHEVSTV-----SHADADCFVCLVSHGEGN 125
QY 320 SVYGVYD-----QTHSGPLPHIRRMFGDSCPYLAGPKMFFIQ-----NY 360
DB 126 HIYADAKIEIQTITGL-----FKGDKCHSLVGRPKFIIOACRGNHQHDVPVPLDV 177
QY 361 VVSEGLNSLLLEVDPAMKNVEFKAKRGLCTVHREADPFWLSLCTADMSSLLEQSHSP 420
DB 178 VDNQTEKLDITNTEVDAAS-----VYTLPGADFLMCMYSVAEGYSHRETAVNG 225
QY 421 SLYLQCLSQKL 431
DB 226 SWYIQDLCEML 236
RESULT 8
ICE3_XENLA
ID ICE3_XENLA STANDARD; PRT; 282 AA.
AC P55866;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Apopain precursor (EC 3.4.22.-) (Cysteine protease CPP32) (Caspase-3)
DE (CASP-3) (XCPP32).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
Xenopodinae; Xenopus.
[1]
SEQUENCE FROM N.A. PubMed-9030578;
MEDLINE-97184166; Yaoita Y., Nakajima K.;
"Induction of apoptosis and CPP32 expression by thyroid hormone in a
myoblastic cell line derived from tadpole tail.";
J. Biol. Chem. 272:5122-5127(1997).
CC -1- FUNCTION: IMPORTANT MEDIATOR OF APOPTOSIS. AT THE ONSET OF
APOPTOSIS IT PROTEOLYTICALLY CLEAVES POLY(ADP-RIBOSE) POLYMERASE
(PARP) AT A 216-ASP-1-GLY-217 BOND (BY SIMILARITY).
CC -1- SUBUNIT: HETERODIMER OF A 17 kDa (P17) AND A 12 kDa (P12)
SUBUNITS.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- MISCELLANEOUS: THE SUBUNITS ARE DERIVED FROM THE PRECURSOR
SEQUENCE BY A PROBABLE AUTOCATALYTIC MECHANISM AND PROBABLY BY
OTHER CASPASES (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
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CC EMBL; D89784; BAA14018.1; -
CC HSSP; P42574; 1PAU.
CC MEROPS; C14.003; -
CC InterPro; IPR002398; ICE.
CC InterPro; IPR002138; ICE_p10.
CC InterPro; IPR001309; ICE_p20.
CC Pfam; PF00656; Peptidase_C14; 1.
CC PRINTS; PR00376; IL1BCENZYME.
CC SMART; SM00115; CASG; 1.
CC PROSITE; PS01122; CASPASE_CYS; 1.
CC PROSITE; PS01121; CASPASE_HIS; 1.
CC PROSITE; PS50207; CASPASE_P10; 1.
CC PROSITE; PS50208; CASPASE_P20; 1.
CC Hydrolase; Thiol protease; Zymogen; Apoptosis.
FT PROPEP 1 23 BY SIMILARITY.
FT CHAIN 186 282 APOPAIN P17 SUBUNIT.
FT CHAIN 187 282 APOPAIN P12 SUBUNIT.
FT ACT_SITE 131 131 BY SIMILARITY.
FT ACT_SITE 174 174 BY SIMILARITY.
FT SEQUENCE 282 AA; 32124 MW; CB390E6980CAB77F CRC64;
Query Match 7.7%; Score 191.5; DB 1; Length 282;
Best Local Similarity 29.4%; Pred. No. 3.6e-05;
Matches 67; Conservative 34; Mismatches 74; Indels 53; Gaps 12;
QY 242 ERYKMKSKPLGICLIID-----CIGNTEL-----LRDFTSLGVEV-----QKFLH 283
DB 46 QNYRTNTPMGKMLIINKNPHSSNMAVRNGTVDALKLHETFTGLGVEVMVNDQK--- 102
QY 284 LSMHGISQILGQFACMPE--HRDYDSFVCLVSRGSGQ--SVYGVYDQTHSGPLH--HIRR 338
DB 103 -----SSDIIGRLAKI SEEDHSKRSPFCALSHGEEDSGICVD-----VPIHKNLTD 152
QY 339 MFMGDCSPYLAGPKMFFIQNYVYVSEGLENSLSLEVDGPGAMKNVEFKAKRGLCTVHRE 398
DB 153 LFRGDRCKTLVGRPKIFFIQ---ACRG--TELDSGIETDSCSEPREIQ-----RIPVE 201
QY 399 ADFPWSLCTADMSSLLEQSHSSPSLYLQCLSQKLRQERKRPLDLHIEL 446
DB 202 ADFLIAYSTVPGYCSWRKMDGGSFWFIQSLCKMKR-----LYGSHLEL 243
RESULT 9
ICEA_XENLA

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ID ICEA_XENLA STANDARD; PRT; 386 AA.
AC P55865;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Interleukin-1 beta convertase homolog A precursor (EC 3.4.22.-)
DE (XICE-A) (Caspase-1A) (CASP-1A).
GN CASP1A.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Yaoita Y., Nakajima K.;
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
CC 1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC 1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
CC 1- SIMILARITY: Contains 1 CARD domain.
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CC -----
DR EMBL; D89783; BAAL4017.1; -;
DR HSSP; P29466; LICE.
DR MEROPS; C14.0PWA;
DR InterPro; IPR001315; CARD.
DR InterPro; IPR002398; ICE.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00856; Peptidase_C14; 1.
DR PRINTS; PR00376; IL1BCENZYME.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS0209; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS0207; CASPASE_P10; 1.
DR PROSITE; PS0208; CASPASE_P20; 1.
KW Hydrolase; Thiol protease; zymogen.
FT PROPEP 1 ? POTENTIAL.
FT CHAIN 2 ? INTERLEUKIN-1 BETA CONVERTASE HOMOLOG A.
FT DOMAIN 22 386 CARD.
FT ACT_SITE 218 218 BY SIMILARITY.
FT ACT_SITE 274 274 BY SIMILARITY.
SQ SEQUENCE 386 AA; 43663 MW; 927C71PC9FED79E6 CRC64;

Query Match
Best Local Similarity 7.7%; Score 190.5; DB 1; Length 386;
Matches 85; Conservative 76; Mismatches 145; Indels 83; Gaps 15;

QY 133 DLVVELEKLVAPQDLLEKLNHRIIDLTQIKYQSQVQAGTSYRNVVLAQAIQK 192
DB 23 DLDDLRKENVLDSEVEHIKES-NTNDRGRAMI-----DSVKKGGDPSNILLSELVK 77
QY 193 SLKDPFNNPRLHN-----GRSKEQLKEQLGAQOQEPVKKSTQSEAFUPQSI 239
DB 78 NHTLAKSLGLHEPPMAPVPIQEHNADTKNKDVGIPCSAEFFK-IQDTQG-----130
QY 240 PEERYKMSKP--LGICLIIDC-----IGNTELLRDTFTSLGYEVQKF 281
DB 131 -DKIYDVRRREGKGLALII-CNEKFENLNERHGAKVDLDGMTKLINL-----LGQVQHPH 184
QY 282 LHLMSHGISQILGQFACHPHEHDYDFVCVLYSRGGSQSVYGV-----QTHSG 330
DB 185 TNLTKTEVMYKMKFAAQEEHADSSTFTVLTMSHGDROGVCGTDSKKTKEKRGQVEVTNL 244

QY 331 LPLHHRFMFGDSCPYLAGKPKMFQIYVYVSEGOLENSLL--EVDGPAMKNVFEKAQ 388
DB 245 LEIDEIFSTFNNVNCKSLRNKPKVITIQ---ACRGENKGGLLVDRDDVASPPLED-----295
QY 389 KRGCLTVHREADFFNSLCTADMSLLSQSHSSPSLYLOCSOKLRQ-ERRKPLDLHLIELN 447
DB 296 -DGLHFVREADFICFCSSPTDPTVSWRDPKGSVFTHLIERKMEYVHAQCPGLDIFLEVQ 354
QY 448 GMYD-----WNSRVSAKEKYVW 466
DB 355 SLFKDKCPNSRSOMPTQERCTLTKKFYLF 383

RESULT 10
ICE2_CHICK
ID ICE2_CHICK STANDARD; PRT; 424 AA.
AC Q98943;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Caspase-2 precursor (EC 3.4.22.-) (CASP-2) (ICH-1 protease) (ICH-1L/1S).
DE 1L/1S).
GN CASP2 OR ICH1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS ICH-1L AND ICH-1S).
RC STRAIN=White leghorn; TISSUE=Ovarian granulosa;
RX MEDLINE=97368127; PubMed=9224894;
RA Johnson A.L., Bridgham J.T., Bergeron L., Yuan J.;
RT "Characterization of the avian Ich-1 cDNA and expression of Ich-1L
RT mRNA in the hen ovary.";
RL Gene 192:227-233(1997).
CC 1- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
CC RESPONSIBLE FOR APOPTOSIS EXECUTION. MIGHT FUNCTION BY EITHER
CC ACTIVATING SOME PROTEINS REQUIRED FOR CELL DEATH OR INACTIVATING
CC PROTEINS NECESSARY FOR CELL SURVIVAL (BY SIMILARITY).
CC 1- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Name=ICH-1L;
CC IsoId=Q98943-1; Sequence=Displayed;
CC Note=Only form found in the ovary;
CC Name=ICH-1S;
CC IsoId=Q98943-2; Sequence=VSP_000803, VSP_000804;
CC 1- PTM: HETERODIMER OF A SMALL AND A LARGE SUBUNIT (BY SIMILARITY).
CC 1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
CC 1- SIMILARITY: Contains 1 CARD domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U64963; AAC29881.1; ALT_INIT.
DR HSSP; P42574; ICP3.
DR MEROPS; C14.006; -;
DR InterPro; IPR001315; CARD.
DR InterPro; IPR002398; ICE.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; IL1BCENZYME.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS0209; CARD; 1.

RA Lark M.W., Nadeau D.P., Suva L.J., Gowen M., Nuttall M.E.;
RT "Potent and selective nonpeptide inhibitors of caspases 3 and 7
RL inhibit apoptosis and maintain cell functionality.";
RN J. Biol. Chem. 275:16007-16014(2000).
RP [9]
RX PROCESSING
RX MEDLINE-96353838; PubMed-8755496;
RA Fernandes-Alnemri T., Armstrong R.C., Krebs J., Srinivasula S.M.,
RA Wang L., Bullrich F., Fritz L.C., Trapani J.A., Tomaselli K.J.,
RA Litwack G., Alnemri E.S.;
RT "In vitro activation of CPP32 and Mch3 by Mch4, a novel human
RT apoptotic cysteine protease containing two FADD-like domains.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:7464-7469(1996).
RN [10]
RP CLEAVAGE OF HUNTINGTIN.
RX MEDLINE-96331285; PubMed-8696339;
RA Goldberg Y.P., Nicholson D.W., Rasper D.M., Kalchman M.A., Koide H.B.,
RA Graham R.K., Bromm M., Kazemi-Esfarjani P., Thornberry N.A.,
RA Vaillancourt J.P., Hayden M.R.;
RT "Cleavage of huntingtin by apopain, a proapoptotic cysteine protease,
RT is modulated by the polyglutamine tract.";
RL Nat. Genet. 13:442-449(1996).
RN [11]
CC -1- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
CC RESPONSIBLE FOR APOPTOSIS EXECUTION. AT THE ONSET OF APOPTOSIS IT
CC PROTEOLYTICALLY CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP) AT A
CC 216-ASP-1-GLY-217 BOND. CLEAVES AND ACTIVATES STEROL REGULATORY
CC ELEMENT BINDING PROTEINS (SREBPS) BETWEEN THE BASIC HELIX-LOOP-
CC HELIX LEUCINE ZIPPER DOMAIN AND THE MEMBRANE ATTACHMENT DOMAIN.
CC CLEAVES AND ACTIVATES CASPASE-6, -7 AND -9. INVOLVED IN THE
CC CLEAVAGE OF HUNTINGTIN.
CC -1- ENZYME REGULATION: INHIBITED BY ISATIN SULFONAMIDES.
CC -1- SUBUNIT: HETERODIMER OF A 17 kDa (P17) AND A 12 kDa (P12) SUBUNIT.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN LUNG, SPLEEN, HEART, LIVER
CC AND KIDNEY. MODERATE LEVELS IN BRAIN AND SKELETAL MUSCLE. AND LOW
CC IN TESTIS. ALSO FOUND IN MANY CELL LINES, HIGHEST EXPRESSION IN
CC CELLS OF THE IMMUNE SYSTEM.
CC -1- PTM: CLEAVAGE BY GRANTZME B, APAF-1, CASPASE-6, -8 AND -10
CC GENERATES THE TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE
CC PROPEPTIDES IS LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE
CC ACTIVATED PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT
CC OF CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR
CC AND VICE VERSA.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
CC
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U13737; AAA65015.1; -
CC EMBL; U13738; AAB60355.1; -
CC EMBL; U26943; AAA74929.1; -
CC EMBL; AJ413269; CAC88866.1; -
CC EMBL; BC016926; AAH16926.1; -
CC PIR; A55315; A55315.
CC PDB; 1PAU; 07-JUL-97.
CC PDB; 1CP3; 24-DEC-97.
CC PDB; 1GFW; 23-JUN-00.
CC MEROPS; C14.003; -
CC Genew; HGNC:1504; CASP3.
CC MIM; 600636; -
CC GO; GO:0004208; F:caspase-3 activity; TAS.
CC GO; GO:0008624; P:induction of apoptosis by extracellular sig. . ; TAS.
CC GO; GO:0008629; P:induction of apoptosis by intracellular sig. . ; TAS.
CC GO; GO:0009405; P:pathogenesis; TAS.
CC InterPro; IPR002398; ICE.
CC InterPro; IPR002138; ICE.p10.
CC InterPro; IPR001309; ICE.p20.
CC Pfam; PF00656; Peptidase_C14; 1.

DR PRINTS; PRO0376; IL1BENZYM. 1
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS0207; CASPASE_P10; 1.
DR PROSITE; PS0208; CASPASE_P20; 1.
KW Hydrolase; Thiol protease; zymogen; Apoptosis; Polymorphism;
KW 3D-structure.
FT PROPEP 1 9
FT CHAIN 10 28
FT CHAIN 29 175
FT CHAIN 176 277
FT ACT_SITE 121 121
FT ACT_SITE 163 163
FT VARIANT 190 190
FT CONFLICT 31 36
FT STRAND 36 36
FT STRAND 43 51
FT HELIX 57 59
FT TURN 60 60
FT TURN 65 66
FT HELIX 67 80
FT TURN 81 82
FT STRAND 84 89
FT HELIX 93 104
FT TURN 105 105
FT TURN 109 110
FT STRAND 111 119
FT STRAND 122 123
FT TURN 124 125
Query Match 7.3%; Score 181; DB 1; Length 277;
Best Local Similarity 26.8%; Pred. No. 0.00016;
Matches 69; Conservative 40; Mismatches 102; Indels 46; Gaps 9;
QY 222 EPVKSIQSEAFLPQSIPEERYKMKKPLGICLIID-----CIGNETEL--L 267
DB 17 EP--KIHGSESMDSIGSLDSYKMDYPENGLCIINNNKFNHKTGTSRSGTVDAAAL 74
QY 268 RDTFTSLGYEQKFLHSMHGISOILGQFACHPEDYDFYCVLYSRGSSQSVYQDT 327
DB 75 RETFRNLKYEVKNKNDLTREEIVELMRDVS-KEDHSKRSFVCVLLSHGEEGIIFG--T 130
QY 328 HSGLPILHRRMFMDGDCPYLAGPKMFTQNVVSEGO--LENSLLEVDGPMKNVEF 385
DB 131 NGPVDLKKITNFRGDCRSLGKPKLFIIQACRGTELDGIGTDSGVDDDMACHK---- 186
QY 386 KAKRGCLTVHREADPFWSLCTADMSLLPQSHSSPSLYLQCLSQKLRQKRPDLHLI- 444
DB 187 -----IPVDAFLYAYSTAPGYYSWRNSKDGSWFIQSLCAMLKQYADK-LEPMHIL 236
QY 445 -----ELNGYMYD 452
DB 237 TRVNRKVATEFESFSFD 253
RESULT 12
ICE3_MOUSE
ID ICE3_MOUSE STANDARD; PRT; 277 AA.
AC P70677; O08668; O9QW14;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Apopain precursor (EC 3.4.22.-) (Cysteine protease CPP32) (Yama
DE protein) (CPP-32) (Caspase-3) (CASP-3) (SREBP cleavage activity 1)
DE (SCA-1) (LICE).
GN CASP3 OR CPP32.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxId=10090;
RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE-96358624; PubMed-8761296;
RA Juan T.S.-C., McNiece I.K., Jenkins N.A., Gilbert D.J., Copeland N.G.,
RA Fletcher F.A.;
RT "Molecular characterization of mouse and rat CPP32 beta gene encoding
RT a cysteine protease resembling interleukin-1 beta converting enzyme
RT and CED-3.";
RL Oncogene 13:749-755(1996).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE-97224429; PubMed-9070890;
RA Mukasa T., Urabe K., Momoi M.Y., Kimura I., Momoi T.;
RT "Specific expression of CPP32 in sensory neurons of mouse embryos and
RT activation of CPP32 in the apoptosis induced by a withdrawal of
RT NGF.";
RL Biochem. Biophys. Res. Commun. 231:770-774(1997).
[3]
RP SEQUENCE FROM N.A.
RX STRAIN-C3H/Ad;
RX MEDLINE-97190206; PubMed-9038361;
RA van de Creen W., Vandenabeele P., Declercq W., van den Brande I.,
RA van Leo G., Molemans F., Schotte P., van Criekinge W., Beyaert R.,
RA Fiers W.;
RT "Characterization of seven murine caspase family members.";
RL FEBS Lett. 403:61-69(1997).
[4]
RP SEQUENCE FROM N.A.
RX TISSUE-Brain;
RA Fernandes-Alnemri T., Litwack G., Alnemri E.S.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
[5]
RP SEQUENCE OF 58-277 FROM N.A.
RA Denis F., Alam A., Cohen L., Hartgers F., Braun M., Martinez O.,
RA Fortin J.-P., Sekaly R.-P.;
RT "Multiple pathways of apoptosis converging on the CPP32 protease.";
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
CC RESPONSIBLE FOR APOPTOSIS EXECUTION AT THE ONSET OF APOPTOSIS IT
CC PROTEOLYTICALLY CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP) AT A
CC 216-ASP-1-GLY-217 BOND. CLEAVES AND ACTIVATES STEROL REGULATORY
CC ELEMENT BINDING PROTEINS (SREBPS) BETWEEN THE BASIC HELIX-LOOP-
CC HELIX LEUCINE ZIPPER DOMAIN AND THE MEMBRANE ATTACHMENT DOMAIN.
CC CLEAVES AND ACTIVATES CASPASE-6, -7 AND -9 (BY SIMILARITY).
CC CLEAVES IL-1 BETA BETWEEN AN ASP AND AN ALA, RELEASING THE MATURE
CC CYTOKINE WHICH IS INVOLVED IN A VARIETY OF INFLAMMATORY PROCESSES.
CC -1- SUBUNIT: HETERODIMER OF A 17 kDa (P17) AND A 12 kDa (P12) SUBUNIT
CC (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN SPLEEN, LUNG, LIVER,
CC KIDNEY AND HEART. LOWER EXPRESSION IN BRAIN, SKELETAL MUSCLE AND
CC TESTIS.
CC -1- PTM: CLEAVAGE BY GRANTYME B, CASPASE-6, -8 AND -10 GENERATES THE
CC TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTIDES IS
CC LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED
CC PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
CC CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR AND
CC VICE VERSA (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; U54803; AAC52768.1; -
DR EMBL; U54802; AAC52768.1; JOINED.
DR EMBL; U49929; AAC52764.1; -
DR EMBL; D86352; BAA21727.1; -
DR EMBL; Y13086; CAA73528.1; -
DR EMBL; U19522; AAC53196.1; -

DR EMBL; U63720; AAD09504.1; -
DR PIR; JC5410; JC5410.
DR HSSP; P42574; 1PAU.
DR MEROPS; C14.003; -
DR MGD; MGI:107739; Casp3.
DR InterPro; IPR002398; ICE.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; IL1BCENZME.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS0207; CASPASE_P10; 1.
DR PROSITE; PS0208; CASPASE_P20; 1.
KW Hydrolase; Thiol protease; zymogen; Apoptosis.
FT PROPEP 1 9
FT PROPEP 10 28
FT CHAIN 29 175
FT CHAIN 176 277
FT ACT_SITE 121 121
FT ACT_SITE 163 163
FT CONFLICT 17 17
FT CONFLICT 51 51
FT CONFLICT 63 65
FT CONFLICT 84 84
FT CONFLICT 95 95
FT CONFLICT 97 97
FT CONFLICT 128 128
FT CONFLICT 135 135
FT CONFLICT 231 231
FT CONFLICT 262 262
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Query Match 7.3%; Score 180.5; DB 1; Length 277;
Best Local Similarity 29.0%; Pred. No. 0.00017;
Matches 64; Conservative 34; Mismatches 88; Indels 35; Gaps 10;
Qy 226 KSIQESAFPLQSPTEERYKMKRPLGICLIID-----CIGNETEL--LRDTF 271
Db 25 KSV-DSGIIYLDSS-----YKMDYPEMGICIIINKNFKHSTGMSRSRGTVDAAANLRETF 78
Qy 272 TSLGYEQKFLHLSMHGTSQILGQFACMPERDYSFVCLVSVRGSGSVGVQDTHSGL 331
Db 79 MGLAYQVKNKNDLTREDILELMDSVS-KEDSKRSSFCVILSHGDEGIYV---TNGPV 134
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Db 135 ELKKLTFFRGDYCRSLTGPKPLFIQ---ACRG-TELDCCGIETDSGT--DEEMACQK-- 186
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AC Q60431;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Apopain precursor (EC 3.4.22.-) (Cysteine protease CPP32) (Yama
DE protein) (CPP-32) (Caspase-3) (SREBP cleavage activity 1)
DE (SCA-1).
GN CASP3 OR CPP32.
OS Cricetus longicaudatus (Long-tailed hamster) (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetus.
OX NCBI_TaxID=10030;
RN [1]
RP SEQUENCE FROM N.A.

Search completed: August 13, 2003, 16:40:19
Job time : 21.5421 secs

11/29/99
PCT/IL
226198
5/1/97
313197

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OM protein - protein search, using sw model

Run on: August 13, 2003, 16:40:24 ; Search time 28.7589 Seconds
(without alignments)
706.188 Million cell updates/sec

Title: US-09-380-546A-2
Perfect score: 2473
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2468	99.8	480	3	US-08-795-088A-2
2	2412	97.5	480	4	US-09-069-023-34
3	2265.5	91.6	445	3	US-08-859-167-2
4	2265.5	91.6	445	3	US-09-109-273-2
5	2265.5	91.6	445	3	US-09-276-993-2
6	2265.5	91.6	445	4	US-09-723-450-2
7	1007	40.7	221	3	US-09-382-155-17
8	1007	40.7	221	3	US-09-074-044A-17
9	417	16.9	84	3	US-09-074-044A-2
10	410	16.6	479	4	US-08-983-502-7
11	410	16.6	479	4	US-09-516-747-7
12	410	16.6	479	5	PCT-US96-10521-7
13	408	16.5	479	2	US-08-807-200-12
14	408	16.5	479	3	US-09-001-777-12
15	406	16.4	479	3	US-08-852-782-3
16	404.5	16.4	464	4	US-08-983-502-18
17	404.5	16.4	464	4	US-09-516-747-18
18	404.5	16.4	464	5	PCT-US96-10521-18
19	403	16.3	84	3	US-09-382-155-28
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22	403	16.3	479	3	US-09-074-044A-26
23	400	16.2	479	3	US-09-382-155-27
24	397	16.1	479	3	US-09-382-155-27
25	392	15.9	479	3	US-09-382-155-26
26	384	15.5	78	3	US-09-382-155-1
27	384	15.5	78	3	US-09-074-044A-1

28	381.5	15.4	496	1	US-08-665-220-4	Sequence 4, Appl1
29	381.5	15.4	496	3	US-09-291-692-4	Sequence 4, Appl1
30	370.5	15.0	476	4	US-09-561-756-27	Sequence 27, Appl1
31	370.5	15.0	476	4	US-09-227-721-27	Sequence 27, Appl1
32	329	13.3	389	2	US-08-618-408B-4	Sequence 4, Appl1
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34	318.5	12.9	479	1	US-08-665-220-2	Sequence 2, Appl1
35	318.5	12.9	479	3	US-09-291-692-2	Sequence 2, Appl1
36	318.5	12.9	479	4	US-09-561-756-33	Sequence 33, Appl1
37	318.5	12.9	479	4	US-09-227-721-33	Sequence 33, Appl1
38	274	11.1	335	4	US-08-983-502-16	Sequence 16, Appl1
39	274	11.1	335	4	US-09-516-747-16	Sequence 16, Appl1
40	274	11.1	335	5	PCT-US96-10521-16	Sequence 16, Appl1
41	246.5	10.0	286	4	US-09-360-017-1	Sequence 2, Appl1
42	246	9.9	389	4	US-08-724-378D-2	Sequence 2, Appl1
43	238	9.6	389	4	US-08-724-378D-3	Sequence 3, Appl1
44	231.5	9.4	241	3	US-09-382-155-21	Sequence 21, Appl1
45	231.5	9.4	241	3	US-09-074-044A-21	Sequence 21, Appl1

ALIGNMENTS

RESULT 1
US-08-795-088A-2
; Sequence 2, Application US/08795088A
; Patent No. 6242569
; GENERAL INFORMATION:
; APPLICANT: Sul, Hong-Bing
; APPLICANT: Goedel, David V.
; TITLE OF INVENTION: Regulators of Apoptosis
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Science & Technology Law Group
; STREET: 75 Denise Drive
; CITY: Hillsborough
; STATE: California
; COUNTRY: USA
; ZIP: 94010
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,088A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 343-4341
; TELEFAX: (650) 343-4342
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 480 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
US-08-795-088A-2

Query Match 99.8%; Score 2468; DB 3; Length 480;
Best Local Similarity 99.8%; Pred. No. 1.2e-230;
Matches 479; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MSAEVIHQVEALDDEKEMLLFCRDVAIDVVPVPPNRDLDLILRERKLSVGDIAELLY 60
Db 1 MSAEVIHQVEALDDEKEMLLFCRDVAIDVVPVPPNRDLDLILRERKLSVGDIAELLY 60
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Qy 121 GRGKISKEKSFLLDVLVELEKLNVLAPQLDLLEKLNHRIIDLTKTIQYKQSVQAGT 180
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Db 181 SYRNLVQAATQKSLKDPNNFRLHNGRSKEQRLKEQIQAQOEPVKKSIQSEAFLPQIP 240
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Db 241 EERYKMKSKPLGICLIIDCIGNETELLRTFTSLGYEVQKFLHLSMHGISOILGQFACMP 300
Qy 301 EHRDYSFVCLVSRGGSQSYGVQDQTHSGPLHRIHRRMFMDSCPYLAGKPKMFFIQNY 360
Db 301 EHRDYSFVCLVSRGGSQSYGVQDQTHSGPLHRIHRRMFMDSCPYLAGKPKMFFIQNY 360
Qy 361 VVSEGLSLLVDGPKAMNVEFKAKRGCLCTVHREADFFWSLCTADMSLLSQSHSSP 420
Db 361 VVSEGLSLLVDGPKAMNVEFKAKRGCLCTVHREADFFWSLCTADMSLLSQSHSSP 420
Qy 421 SLYLQCLSQKLRQERKRPDLDLHIELNGMYMDWNSRVSAREKYYVWLQHTLRKKLILSYT 480
Db 421 SLYLQCLSQKLRQERKRPDLDLHIELNGMYMDWNSRVSAREKYYVWLQHTLRKKLILSYT 480

RESULT 2
US-09-069-023-34
; Sequence 34, Application US/09069023A
; Patent No. 6348573
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; APPLICANT: Koseki, Takeyoshi
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
; TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
; FILE REFERENCE: UM-03333
; CURRENT APPLICATION NUMBER: US/09/069,023A
; CURRENT FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 34
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-069-023-34

Query Match 97.5%; Score 2412; DB 4; Length 480;
Best Local Similarity 97.7%; Pred. No. 3.3e-225;
Matches 469; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MSAEVIHQVEEALDTDEKEMLLFCRDVAIDVPPNVRDLIDLIRERKLSVGLAELLY 60
Db 1 MSAEVIHQVEEALDTDEKEMLLFCRDVAIDVPPNVRDLIDLIRERKLSVGLAELLY 60
Qy 61 RVRFDLLKRLKMDRAVETHLRNPHLVSDYVLMAEIGEDLDKSDVSSLIPLMKDYM 120
Db 61 RVRFDLLKRLKMDRAVETHLRNPHLVSDYVLMAEIGEDLDKSDVSSLIPLMKDYM 120
Qy 121 GRGKISKEKSFLLDVLVELEKLNVLAPQLDLLEKLNHRIIDLTKTIQYKQSVQAGT 180
Db 121 GRGKISKEKSFLLDVLVELEKLNVLAPQLDLLEKLNHRIIDLTKTIQYKQSVQAGT 180
Qy 181 SYRNLVQAATQKSLKDPNNFRLHNGRSKEQRLKEQIQAQOEPVKKSIQSEAFLPQIP 240
Db 181 SYRNLVQAATQKSLKDPNNFRLHNGRSKEQRLKEQIQAQOEPVKKSIQSEAFLPQIP 240
Qy 241 EERYKMKSKPLGICLIIDCIGNETELLRTFTSLGYEVQKFLHLSMHGISOILGQFACMP 300
Db 241 EERYKMKSKPLGICLIIDCIGNETELLRTFTSLGYEVQKFLHLSMHGISOILGQFACMP 300

Qy 301 EHRDYSFVCLVSRGGSQSYGVQDQTHSGPLHRIHRRMFMDSCPYLAGKPKMFFIQNY 360
Db 301 EHRDYSFVCLVSRGGSQSYGVQDQTHSGPLHRIHRRMFMDSCPYLAGKPKMFFIQNY 360
Qy 361 VVSEGLSLLVDGPKAMNVEFKAKRGCLCTVHREADFFWSLCTADMSLLSQSHSSP 420
Db 361 VVSEGLSLLVDGPKAMNVEFKAKRGCLCTVHREADFFWSLCTADMSLLSQSHSSP 420
Qy 421 SLYLQCLSQKLRQERKRPDLDLHIELNGMYMDWNSRVSAREKYYVWLQHTLRKKLILSYT 480
Db 421 SLYLQCLSQKLRQERKRPDLDLHIELNGMYMDWNSRVSAREKYYVWLQHTLRKKLILSYT 480

RESULT 3
US-08-859-167-2
; Sequence 2, Application US/08859167
; Patent No. 6037461
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Enad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: FADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF
; TITLE OF INVENTION: USING THE SAME, AND COMPOSITIONS FOR AND METHODS
; TITLE OF INVENTION: OF MAKING THE SAME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6037461rls
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: WINDOWS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,167
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: DeLuca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: RJU-
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 445 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-859-167-2

Query Match 91.6%; Score 2265.5; DB 3; Length 445;
Best Local Similarity 92.5%; Pred. No. 4.6e-211;
Matches 444; Conservative 1; Mismatches 0; Indels 35; Gaps 1;

Qy 1 MSAEVIHQVEEALDTDEKEMLLFCRDVAIDVPPNVRDLIDLIRERKLSVGLAELLY 60
Db 1 MSAEVIHQVEEALDTDEKEMLLFCRDVAIDVPPNVRDLIDLIRERKLSVGLAELLY 60
Qy 61 RVRFDLLKRLKMDRAVETHLRNPHLVSDYVLMAEIGEDLDKSDVSSLIPLMKDYM 120
Db 61 RVRFDLLKRLKMDRAVETHLRNPHLVSDYVLMAEIGEDLDKSDVSSLIPLMKDYM 120
Qy 121 GRGKISKEKSFLLDVLVELEKLNVLAPQLDLLEKLNHRIIDLTKTIQYKQSVQAGT 180
Db 121 GRGKISKEKSFLLDVLVELEKLNVLAPQLDLLEKLNHRIIDLTKTIQYKQSVQAGT 180
Qy 181 SYRNLVQAATQKSLKDPNNFRLHNGRSKEQRLKEQIQAQOEPVKKSIQSEAFLPQIP 240
Db 181 SYRNLVQAATQKSLKDPNNFRLHNGRSKEQRLKEQIQAQOEPVKKSIQSEAFLPQIP 240

Db 181 SYRNVQAAIQSLKDPSPNNFR-----SIP 205

QY 241 EERYKMSKPLGICLIIDICIGNETELLRTFTSLGYEVQKFLHLSMHGISQILGQFACMP 300

Db 206 EERYKMSKPLGICLIIDICIGNETELLRTFTSLGYEVQKFLHLSMHGISQILGQFACMP 265

QY 301 EHRDYSFVCVLVSRGSGSVYGVDTHTSGLPLHHIRRMFMGDSQPYLAGKPKMFFIQNY 360

Db 266 EHRDYSFVCVLVSRGSGSVYGVDTHTSGLPLHHIRRMFMGDSQPYLAGKPKMFFIQNY 325

QY 361 VVSEGLENSLLEVDGPAMKNVFEKAKRGGLCTVHREADFFWSLCTADMSLLEQSHSP 420

Db 326 VVSEGLENSLLEVDGPAMKNVFEKAKRGGLCTVHREADFFWSLCTADMSLLEQSHSP 385

QY 421 SLYLOCSOKLQKROERKRPDLDLHIELNGYMYDMNSRVSAKEYYVWLQHTLRKKLLSYT 480

Db 386 SLYLOCSOKLQKROERKRPDLDLHIELNGYMYDMNSRVSAKEYYVWLQHTLRKKLLSYT 445

RESULT 4

US-09-109-273-2

; Sequence 2, Application US/09109273

; Patent No. 6063760

; GENERAL INFORMATION:

; APPLICANT: Alnemri, Emad S.

; APPLICANT: Fernandez-Alnemri, Teresa

; TITLE OF INVENTION: FADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF

; TITLE OF INVENTION: USING THE SAME, AND COMPOSITIONS FOR AND METHODS

; NUMBER OF SEQUENCES: 17

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6063760r1s

; STREET: One Liberty Place, 46th floor

; CITY: Philadelphia

; STATE: PA

; COUNTRY: USA

; ZIP: 19103

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: WINDOWS

; SOFTWARE: WordPerfect

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/109,273

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/859,167

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Deluca, Mark

; REGISTRATION NUMBER: 33,229

; REFERENCE/DOCKET NUMBER: TJU-

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (215) 568-3100

; TELEFAX: (215) 568-3439

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 445 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-09-109-273-2

Query Match 91.6%; Score 2265.5; DB 3; Length 445;

Best Local Similarity 92.5%; Pred. No. 4.6e-211;

Matches 444; Conservative 1; Mismatches 0; Indels 35; Gaps 1;

QY 1 MSAEVIHQVEALDVTDEKEMLLFLCRDVAIDVVPPNVRLLDILRGRKLSVGDLAELLY 60

Db 1 MSAEVIHQVEALDVTDEKEMLLFLCRDVAIDVVPPNVRLLDILRGRKLSVGDLAELLY 60

QY 61 RVRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIIFLMKDYM 120

Db 61 RVRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIIFLMKDYM 120

QY 121 GRGKTSKESKSFDDLVLVVELEKLNLVAPDQDLLEKCLKNHRIIDLTKIKYKOSVOGAGT 180

Db 121 GRGKTSKESKSFDDLVLVVELEKLNLVAPDQDLLEKCLKNHRIIDLTKIKYKOSVOGAGT 180

QY 181 SYRNVQAAIQSLKDPSPNNFR-----SIP 240

Db 181 SYRNVQAAIQSLKDPSPNNFR-----SIP 205

QY 241 EERYKMSKPLGICLIIDICIGNETELLRTFTSLGYEVQKFLHLSMHGISQILGQFACMP 300

Db 206 EERYKMSKPLGICLIIDICIGNETELLRTFTSLGYEVQKFLHLSMHGISQILGQFACMP 265

QY 301 EHRDYSFVCVLVSRGSGSVYGVDTHTSGLPLHHIRRMFMGDSQPYLAGKPKMFFIQNY 360

Db 266 EHRDYSFVCVLVSRGSGSVYGVDTHTSGLPLHHIRRMFMGDSQPYLAGKPKMFFIQNY 325

QY 361 VVSEGLENSLLEVDGPAMKNVFEKAKRGGLCTVHREADFFWSLCTADMSLLEQSHSP 420

Db 326 VVSEGLENSLLEVDGPAMKNVFEKAKRGGLCTVHREADFFWSLCTADMSLLEQSHSP 385

QY 421 SLYLOCSOKLQKROERKRPDLDLHIELNGYMYDMNSRVSAKEYYVWLQHTLRKKLLSYT 480

Db 386 SLYLOCSOKLQKROERKRPDLDLHIELNGYMYDMNSRVSAKEYYVWLQHTLRKKLLSYT 445

RESULT 5

US-09-276-993-2

; Sequence 2, Application US/09276993

; Patent No. 6207801

; GENERAL INFORMATION:

; APPLICANT: Alnemri, Emad S.

; APPLICANT: Fernandez-Alnemri, Teresa

; TITLE OF INVENTION: FADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF

; TITLE OF INVENTION: USING THE SAME, AND COMPOSITIONS FOR AND METHODS

; NUMBER OF SEQUENCES: 17

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6207801r1s

; STREET: One Liberty Place, 46th floor

; CITY: Philadelphia

; STATE: PA

; COUNTRY: USA

; ZIP: 19103

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: WINDOWS

; SOFTWARE: WordPerfect

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/276,993

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/859,167

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Deluca, Mark

; REGISTRATION NUMBER: 33,229

; REFERENCE/DOCKET NUMBER: TJU-

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (215) 568-3100

; TELEFAX: (215) 568-3439

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 445 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-09-276-993-2

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Query Match 91.6%; Score 2265.5; DB 3; Length 445;
Best Local Similarity 92.5%; Pred. No. 4.6e-211;
Matches 444; Conservative 1; Mismatches 0; Indels 35; Gaps 1;

Qy 1 MSAEVIHQVEALDTDEKEMLLFCRDVAIDVPPNVRDLDLILRERKLSVGDLAELLY 60
Db 1 MSAEVIHQVEALDTDEKEMLLFCRDVAIDVPPNVRDLDLILRERKLSVGDLAELLY 60
Qy 61 RVRFDLLKRLKMDRAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIPLMKDYM 120
Db 61 RVRFDLLKRLKMDRAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIPLMKDYM 120
Qy 121 GRGKISKEKSFDLVVELEKLNIVAPQDLDLLEKLNIRHIDLTKTIKYKQSVQAGT 180
Db 121 GRGKISKEKSFDLVVELEKLNIVAPQDLDLLEKLNIRHIDLTKTIKYKQSVQAGT 180
Qy 181 SYRNVLOAAIOKSLKDPNNFRLHNGRSKQRLKEQLGAQOEPVKYSIQSEAFPLPOSIP 240
Db 181 SYRNVLOAAIOKSLKDPNNFRLHNGRSKQRLKEQLGAQOEPVKYSIQSEAFPLPOSIP 240
Qy 241 EERYKMSKPLGICLIIDCIGNETELLRTDFTSLGYEVQKFLHLSMHGISOILGQFACMP 300
Db 241 EERYKMSKPLGICLIIDCIGNETELLRTDFTSLGYEVQKFLHLSMHGISOILGQFACMP 300
Qy 206 EERYKMSKPLGICLIIDCIGNETELLRTDFTSLGYEVQKFLHLSMHGISOILGQFACMP 265
Db 206 EERYKMSKPLGICLIIDCIGNETELLRTDFTSLGYEVQKFLHLSMHGISOILGQFACMP 265
Qy 301 EHRDYSFVCLVSRGSGSQSVYGDQTHSGPLHRIHRRMFMDGSCPYLAGKPKMFFIQNY 360
Db 301 EHRDYSFVCLVSRGSGSQSVYGDQTHSGPLHRIHRRMFMDGSCPYLAGKPKMFFIQNY 360
Qy 266 EHRDYSFVCLVSRGSGSQSVYGDQTHSGPLHRIHRRMFMDGSCPYLAGKPKMFFIQNY 325
Db 266 EHRDYSFVCLVSRGSGSQSVYGDQTHSGPLHRIHRRMFMDGSCPYLAGKPKMFFIQNY 325
Qy 361 VVSEGLENSLLEVDGPKMKNVEFKAKRGCLCTVHREADFFWSLCTADMSLLEQSHSP 420
Db 361 VVSEGLENSLLEVDGPKMKNVEFKAKRGCLCTVHREADFFWSLCTADMSLLEQSHSP 420
Qy 326 VVSEGLENSLLEVDGPKMKNVEFKAKRGCLCTVHREADFFWSLCTADMSLLEQSHSP 385
Db 326 VVSEGLENSLLEVDGPKMKNVEFKAKRGCLCTVHREADFFWSLCTADMSLLEQSHSP 385
Qy 421 SLXQLCSQKLQERKRPDLHLHIELNGYMYDMNSRVSAREKYYVWLQHTLRKKLILSYT 480
Db 421 SLXQLCSQKLQERKRPDLHLHIELNGYMYDMNSRVSAREKYYVWLQHTLRKKLILSYT 480
Qy 386 SLXQLCSQKLQERKRPDLHLHIELNGYMYDMNSRVSAREKYYVWLQHTLRKKLILSYT 445
Db 386 SLXQLCSQKLQERKRPDLHLHIELNGYMYDMNSRVSAREKYYVWLQHTLRKKLILSYT 445

RESULT 6
US-09-723-450-2
; Sequence 2, Application US/09723450
; Patent No. 6576751
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: Fadd-Like Anti-Apoptotic Molecules, Methods Of Using The Same, And
; FILE REFERENCE: TJU2445
; CURRENT APPLICATION NUMBER: US/09/723,450
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/276,993
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 08/859,167
; PRIOR FILING DATE: 1997-05-20
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Artificial Sequence
; NAME/KEY: misc feature
; OTHER INFORMATION: No. 6576751el Sequence
US-09-723-450-2

Query Match 91.6%; Score 2265.5; DB 4; Length 445;
Best Local Similarity 92.5%; Pred. No. 4.6e-211;
Matches 444; Conservative 1; Mismatches 0; Indels 35; Gaps 1;

Qy 1 MSAEVIHQVEALDTDEKEMLLFCRDVAIDVPPNVRDLDLILRERKLSVGDLAELLY 60
Db 1 MSAEVIHQVEALDTDEKEMLLFCRDVAIDVPPNVRDLDLILRERKLSVGDLAELLY 60
Qy 61 RVRFDLLKRLKMDRAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIPLMKDYM 120
Db 61 RVRFDLLKRLKMDRAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIPLMKDYM 120

Query Match 91.6%; Score 2265.5; DB 3; Length 445;
Best Local Similarity 92.5%; Pred. No. 4.6e-211;
Matches 444; Conservative 1; Mismatches 0; Indels 35; Gaps 1;

Qy 1 MSAEVIHQVEALDTDEKEMLLFCRDVAIDVPPNVRDLDLILRERKLSVGDLAELLY 60
Db 1 MSAEVIHQVEALDTDEKEMLLFCRDVAIDVPPNVRDLDLILRERKLSVGDLAELLY 60
Qy 61 RVRFDLLKRLKMDRAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIPLMKDYM 120
Db 61 RVRFDLLKRLKMDRAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIPLMKDYM 120
Qy 121 GRGKISKEKSFDLVVELEKLNIVAPQDLDLLEKLNIRHIDLTKTIKYKQSVQAGT 180
Db 121 GRGKISKEKSFDLVVELEKLNIVAPQDLDLLEKLNIRHIDLTKTIKYKQSVQAGT 180
Qy 181 SYRNVLOAAIOKSLKDPNNFRLHNGRSKQRLKEQLGAQOEPVKYSIQSEAFPLPOSIP 240
Db 181 SYRNVLOAAIOKSLKDPNNFRLHNGRSKQRLKEQLGAQOEPVKYSIQSEAFPLPOSIP 240
Qy 241 EERYKMSKPLGICLIIDCIGNETELLRTDFTSLGYEVQKFLHLSMHGISOILGQFACMP 300
Db 241 EERYKMSKPLGICLIIDCIGNETELLRTDFTSLGYEVQKFLHLSMHGISOILGQFACMP 300
Qy 206 EERYKMSKPLGICLIIDCIGNETELLRTDFTSLGYEVQKFLHLSMHGISOILGQFACMP 265
Db 206 EERYKMSKPLGICLIIDCIGNETELLRTDFTSLGYEVQKFLHLSMHGISOILGQFACMP 265
Qy 301 EHRDYSFVCLVSRGSGSQSVYGDQTHSGPLHRIHRRMFMDGSCPYLAGKPKMFFIQNY 360
Db 301 EHRDYSFVCLVSRGSGSQSVYGDQTHSGPLHRIHRRMFMDGSCPYLAGKPKMFFIQNY 360
Qy 266 EHRDYSFVCLVSRGSGSQSVYGDQTHSGPLHRIHRRMFMDGSCPYLAGKPKMFFIQNY 325
Db 266 EHRDYSFVCLVSRGSGSQSVYGDQTHSGPLHRIHRRMFMDGSCPYLAGKPKMFFIQNY 325
Qy 361 VVSEGLENSLLEVDGPKMKNVEFKAKRGCLCTVHREADFFWSLCTADMSLLEQSHSP 420
Db 361 VVSEGLENSLLEVDGPKMKNVEFKAKRGCLCTVHREADFFWSLCTADMSLLEQSHSP 420
Qy 326 VVSEGLENSLLEVDGPKMKNVEFKAKRGCLCTVHREADFFWSLCTADMSLLEQSHSP 385
Db 326 VVSEGLENSLLEVDGPKMKNVEFKAKRGCLCTVHREADFFWSLCTADMSLLEQSHSP 385
Qy 421 SLXQLCSQKLQERKRPDLHLHIELNGYMYDMNSRVSAREKYYVWLQHTLRKKLILSYT 480
Db 421 SLXQLCSQKLQERKRPDLHLHIELNGYMYDMNSRVSAREKYYVWLQHTLRKKLILSYT 480
Qy 386 SLXQLCSQKLQERKRPDLHLHIELNGYMYDMNSRVSAREKYYVWLQHTLRKKLILSYT 445
Db 386 SLXQLCSQKLQERKRPDLHLHIELNGYMYDMNSRVSAREKYYVWLQHTLRKKLILSYT 445

RESULT 7
US-09-382-155-17
; Sequence 17, Application US/09382155B
; Patent No. 6160095
; GENERAL INFORMATION:
; APPLICANT: CHAUDHARY, PREET M
; TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NF-KB, JNK AND APOPTOSIS
; FILE REFERENCE: Chaudhary
; CURRENT APPLICATION NUMBER: US/09/382,155B
; CURRENT FILING DATE: 1999-08-24
; EARLIER APPLICATION NUMBER: 09/074,044
; EARLIER FILING DATE: 1998-05-07
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-382-155-17

Query Match 40.7%; Score 1007; DB 3; Length 221;
Best Local Similarity 99.5%; Pred. No. 1.5e-89;
Matches 202; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSAEVIHQVEALDTDEKEMLLFCRDVAIDVPPNVRDLDLILRERKLSVGDLAELLY 60
Db 1 MSAEVIHQVEALDTDEKEMLLFCRDVAIDVPPNVRDLDLILRERKLSVGDLAELLY 60
Qy 61 RVRFDLLKRLKMDRAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIPLMKDYM 120
Db 61 RVRFDLLKRLKMDRAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIPLMKDYM 120
Qy 121 GRGKISKEKSFDLVVELEKLNIVAPQDLDLLEKLNIRHIDLTKTIKYKQSVQAGT 180
Db 121 GRGKISKEKSFDLVVELEKLNIVAPQDLDLLEKLNIRHIDLTKTIKYKQSVQAGT 180
Qy 181 SYRNVLOAAIOKSLKDPNNFRL 203
Db 181 SYRNVLOAAIOKSLKDPNNFRL 203

RESULT 8
US-09-074-044a-17
; Sequence 17, Application US/09074044a
```

```

; Patent No. 6207458
; GENERAL INFORMATION:
; APPLICANT: CHAUDHARY, PREET M
; APPLICANT: HOOD, LEROY
; TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NK-KB, JNK AND
; TITLE OF INVENTION: APOPTOSIS PATHWAYS AND METHODS OF USING THE SAME
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS
; STREET: 2405 GRAND BLVD., SUITE 400
; CITY: KANSAS CITY
; STATE: MISSOURI
; COUNTRY: USA
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/074,044A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: COLLINS, JOHN M
; REGISTRATION NUMBER: 26,262
; REFERENCE/DOCKET NUMBER: 26588
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 816/474-9050
; TELEFAX: 816/474-9057
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 221 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
;
US-09-074-044A-17

Query Match 40.7%; Score 1007; DB 3; Length 221;
Best Local Similarity 99.5%; Pred. No. 1.5e-89;
Matches 202; Conservative 1; Mismatches 0; Indels 0; Gaps

QY 1 MSAEVIHQVEEALDPTDEKEMLLFLCRDVAIDVPPNVRDLDDLRLRERKLSVGDIAELLY
DB 1 MSAEVIHQVEEALDPTDEKEMLLFLCRDVAIDVPPNVRDLDDLRLRERKLSVGDIAELLY
QY 61 RYVRFDLLKRLKMDRKAVETHLLRNPHLSVDRYVLMAEIGEDLDKSDVSSLIFLMKDY
DB 61 RYVRFDLLKRLKMDRKAVETHLLRNPHLSVDRYVLMAEIGEDLDKSDVSSLIFLMKDY
QY 121 GRGKTSKEKSFLLDLVVELEKLNLPADQLDLEKLNHRIIDLTKTKQKSVQAGAT
DB 121 GRGKTSKEKSFLLDLVVELEKLNLPADQLDLEKLNHRIIDLTKTKQKSVQAGAT
QY 181 SYRNVLAQAIQSLKDPNNFRL 203
DB 181 SYRNVLAQAIQSLKDPNNFRL 203

RESULT 9
US-09-074-044A-2
; Sequence 2, Application US/09074044A
; Patent No. 6207458
; GENERAL INFORMATION:
; APPLICANT: CHAUDHARY, PREET M
; APPLICANT: HOOD, LEROY
; TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NK-KB, JNK AND
; TITLE OF INVENTION: APOPTOSIS PATHWAYS AND METHODS OF USING THE SAME
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:

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; FILING DATE: 16-JAN-1998
 ; PRIOR APPLICATION DATA: PCT/US96/10521
 ; APPLICATION NUMBER: 14-JUN-1996
 ; FILING DATE: 14-JUN-1996
 ; PRIOR APPLICATION DATA: IL 114,615
 ; APPLICATION NUMBER: 16-JUL-1995
 ; FILING DATE: 16-JUL-1995
 ; PRIOR APPLICATION DATA: IL 114,986
 ; APPLICATION NUMBER: 17-AUG-1995
 ; FILING DATE: 17-AUG-1995
 ; PRIOR APPLICATION DATA: IL 115,319
 ; APPLICATION NUMBER: 14-SEP-1995
 ; FILING DATE: 14-SEP-1995
 ; PRIOR APPLICATION DATA: IL 116,588
 ; APPLICATION NUMBER: 27-DEC-1995
 ; FILING DATE: 27-DEC-1995
 ; PRIOR APPLICATION DATA: IL 117,932
 ; APPLICATION NUMBER: 16-APR-1996
 ; FILING DATE: 16-APR-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Browdy, Roger L.
 ; REGISTRATION NUMBER: 25,618
 ; REFERENCE/DOCKET NUMBER: WALLACH-19
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 628-5197
 ; TELEFAX: (202) 737-3528
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 479 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-983-502-7

Query Match 16.68; Score 410; DB 4; Length 479;
 Best Local Similarity 26.18; Pred. No. 3.9e-31;
 Matches 137; Conservative 106; Mismatches 172; Indels 110; Gaps 22;
 QY 6 IHVVEALDTDEKEMLLFLCRDVAIDVPPN---VRDLDDI---LRERGLSVGDLA-- 56
 DB 7 LYDGEQDSDSDASLAF---SLDIYIPQKQPKIDALMLFORQKRMLESNLSFL 62
 QY 57 -ELLYRVRRFDLLKRLKMDKAVETHLLRNP--HLVSDYRVLMMAEIGEDLDKSDVSSLI 113
 DB 63 KELLFRINRLDLLTYLNTKREEMERE-LQTPGGAQISAVRVMLYQISEEVSRLSFK 121
 QY 114 FLMDYMGKGIKSEKSFLLDVLEKLNVLVAPDQLDLLEKLNHRIIDLTKIKYKQ 173
 DB 122 FLIQEISKKLDMDMLDIFEMERKVLIGEGKDLKRVCAQINKSLKI-INDYEE 180
 QY 174 -----SVQAGTSYRNVLQAATQKSLKDPNNFRLHNGRSKQRLKEQLGAQOEPVK 226
 DB 181 FSKERSSSLEGPDSFNGELCGVMTISDSPRE-----NETEL--- 214
 QY 227 SIQSEAPLPQSIPEERYKMKSKPLGICLIIDICG-----NETEL--- 266
 DB 215 --QDS----QTL-DKYQMKSKRGYGLIINNHNFAKREKVPKLHSIRDRNGTHLDAG 268
 QY 267 -LRDTFTSLGVEQKFLHLSMHGISQILQOPACMPHEHRDYSFVCVLVSRGSGSVYGV 325
 DB 269 ALTTTFELHFEIAPHDDCTVEQIYEILKIYQLM-DHSNMDCFICCLSHGDKGIITYGT 327
 QY 326 QTHSGPLPHHRRFMGDSQPYLAGKPKMFFIQ-----NY---VYSEGLQENSSLLVED- 376
 DB 328 GOEA--PIYELTSQTLGKSLAGKPKVFIQACQDNQKQIPVETDSEQPYLEMDL 385
 QY 377 -GPAKNVFEKQKGLCTVHREADFWSLCTADMSLLEQSHSPSYLYLQCLSKLROE- 434
 DB 386 SSPQTRYIP-----DEADFLIGMATVNCVSYRNPAEGTWTYIQLCSLRERC 433
 QY 435 -RKRPDLDLHLNAGYWDNWSRYSAKE--KYIYWLQHTLRKLI 476

Db 434 PRGDDILTILTEVN---YEYSNKDDKKNMGKOMPQPTFTLRKKLV 475
 RESULT 11
 US-09-516-747-7
 ; Sequence 7, Application US/09516747
 ; Patent No. 6586571
 ; GENERAL INFORMATION:
 ; APPLICANT: David WALLACH
 ; Mark P. BOLDIN
 ; Tanya M. GONCHAROV
 ; Yury V. GOLTSEV
 ; TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS RECEPTORS
 ; AND OTHER PROTEINS
 ; NUMBER OF SEQUENCES: 34
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Browdy and Neimark
 ; STREET: 419 Seventh Street N.W., Ste. 300
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20004
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/516,747
 ; FILING DATE: 01-Mar-2000
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/983,502
 ; FILING DATE: <Unknown>
 ; APPLICATION NUMBER: IL 114,615
 ; FILING DATE: 16-JUL-1995
 ; APPLICATION NUMBER: IL 114,986
 ; FILING DATE: 17-AUG-1995
 ; APPLICATION NUMBER: IL 115,319
 ; FILING DATE: 14-SEP-1995
 ; APPLICATION NUMBER: IL 116,588
 ; FILING DATE: 27-DEC-1995
 ; APPLICATION NUMBER: IL 117,932
 ; FILING DATE: 16-APR-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Browdy, Roger L.
 ; REGISTRATION NUMBER: 25,618
 ; REFERENCE/DOCKET NUMBER: WALLACH-19
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 628-5197
 ; TELEFAX: (202) 737-3528
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 479 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
 US-09-516-747-7

Query Match 16.68; Score 410; DB 4; Length 479;
 Best Local Similarity 26.18; Pred. No. 3.9e-31;
 Matches 137; Conservative 106; Mismatches 172; Indels 110; Gaps 22;
 QY 6 IHVVEALDTDEKEMLLFLCRDVAIDVPPN---VRDLDDI---LRERGLSVGDLA-- 56
 DB 7 LYDGEQDSDSDASLAF---SLDIYIPQKQPKIDALMLFORQKRMLESNLSFL 62
 QY 57 -ELLYRVRRFDLLKRLKMDKAVETHLLRNP--HLVSDYRVLMMAEIGEDLDKSDVSSLI 113
 DB 63 KELLFRINRLDLLTYLNTKREEMERE-LQTPGGAQISAVRVMLYQISEEVSRLSFK 121
 QY 114 FLMDYMGKGIKSEKSFLLDVLEKLNVLVAPDQLDLLEKLNHRIIDLTKIKYKQ 173


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122 FLQEEISCKLDDNNLLDIFTEMKRVILGKGLDILKRVCAQINKSLKTI-INDYEE 180
174 -----SVQAGCTSYRNVLQAAIQKSLKDPNSNFRHLNRSKEQRLKEQLGAQOEPVK 226
181 FSKERSSSLEGSDFESNGEELCGVMTISDSPRE----- 214
227 SIQESAFILPQSIPPEERYKMKSPGLGICLIIDCIG-----NETEL--- 266
215 --QDSSES--QTL-DKVOYQMKSPRGYCLIIHNNHFAKAREKVPKLSIRDRNGTHLDAG 268
267 -LRDTFTSLGYEVOKFLHLSMHGISOILGQFACMPHEDYDVFVCLVSRGGSQSVYGV 325
269 ALTTTEELHFEIKPHDDCTVEQIYELIKYQLM-DHSNMDCFICILSHGDKGIYGT 327
326 QTHSGPLHHRMFMDGSCPYLAGPKMFFFIO-----NY---VSEGOLENSLLEVD- 376
328 GQEA--PIYELTSQFTGLKPSLAGPKVFFIQACQGDNYQKGPVETDSEEQPYLEMDL 385
377 -GPMKNVFEKAKRGKGLCTVHREADFWLSICTADMSLLEQSHSPSLYLQCLSKLRQE- 434
386 SSPQTRYIP-----DEADFLGMATVNNCVSYRNPAEGTWYIQSLQSLRERC 433
435 -RRRPLDLHLIELNGYMDWNSRVSAKE--KYVWLQHTLRKKLI 476
434 PRGDDILTILTEVN---YEVSNDKDKKNGKMPQPTFTLRKKLV 475

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RESULT 12

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PCT-US96-10521-7
; Sequence 7, Application PC/TUS9610521
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS RECEPTORS
; TITLE OF INVENTION: AND OTHER PROTEINS
; NUMBER OF SEQUENCES: 34
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10521
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 114,615
; FILING DATE: 16-JUL-1995
; PRIOR APPLICATION DATA: IL 114,986
; APPLICATION NUMBER: IL 117,932
; FILING DATE: 17-AUG-1995
; APPLICATION NUMBER: IL 115,319
; FILING DATE: 14-SEP-1995
; APPLICATION NUMBER: IL 116,588
; FILING DATE: 27-DEC-1995
; APPLICATION NUMBER: IL 117,932
; FILING DATE: 16-APR-1996
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 479 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US96-10521-7

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Query Match 16.6%; Score 410; DB 5; Length 479;
Best Local Similarity 26.1%; Pred. No. 3.9e-31;
Matches 137; Conservative 106; Mismatches 172; Indels 110; Gaps 22;

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QY 6 IHQVEALDTDEKEMLLFCROVAIDVPPN-----VRDLIDI---LRERKLSQVGLA-- 56
DB 7 LXDIGQLDSEDLASLKL-----SLDYIPQKOEPIKDALMLQRLQKRMLESNFL 62
QY 57 -ELLYVVRFDLLKRLKMDRKAVETHLLRNP--HLVSDYRVLMARIGEDLDKSDVSSLI 113
DB 63 KELLFRINRDLITTYLNRKEEMERE-LQTPQRAQISATYRWMLYQISEEVSRELSKSF 121
QY 114 FLKDYMGKGIKSKESFLDVLVVELEKLNVLAPDQLDLLEKCLKNHRIIDKTKIQYKQ 173
DB 122 FLQEEISCKLDDNNLLDIFTEMKRVILGKGLDILKRVCAQINKSLKTI-INDYEE 180
QY 174 -----SVQAGCTSYRNVLQAAIQKSLKDPNSNFRHLNRSKEQRLKEQLGAQOEPVK 226
DB 181 FSKERSSSLEGSDFESNGEELCGVMTISDSPRE----- 214
QY 227 SIQESAFILPQSIPPEERYKMKSPGLGICLIIDCIG-----NETEL--- 266
DB 215 --QDSSES--QTL-DKVOYQMKSPRGYCLIIHNNHFAKAREKVPKLSIRDRNGTHLDAG 268
QY 267 -LRDTFTSLGYEVOKFLHLSMHGISOILGQFACMPHEDYDVFVCLVSRGGSQSVYGV 325
DB 269 ALTTTEELHFEIKPHDDCTVEQIYELIKYQLM-DHSNMDCFICILSHGDKGIYGT 327
QY 326 QTHSGPLHHRMFMDGSCPYLAGPKMFFFIO-----NY---VSEGOLENSLLEVD- 376
DB 328 GQEA--PIYELTSQFTGLKPSLAGPKVFFIQACQGDNYQKGPVETDSEEQPYLEMDL 385
QY 377 -GPMKNVFEKAKRGKGLCTVHREADFWLSICTADMSLLEQSHSPSLYLQCLSKLRQE- 434
DB 386 SSPQTRYIP-----DEADFLGMATVNNCVSYRNPAEGTWYIQSLQSLRERC 433
QY 435 -RRRPLDLHLIELNGYMDWNSRVSAKE--KYVWLQHTLRKKLI 476
DB 434 PRGDDILTILTEVN---YEVSNDKDKKNGKMPQPTFTLRKKLV 475

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RESULT 13

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US-08-807-200-12
; Sequence 12, Application US/08807200
; Patent No. 5837837
; GENERAL INFORMATION:
; APPLICANT: Hunter, John J.
; APPLICANT: Shigjan, Andrew W.
; APPLICANT: Wong, Grace H.W.
; TITLE OF INVENTION: NOVEL FORMS OF CASPASE-8 AND
; TITLE OF INVENTION: USES THEREFOR
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/807,200
; FILING DATE: 27-FEB-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/021001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070

```

```
;
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 479 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-807-200-12

Query Match          16.5%; Score 408; DB 2; Length 479;
Best Local Similarity 26.1%; Pred. No. 6.1e-31;
Matches 137; Conservative 105; Mismatches 173; Indels 110; Gaps 22;

QY 6 IHVVEALDTDEKEMLLFLCRDVAIDVVPPN-----VRDLDDI---LRERGLKLSVGDLA-- 56
DB 7 LYDIGEQDSEDLASLAKFL-----SLDYIPQRKQEPKIDALMLFQRLQEKRMLESNLSFL 62
QY 57 -ELLYRVRRFDLLKRILKMDRKAVETHLLRNP--HLVSDYRVLMAEIGEDLDKSDVSSLI 113
DB 63 KELLFRINRLDLLTYLNTKREEMERE-LQTPGRAQISAYRVMLYQISEEVSRLSFK 121
QY 114 FLMDYMGGRGKISKEKSFLLVLEKLNLPDQLLEKLNHRIIDLTKTIOKYQ 173
DB 122 FLQEEISKCKLDDMDNLLDIFIEWKRVILGEGKLDILKRVCAQINKSLKI-INDYEE 180
QY 174 -----SVQAGTSYRNVLQAAIQSLKDPNSNFRHLNHRGSKQRLKEQLGAQOEPVK 226
DB 181 FSKERSSSLEGSPDFSNGEELCGVMTISDSPRE-----NETEL--- 266
QY 227 SIQSEAFPLPOSIPERYKMKSPGLICLIIDICIG-----NETEL--- 266
DB 215 --QDSES---QTL-DKVYQMKSKPRGYCLIIINNHFARAKREKVPKLHSIRDRNGTHLDAG 268
QY 267 -LRDTFTSLGYEVOKFLHLSMHGISOILGQFACMPHEHRDYDSFVCLVSRGSGSVYGD 325
DB 269 ALTTTFEELHFEIRPHDCTVEQIYEILKIYQLM-DHSNMDCFICCLSHGDKGIYGT 327
QY 326 QTHSGLPLHRIIRFMGDCSPYLAGPKMFFIQ-----NY---VVEGQLENSLSLEVD- 376
DB 376 QTHSGLPLHRIIRFMGDCSPYLAGPKMFFIQ-----NY---VVEGQLENSLSLEVD- 376
QY 377 -GPAKNVFEKRAQKRGCTVHREADFWSLCTADMSLLEQSHSPSYLVLCLOKLRQE- 434
DB 386 SSPQTRYIP-----DEADFLGMATVNCVSYRNPAGCTWTIQLSCLSLRRC 433
QY 435 -RKRPDLHLIELNGYMYDWSRYSAKE--KYVWLQHTLRKKLI 476
DB 434 PRGDDILTILTEVN---YEVSNDKDDKKNMGKQMPQPTFTLRKKLV 475
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```
RESULT 14
US-09-001-777-12
; Sequence 12, Application US/09001777
; Patent No. 6172190
; GENERAL INFORMATION:
; APPLICANT: Hunter, John J.
; APPLICANT: Shyjan, Andrew W.
; APPLICANT: Wong, Grace H.W.
; TITLE OF INVENTION: NOVEL FORMS OF CASPASE-8 AND USES THEREOF
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
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;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/001.777
; FILING DATE: 31-DEC-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/807,200
; FILING DATE: 27-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 07334/021002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 479 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-09-001-777-12

Query Match          16.5%; Score 408; DB 3; Length 479;
Best Local Similarity 26.1%; Pred. No. 6.1e-31;
Matches 137; Conservative 105; Mismatches 173; Indels 110; Gaps 22;

QY 6 IHVVEALDTDEKEMLLFLCRDVAIDVVPPN-----VRDLDDI---LRERGLKLSVGDLA-- 56
DB 7 LYDIGEQDSEDLASLAKFL-----SLDYIPQRKQEPKIDALMLFQRLQEKRMLESNLSFL 62
QY 57 -ELLYRVRRFDLLKRILKMDRKAVETHLLRNP--HLVSDYRVLMAEIGEDLDKSDVSSLI 113
DB 63 KELLFRINRLDLLTYLNTKREEMERE-LQTPGRAQISAYRVMLYQISEEVSRLSFK 121
QY 114 FLMDYMGGRGKISKEKSFLLVLEKLNLPDQLLEKLNHRIIDLTKTIOKYQ 173
DB 122 FLQEEISKCKLDDMDNLLDIFIEWKRVILGEGKLDILKRVCAQINKSLKI-INDYEE 180
QY 174 -----SVQAGTSYRNVLQAAIQSLKDPNSNFRHLNHRGSKQRLKEQLGAQOEPVK 226
DB 181 FSKERSSSLEGSPDFSNGEELCGVMTISDSPRE-----NETEL--- 266
QY 227 SIQSEAFPLPOSIPERYKMKSPGLICLIIDICIG-----NETEL--- 266
DB 215 --QDSES---QTL-DKVYQMKSKPRGYCLIIINNHFARAKREKVPKLHSIRDRNGTHLDAG 268
QY 267 -LRDTFTSLGYEVOKFLHLSMHGISOILGQFACMPHEHRDYDSFVCLVSRGSGSVYGD 325
DB 269 ALTTTFEELHFEIRPHDCTVEQIYEILKIYQLM-DHSNMDCFICCLSHGDKGIYGT 327
QY 326 QTHSGLPLHRIIRFMGDCSPYLAGPKMFFIQ-----NY---VVEGQLENSLSLEVD- 376
DB 376 QTHSGLPLHRIIRFMGDCSPYLAGPKMFFIQ-----NY---VVEGQLENSLSLEVD- 376
QY 377 -GPAKNVFEKRAQKRGCTVHREADFWSLCTADMSLLEQSHSPSYLVLCLOKLRQE- 434
DB 386 SSPQTRYIP-----DEADFLGMATVNCVSYRNPAGCTWTIQLSCLSLRRC 433
QY 435 -RKRPDLHLIELNGYMYDWSRYSAKE--KYVWLQHTLRKKLI 476
DB 434 PRGDDILTILTEVN---YEVSNDKDDKKNMGKQMPQPTFTLRKKLV 475
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RESULT 15
US-08-852-782-3
; Sequence 3, Application US/08852782
; Patent No. 6008042
; GENERAL INFORMATION:
; APPLICANT: Vishva Dixit, Kristine Kikly, Jian Ni, Craig Rosen and
; APPLICANT: Steven Ruben
; TITLE OF INVENTION: INTERLEUKIN-1 BETA CONVERTING ENZYME LIKE APOPTOTIC PR
; NUMBER OF SEQUENCES: 3
```

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Smithkline Beecham Corporation
;; STREET: 709 Swedeland Road
;; CITY: King of Prussia
;; STATE: PA
;; COUNTRY: USA
;; ZIP: 19406-2799
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: PastSeq Version 1.5
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/852,782
;; FILING DATE:
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 60/019,365
;; FILING DATE: 05 JUNE 1996
;; APPLICATION NUMBER: 60/017,454
;; FILING DATE: 17 MAY 1996
;; APPLICATION NUMBER: 60/017,914
;; FILING DATE: 16 MAY 1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Han, William T
;; REGISTRATION NUMBER: 34,344
;; REFERENCE/DOCKET NUMBER: P50484-2
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 610-270-5219
;; TELEFAX: 610-270-5090
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 479 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; HYPOTHEtical: NO
;; ANTI-SENSE: NO
;; FRAGMENT TYPE: N-terminal
;; ORIGINAL SOURCE:
US-08-852-782-3

Query Match 16.4%; Score 406; DB 3; Length 479;
Best Local Similarity 26.1%; Pred. No. 9.5e-31;
Matches 137; Conservative 105; Mismatches 173; Indels 110; Gaps 22;
QY 6 IHQVEALDTDEKEMLLFLCRDVAIDVPPN---VRDLIDI---LRERKLSVGLA--- 56
DB 7 LYDIGQLDSEDLASLKLFL-----SLDIYIPQRKEPIKDALMLFORLQEKRLMEESNLSFL 62
QY 57 -ELLYRVRFDLRLKRLKMDRAKAVETHLLRNP--HLVSDYRVLMAEIGEDLDKSDVSSLI 113
DB 63 KELLFRINRDLITTYLNTKRKEMERE-LQTPCRAQISAYRVMLYQISEVSRSELRSFK 121
QY 114 FLAKDVMGRGKISKESKESFDLDVVELEKLNVLAPDQDLLEKCLKNHRIIDLTKIKQYKQ 173
DB 122 FLIQEISCKLDDDDNNLLDITFEMEKRVILGEGKLDILKRVCAQINKSLKI-INDYEE 180
QY 174 -----SYOGACTSYRVNVLQAAIQKSLKDPNPNFLHNGRSKEQLKQLGAQEPVK 226
DB 181 FSKERSSSLESPDFSNSEELGVMTISDSPRE----- 214
QY 227 SIQSEAFUPQSIPERYKMKSKPLGICLIIDICG-----NETEL--- 266
DB 215 --QDSES---QTL-DKVIQMKSKPRGYCLIIINHNFAKAREKVPKLSHTRDRNGTHLDAG 268
QY 267 -LRDTFTSLGYEVQKFLHLSMHGISQILGQFACMPHRDYSFVCVLSRGGSSQSVGYD 325
DB 269 ALTTTFEELHFEIKPHDDCTVQEIYELIKIYQL-DHSNMDCFICCLSHGDKGIYGT 327
QY 326 QTHSGPLHLHRRMFMDGSCPYLAGPKMFFIQ-----NY-----VVSEGLENSLLEVD- 376

DB 328 GQEP--PIYELTSQFTGLKCPSLAGRPKVFFIQAQGDNYQKGIPIVETDSEEQPYLEMDL 385
QY 377 -GPAMKNVEFKAQKRGCLCTVHREADFFWSLCTADMSLLLEQSHSSPSLYLQCLLSQKLRQE- 434
DB 386 SSPQTRYIP-----DEADFLMGATVNNCVSYRNPAEGTWYIQLWSLQSRERC 433
QY 435 -RRPLLDLHLIELNGYMYDMNSRVSAKE--KYVVMQLQHTLRKKLI 476
DB 434 PRGDDILITLITVN---YEVSNKDDKKNGKQMPQPTFTLRKKLV 475

Search completed: August 13, 2003, 16:45:03
Job time : 29.7589 secs

A:Status: preliminary; translated from GB/EMBL/DBD

A:Molecule type: mRNA

A:Residues: 1-212 <RES>

A:Cross-references: EMBL:U34685; NID:gl1004370; PIDN:AAC52261.1; PID:gl1004371

C:Keywords: cysteine proteinase; hydrolase

Query Match 7.5%; Score 184.5; DB 2; Length 212;
Best Local Similarity 29.1%; Pred. No. 4.8e-05;
Matches 60; Conservative 36; Mismatches 81; Indels 29; Gaps 8;

QY 241 EERYKMKSKPLGICLIID-----CIGNETEL-----LRDFTSLGYEVQKFLHLM 286
DB 5 DSSYKMDYPEMGLCIIINNNFKHSTGMSARNGTDVDAANLRETFMALKYEVNRKNLDLR 64
QY 287 HGISOILGQACPMPEHRDYDFVCLVSRGSGSQSVYGVQDTHSGPLHLHRRMFMGDSQP 346
DB 65 EEIMELMDSVS-KEDHSKRSSFVCLVSHGDEGVIFG---TNGPVDLKLKTSFPRGDYCR 120
QY 347 YLACKPKMFFIQTNYVSEGLENSLLEVDGPMKNVFEFAKRGKGLCTVIREADFFWSLC 406
DB 121 SLTGKPKLFITQ---ACRG-TELDSTGTDGADDDV---ACOKKPV-----EADFLYAYS 169
QY 407 TADMSLLEQSSPSLVLCQLSQKLR 432
DB 170 SAPGYSWRNSRGGSWFIQSLCAMLK 195

RESULT 3

JC5410

CPP32 protein - mouse

C:Species: Mus musculus (house mouse)

C:Date: 10-Jun-1997 #sequence_revision 18-Jul-1997 #text_change 17-Mar-1999

R:Accession: JC5410

R:Mukasa, T.; Urabe, K.; Momoi, M.Y.; Kimura, I.; Momoi, T.

Biochem. Biophys. Res. Commun. 231, 770-774, 1997

A:Title: Specific expression of Cpp32 in sensory neurons of mouse embryos and activation

A:Reference number: JC5410; MUID:97224429; PMID:9070890

A:Accession: JC5410

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-277 <MUK>

A:Cross-references: DDBJ:D86352

A:Experimental source: embryo

C:Comment: This protein is involved in the apoptosis of dorsal root ganglia neurons.

Query Match 7.3%; Score 181.5; DB 2; Length 277;
Best Local Similarity 27.6%; Pred. No. 0.00011;
Matches 67; Conservative 37; Mismatches 104; Indels 35; Gaps 10;

QY 204 HNGRSKEQRLKEQLGAQOEYKKSIOEAEFLPOSIPERYKMKSKPLGICLI----- 257
DB 3 NNTSVDSKSNINFGVKTIGHGSKSV-DSGIYLDSS-----YKMDYPMGICIIITNKNFH 56
QY 258 -----DCIGNETEL--LRDFTSLGYEVQKFLHLMHGISOILGQACPMPEHRDYDSFV 309
DB 57 KSTGMSRSGTDVDAANLRETFMGLKYEVRKNLDTREEIMELMDSVS-KEDHSKRSSFV 115
QY 310 CVLVSRGSGSQSVYGVQDTHSGPLHLHRRMFMPMGDSCPYLAGPKMFFIQTNYVSEGOLEN 369
DB 116 CVILSHGDEGVIFG---TNGPVDLKLKTSFPRGDYCRSLTGKPKLFITQ---ACRG-TEL 168
QY 370 SSLLEVDPKMKNVFEFAKRGKGLCTVIREADFFWSLCTADMSLLEQSSPSLVLCQLSQ 429
DB 169 DCGIETDSGT--DEMAQCK-----IPVEADFLYAYSTAPGYSWRNSKDGSWFIQSLCS 221
QY 430 KLR 432
DB 222 MLK 224

RESULT 4

A55315

cysteine proteinase (EC 3.4.22.-) Cpp32 precursor - human

N:Alternate names: cysteine proteinase CPP32

C:Species: Homo sapiens (man)

C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 01-Dec-2000

A:Accession: A55315; S58999; I39005

R:Fernandes-Alnemri, T.; Litwack, G.; Alnemri, E.S.

J. Biol. Chem. 269, 30761-30764, 1994

A:Title: CPP32, a novel human apoptotic protein with homology to Caenorhabditis elega

A:Reference number: A55315; MUID:95074098; PMID:7983002

A:Accession: A55315

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-277 <PER>

A:Cross-references: GB:U13737; NID:9561665; PIDN:AAA65015.1; PID:9561666

R:Nicholson, D.W.; Ali, A.; Thornberry, N.A.; Vaillancourt, J.P.; Ding, C.K.; Gallant

; Yu, V.L.; Miller, D.K.

Nature 376, 37-43, 1995

A:Title: Identification and inhibition of the ICE/CED-3 protease necessary for mamma

A:Reference number: S58999; MUID:95319529; PMID:7596430

A:Accession: S58999

A:Molecule type: protein

A:Residues: 29-46; 176-189, 'E', 191-193 <NIC>

R:Tewari, M.; Quan, L.T.; O'Rourke, K.; Desnoyers, S.; Zeng, Z.; Beidler, D.R.; Poiri

Cell 81, 801-809, 1995

A:Title: Yama/CPP32 beta, a mammalian homolog of CED-3, is a CrmA-inhibitable proteas

A:Reference number: A56924; MUID:95292347; PMID:7774019

A:Accession: I39005

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-189, 'E', 191-277 <RES>

A:Cross-references: EMBL:U26943; NID:9857568; PIDN:AAA74929.1; PID:9857569

C:Keywords: apoptosis; cysteine proteinase; hydrolase; lymphocyte

Query Match 7.3%; Score 181; DB 2; Length 277;
Best Local Similarity 26.8%; Pred. No. 0.00012;
Matches 69; Conservative 40; Mismatches 102; Indels 46; Gaps 9;

QY 222 EPYKKSIOEAEFLPOSIPERYKMKSKPLGICLIID-----CIGNETEL--L 267
DB 17 EP--KIITHSESMDSGISLONSRYKMDYPEMGLCIIINNNFKHSTGMSRSGTDVDAANL 74
QY 268 RDTFTSLGYEVQKFLHLMHGISOILGQACPMPEHRDYDFVCLVSRGSGSQSVYGVQDT 327
DB 75 REIFRNLYKYEVRKNLDTREEIVELMRDVS-KEDHSKRSSFVCLVSHGEGGIIFG--T 130
QY 328 HSGPLHLHRRMFMPMGDSCPYLAGPKMFFIQTNYVSEGO--LENSLLEVDGPMKNVFE 385
DB 131 NGPVDLKKITNFFRGDRCSLTGKPKLFITQACRGTELDGCIETDSGVDDDMACHK---- 186
QY 386 KAQRGLCTVIREADFFWSLCTADMSLLEQSSPSLVLCQLSQKLRQERKRPILLDLHI- 444
DB 187 -----IPVDADFLYAYSTAPGYSWRNSKDGSWFIQSLCAMLKQYADK-LEFPHIL 236
QY 445 -----ELNGYMYD 452
DB 237 TRVNRKVATEPESFSFD 253

RESULT 5

S64710

cysteine proteinase (EC 3.4.22.-) Cpp32 - Chinese hamster

C:Species: Crictetus griseus (Chinese hamster)

C:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 05-Nov-1999

C:Accession: S64710; S72395

R:Wang, X.; Zelenski, N.G.; Yang, J.; Sakai, J.; Brown, M.S.; Goldstein, J.L.

EMBO J. 15, 1012-1020, 1996

A:Title: Cleavage of sterol regulatory element binding proteins (SREBPs) by CPP32 dur

A:Reference number: S64710; MUID:96183185; PMID:8605870

A:Accession: S64710

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-277 <WAN>

A:Cross-references: EMBL:U27463

R:Wang, X.

submitted to the EMBL Data Library, May 1995
A:Reference number: S72395
A:Accession: S72395
A:Molecule type: mRNA
A:Residues: 1-79, 'A', 81-146, 'Y', 148-277 <NAW>
A:Cross-references: EMBL:U27463; NID:g1244443; PIDN:AAB01511.1; PID:g1244444
C:Keywords: apoptosis; cysteine proteinase; hydrolase

Query Match 7.3%; Score 179.5; DB 2; Length 277;
Best Local Similarity 27.4%; Pred. No. 0.00015;
Matches 61; Conservative 36; Mismatches 93; Indels 33; Gaps 6;
QY 226 KSIQSEAPLPPOSIEPEERYKMKSKPLGICLIID-----CIGNETEL--LRDPF 271
DB 19 KTIHSGKSDSYLDSSYKMDYPENGVCIINNNHFKSTGMTPRSGTDVDAAKLRETF 78
QY 272 TSLGVEVOKFLHLSMHGISOILQGFACMPHEDYDFVCVLVSRGSSQSVYGVDTQTHSLG 331
DB 79 MNLKYEVRNKNDLTREETIEVELM-KNASKEDHRSFVCVILSHGDEGVIFGTD---GPI 134
QY 332 PLHHIRRMFMGDCPYLAGKPKMFFIIONYVVSEGO--LENSLLEVDGPKAMNVEFKAOK 389
DB 135 DLKLTYSYFRGDRCSRSLGKPKLFIQACRGTELDGIGTDSGTEDDMTCQK-----186
QY 390 RGLCTVHREADFWSLCTADMSLLEQSHSPSYLYLQCLSQKLR 432
DB 187 -----IPVEADFLYATAPGYISWRNPRDGSFWFIQSLCSMLK 224

RESULT 6
JC6507
caspase-2 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C:Accession: JC6507
R:Sato, N.; Milligan, C.E.; Uchiyama, Y.; Oppenheim, R.W.
Gene 202, 127-132, 1997
A:Title: Cloning and expression of the cDNA encoding rat caspase-2.
A:Reference number: JC6507; MUID:98087427; PMID:9427555
A:Accession: JC6507
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-452 <SNA>
A:Cross-references: GB:U77933; NID:g2769705; PIDN:AAB96379.1; PID:g2769706

Query Match 7.2%; Score 177.5; DB 2; Length 452;
Best Local Similarity 22.4%; Pred. No. 0.00039;
Matches 97; Conservative 65; Mismatches 166; Indels 105; Gaps 18;
QY 84 LRNPHLVSYRVLMABIGEDLDKSDVSSLIPLMKDYMGKISKESKSFIDLVLVELEKLN 143
DB 40 LKKNRVVLAKOLLSELLEHLEKDIITL--EMRELIQ----AKGVSFSQ---NVELLN 90
QY 144 V---APDQDLLEKCLKNI---HRID-LTKTKIQKQSVQAGTYSRVNVLQAAIQSLKD 196
DB 91 LPRGPGQAFDAFCEALRETQGHLEDLTLTTLSQIHILPPLSCDYSLSPFVSCSC-P 149
QY 197 PSNNFRLHNGRSKEQRLKEQLGAQOEPVKKSIOEAFLPQSIPEERYKMKSKPLGICLI 256
DB 150 PHKQSLSTD-TMESHSLDNGDGPCLQVPCPTE-----FYQAHYQLAYRLQSQPGLALV 204
QY 257 IDCI-----GNETE--LLRDTFTSLGYEVQKFLHLSMHGISQILQGFACMPRH 302
DB 205 MSNVHFTGKOLEFRSGGDVDTLTLVTLFKLLGVNVHLYDQTAEMQEKLNQFALQPAH 264
QY 303 RYDSEFVCLVSRGSSQSVYGVDTQTHSGPLHHRMFMGDCSCPYLAKGPKMFFQ----358
DB 265 RVTDSCTVALLSHGVEGGIYGVDD--GKLIQIQEVFLFDNANCPSLQNKPRMFFQACRG 322
QY 359 -----NVYVSEGLENSSS-----LLEVDGPKAMK-----NVEFKAOKR 390
DB 323 DETDRGVDDQDGKNAQSPGCEESDAGKEELMKMLPFRSDMICGYACLKGNAMNRTKR 382

QY 391 GLCTVHREADFWSLCTADMSLLEQSHSPSYLYLQCLSQKLRKRRLPDLHLHIELNGYM 450
DB 383 G-----SWTIEALTQVFSER-----ACDMHVA--DML 407
QY 451 YDWNRSVSAKEY 463
DB 408 VKVNALIKEREGY 420

RESULT 7
A54821
apoptosis regulator ICH-1, stimulatory form L - human
C:Species: Homo sapiens (man)
C:Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 17-Mar-1999
C:Accession: A54821
R:Wang, L.; Miura, M.; Bergeron, L.; Zhu, H.; Yuan, J.
Cell 78, 739-750, 1994
A:Title: Ich-1, an Ice/Ced-3-related gene, encodes both positive and negative regulat
A:Reference number: A54821; MUID:94373811; PMID:8087842
A:Accession: A54821
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-435 <WAN>
A:Cross-references: GB:U13021; NID:g537291; PID:g537292
C:Keywords: alternative splicing; apoptosis

Query Match 7.1%; Score 175.5; DB 2; Length 435;
Best Local Similarity 22.0%; Pred. No. 0.00049;
Matches 91; Conservative 70; Mismatches 187; Indels 65; Gaps 15;
QY 84 LRNPHLVSYRVLMABIGEDLDKSDVSSLIPLMKDYMGKISKESKSFIDLVLVELEKLN 143
DB 23 LKKNRVVLAKOLLSELLEHLEKDIITL--EMRELIQ----AKGVSFSQ---NVELLN 73
QY 144 V---APDQDLLEKCL---KNTRID-LTKTKIQKQSVQAGTYSRVNL-----QAAI 190
DB 74 LPRGPGQAFDAFCEALRETQGHLEDLTLTTLSGQIHLVPLPSCDYSLSPFVSCSCPL 133
QY 191 QKSLADPSNNFRLHNGRSKEQRLKEQLGAQOEPVKKSIOEAFLPQSIPEERYKMKSKP 250
DB 134 YKKL-----RLSTDVHSLDNKDGVPCLQVPCPTEFFQTHFQLAYRLQSRP 181
QY 251 LGICLIIDCI--GNETEL-----LRDTFTSLGYEVQKFLHLSMHGISQILQGF 296
DB 182 RGLALVLSNVHFTGEKELEFRSGGDVDTLTLVTLFKLLGYDVHVLCDQTAEMQEKLN 241
QY 297 ACMPEHRDYDFVCLVSRGSSQSVYGVDTQTHSGPLHHRMFMGDCSCPYLAKGPKMEF 356
DB 242 AQLPAHRVTDSCIVALLSHGVEGAIYGVDD--GKLIQIQEVFLFDNANCPSLQNKPRMFF 299
QY 357 IQNYVYSEGLENSSLLEVDG-----PAMKNVEFKAOKRGLCTVHREADFWSLCTADM 410
DB 300 IQ---ACRGETDRGVDDQDGKNNHAGSPGCEESDAGKEELPKMRLPFRSDMICGYACLK 356
QY 411 SLLEQSHSPSYLYLQCLSQKLRKRRLPDLHLHIELNGYMWNRSVSAKEY 463
DB 357 TAAMRNTKRSWTIEALQAVFSER-----ACDMHVA--DMLVKVNALIKEREGY 403

RESULT 8
B54821
apoptosis regulator ICH-1, suppressive form S - human
C:Species: Homo sapiens (man)
C:Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 17-Mar-1999
C:Accession: B54821
R:Wang, L.; Miura, M.; Bergeron, L.; Zhu, H.; Yuan, J.
Cell 78, 739-750, 1994
A:Title: Ich-1, an Ice/Ced-3-related gene, encodes both positive and negative regulat
A:Reference number: A54821; MUID:94373811; PMID:8087842
A:Accession: B54821
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-312 <WAN>

A:Cross-references: GB:U10322
C:Keywords: alternative splicing; apoptosis

Query Match
Best Local Similarity 6.9%; Score 171; DB 2; Length 312;
Matches 76; Conservative 49; Mismatches 127; Indels 50; Gaps 11;

QY 84'LRNPHLYSDYRVLMKDYMGKISKEKSFLLDVLVELEKLN 143
DB 9 LKKNRVVLAKLLSLEHLEKDIITL--EMRELQ-----AKVGSFSQ---NVELNL 59
QY 144 V---APQDLLEKCL---KNHRIID-LKTKIQYKQSVQAGTSYRNVL-----QAAI 190
DB 60 LPKRGPQAFDAFCALRETKOCHLEDMLLTLSGLQHVLPPLSCDYDLSLFPVCECPL 119
QY 191 QSKLQPSNNPRLNNGRSKEQLKEQLGAQOPEYKKSQISEAFLPQSIPEERYKMKSKP 250
DB 120 YKKL-----RLSTDVHSLDNKDPVCLQVKPCTPEFYQTHFLAYRLQSRP 167
QY 251 LGICLIIDCI--GNETE-----LRDTFTSLGYEVQKFLHLSMHGISQILQGF 296
DB 168 RGLALVLSNVHFTGEKEKLEFRSGDGDVHSTLTTLTKLLGYDVHVLCDQTAQEMQEKQNF 227
QY 297 ACMPEHRDYDFVCVLYSRGSSQSYGVDPQTHSLPLHHRMFWMGSCPYLACKPKMFF 356
DB 228 AOLPAHRVYDSCIVALLSHGVEGAIYGVDP--GKLLQEQEVQLFDNANCPSLQNKPMFF 285
QY 357 IQ 358
DB 286 IQ 287

RESULT 9
S55668
hypothetical protein E8 - equine herpesvirus 2
C:Species: equine herpesvirus 2
C:Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 08-Oct-1999
C:Accession: S55668
R:Telford, E.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.
J. Mol. Biol. 249, 520-528, 1995
A:Title: The DNA sequence of equine herpesvirus 2.
A:Reference number: S55594; MUID:95302501; PMID:7783207
A:Accession: S55668
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-171 <TEL>
A:Cross-references: GB:U08024; NID:g695172; PIDN:AAC13862.1; PID:g695247
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1995
C:Superfamily: equine herpesvirus 2 hypothetical protein E8

Query Match
Best Local Similarity 6.9%; Score 170.5; DB 2; Length 171;
Matches 55; Conservative 22; Mismatches 72; Indels 19; Gaps 5;

QY 12 ALDTEKEMLLFCRDVAIDVPPN-----VRDLTLRLRGRKLSVGDIAELLYRVRRF 65
DB 12 SLDEDETFYLYLCLDLL-----KNKGEFQCTRADPFSLDYACLSAANQMLLFYRGL 66
QY 66 DLLKRLKMDKRAVETHLLRNPHLYSDYRVLMKDYMGKISKEKSFLLDVLVELEKLN 121
DB 67 DLIRRFQQTWTPDSCPRYMP-ICSPFRCMLALVNDVFLSDKEVEEMTFLCAPRLSHLE 125.
QY 122 RGKISKEKSFLLDVLVELEKLNVLAPDQDLLEKCLKNHRIIDLTQ 169
DB 126 PG---SRKSFURLASLLELLEGGDKLTLFLRHLLTTIGRADLVKNLQ 170

RESULT 10
T30762
hypothetical protein 160L - Molluscum contagiosum virus 1
N:Alternate names: MC160L
C:Species: Molluscum contagiosum virus 1
C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 11-May-2000

C:Accession: T30762
R:Senkevich, T.G.; Bugert, J.J.; Sisler, J.R.; Koonin, E.V.; Darai, G.; Moss, B.
Science 273, 813-816, 1996
A:Title: Genome sequence of a human tumorigenic poxvirus: Prediction of specific host
A:Reference number: 220876; MUID:96325459; PMID:8670425
A:Accession: T30762
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-371 <SEN>
A:Cross-references: EMBL:U60315; PIDN:AAC55288.1
C:Genetics:
A:Note: MC160L

Query Match
Best Local Similarity 6.3%; Score 157; DB 2; Length 371;
Matches 52; Conservative 25; Mismatches 81; Indels 16; Gaps 5;

QY 13 LDTEKEMLLFCRDVAIDVPPNVRDLTLRLRGRKLSVGDIAELLYRVRRFLLKRL 72
DB 18 LDASEHEVLRFLCRDVA--PASKTAEDALRALQRRRLTLSSMAELLALRRFDVLYRVF 75
QY 73 KMDKRAVETHLLRNPHLYSDYRVLMKDYMGKISKEKSFLLDVLVELEKLN 128
DB 76 GMTRECAGR--LLGHGFLSQYELQVAAINNVGSEDLEVMC-----LCAGKLLPPSTP 127
QY 129 KSFIDLVLVELEKLNVLAPDQDLLEKCLKNHRIIDLTQKIQ--KYQSVQAGT 180
DB 128 RCLVDLVSALEDAGAIQSDVSVLTVLLHAVCRYDLSVALSAVAHGHTVGVGT 181

RESULT 11
167436
interleukin-1-beta-converting enzyme and ced-3 homolog-1, long isoform - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
C:Accession: I67436
R:Flaws, J.A.; Kugu, K.; Trbovich, A.M.; DeSanti, A.; Tilly, K.I.; Hirshfield, A.N.;
Endocrinology 136, 5042-5053, 1995
A:Title: Interleukin-1-beta-converting enzyme-related proteases (IRPs) and mammalian
nucleosa cells of the ovarian follicle.
A:Reference number: 153300; MUID:96042508; PMID:7588240
A:Accession: I67436
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-182 <RES>
A:Cross-references: EMBL:U34684; NID:g1004369; PIDN:AAC52260.1; PID:g1004369

Query Match
Best Local Similarity 6.0%; Score 148; DB 2; Length 182;
Matches 40; Conservative 16; Mismatches 51; Indels 16; Gaps 3;

QY 250 PLGICLIIDCI-----GNETE--LLRDTFTSLGYEVQKFLHLSMHGISQILQ 295
DB 1 PRGLALVMSNVHFTGEKLEFRSGDGDVHSTLTTLTKLLGYDVHVLCDQTAQEMQEKLN 60
QY 296 FACPEHRDYDFVCVLYSRGSSQSYGVDPQTHSLPLHHRMFWMGSCPYLACKPKMF 355
DB 61 FAQLPAHRVYDSCIVALLSHGVEGAIYGVDP--GKLLQEQEVFLFDNANCPSLQNKPMF 118
QY 356 FIQ 358
DB 119 FIQ 121

RESULT 12
JC7123
caspase-9 long chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 23-Mar-2001
C:Accession: JC7123
R:Fujita, E.; Jinbo, A.; Matuzaki, H.; Konishi, H.; Kikkawa, U.; Momoi, T.
Biochem. Biophys. Res. Commun. 264, 550-555, 1999
A:Title: Akt phosphorylation site found in human caspase-9 is absent in mouse caspase

T47626
structural maintenance of chromosomes (SMC)-like protein - Arabidopsis thaliana
N;Alternate names: protein T5N23.30
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000
C;Accession: T47626
R;Obermaier, B.; Ottenwaelder, B.; Duchemin, D.; Zeitler, K.; Mewes, H.W.; Lemcke, K.;
submitted to the Protein Sequence Database, March 2000
A;Reference number: Z24463
A;Accession: T47626
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1265 <OBE>
A;Cross-references: EMBL:AL138650
A;Experimental source: cultivar Columbia; BAC clone T5N23
C;Genetics:
A;Map position: 3
A;Introns: 147/3; 226/3; 312/3; 392/2; 481/2; 571/3; 620/3; 670/1; 706/1; 752/3; 784/3;
A;Note: T5N23.30

Query Match	5.5%	Score 136;	DB 2;	Length 1265;
Best Local Similarity	20.6%;	Pred. No. 0.81;		
Matches	98;	Conservative	67;	Mismatches 164; Indels 146; Gaps 18;
QY	3	AEVHIOVEEALDDEKEMLLFLCRDVAIDVVPVN-----VRLLDLIRERGK	49	
DB	216	AEKHLRLQEEALKALKRERFTLWOLYNIENDIEKANEDVDSEKSNKQVMRELEFRERAGK	275	
QY	50	LSVGD---LAELYRVRRF---DLKRIILKMDRKAVETHLLRNPHLVSYRVYVMAEIGE	103	
DB	276	RKYEQAKYLEIAQREKKIAAEKSKLGKIYSPWKSQPELLFRFKEEIAARIKAKIETNRK	335	
QY	103	DLKSDVSSLIIFLWKDVMGRGKTSKE-----KSFOLDVLEKLNLVAPD---OLDLEK	154	
DB	336	DVDKRKE-----KGRHSKETEQMOKSIKELNKKMELFNKKRQDSSGKLPMDS	384	
QY	155	CLNKNIURID-----LTKTIQYKYSQVQAGTYSYRNVLQ	187	
DB	385	QLQDYFLRKEEAGMKITKLREHEVLEVRQRTDLEALRNLEENYQOLI-----NRKNDLD	439	
QY	188	AAIQSKLSDPSNNFRLHNGRSKQ---RLKEQLGAQOE-----PVKKSIOESEAF	235	
DB	440	EQI-KFKDRQGEIETSSSKYKNETTSLKTELRLAQEKHVNAREASAKLTRIAELEDQ	498	
QY	236	QPSIPERYKMSKPLGICLIIDICIGNETELLRDFTTSLGYEQVKFHLHSMHGSIQLGQ	295	
DB	499	-SDLTAEYV-----NE-----RDSRLTQAVESLKRFLQGVHGRMTDL--	535	
QY	296	FACMPHEHRDYDSFVCVLVSRGGSQSVGVVDTHSG-----LPLHHR	338	
DB	536	--CRPNKKYN--LATVAMGRFMDVAVDEWNTGKDCIKYLEQRPLPMTFPLQSVRV	591	
QY	339	MFMGDSCPVIAGPKM-----FFQNTYVVSSEGOLENSLLLEV	375	
DB	592	KQYFERLRNIGGTAKLVDVFIQYPLHISEVSKYIYFVLNTSTDEPELKEAVLXAV	646	

Search completed: August 13, 2003, 16:43:46
Job time : 37.4215 secs

Result No.	Score	Query		Length	DB	ID	Description
		Match					
1	2224	89.9	462	4	Q96T84		Q96te4 homo sapien
2	218.5	29.1	218	11	Q99WZ5		Q99mz5 rattus norv
3	598	24.2	418	13	Q8UVG5		Q8uv95 brachydanio
4	437.5	17.7	482	11	Q9JHX4		Q9jhx4 rattus norv
5	418.5	16.9	482	13	Q9OWM1		Q90wul gallus gall
6	402	16.3	476	13	Q91B53		Q91bf3 brachydanio
7	386	15.6	78	6	Q8MJ18		Q8mj18 macaca mulla
8	361	14.6	500	13	Q91B64		Q91b64 xenopus lae
9	342.5	13.8	520	13	Q91B62		Q91b62 xenopus lae
10	334	13.5	522	4	Q81UP5		Q81up5 homo sapien
11	318.5	12.9	479	4	Q8WY08		Q8wy8 homo sapien
12	245	9.9	182	12	Q99CX0		Q99cx0 bovine herp
13	234	9.5	188	12	P88961		P88961 kaposi's sa
14	227	9.2	496	5	Q81749		Q81749 suberites d
15	220.5	8.9	283	13	Q93417		Q93417 gallus gall
16	197.5	-8.0	400	5	Q81TP2		Q81tp2 brachiosteo

Query Match 89.9%; Score 2224; DB 4; Length 462;

Best Local Similarity 99.8%; Pred. No. 1.2e-144;

Matches 434; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 MSAEVIHQVEALDTDEKEMLLFCRDVAIDVPPNVRDLDDILRERKLSVGDLAELLY 60
DB 1 MSAEVIHQVEALDTDEKEMLLFCRDVAIDVPPNVRDLDDILRERKLSVGDLAELLY 60
QY 61 RVRRFDLLKRLKMDRKAVETHLLRNPHLYSDYRVLMAEIGEDLDKSDVSSLIFFLMKDYM 120
DB 61 RVRRFDLLKRLKMDRKAVETHLLRNPHLYSDYRVLMAEIGEDLDKSDVSSLIFFLMKDYM 120
QY 121 GRGKISKEKSFLLVVELEKLNIVAPDQLDLEKLNHRIIDLKTKIQYKQSVGAGT 180
DB 121 GRGKISKEKSFLLVVELEKLNIVAPDQLDLEKLNHRIIDLKTKIQYKQSVGAGT 180
QY 181 SYRNVLOAAIQK-SLKDPSNNFRLHNGR 207
DB 181 SYRNVLOAAIQKSLKDPNNFRLHNGRSKEQRLKEQLGAQOEPVKYSIQSEAFLPQSIP 240
QY 241 EERYKMKSKPLGICLIIDCIGNETELLRTFTSLGYEVQKFLHLSMHGISOILGQFACMP 300
DB 241 EERYKMKSKPLGICLIIDCIGNETELLRTFTSLGYEVQKFLHLSMHGISOILGQFACMP 300
QY 301 EHRDYSFVCLVSRGSSQSYGVQDTHSGPLHRIIRMFMDGSCPYLAGPKPMFFIQNY 360
DB 301 EHRDYSFVCLVSRGSSQSYGVQDTHSGPLHRIIRMFMDGSCPYLAGPKPMFFIQNY 360
QY 361 VVSEGLQENSLLEVDGPAKKNVEFKAKRGKGLCTVHREADFFVSLCTADMSLLEQSHSP 420
DB 361 VVSEGLQENSLLEVDGPAKKNVEFKAKRGKGLCTVHREADFFVSLCTADMSLLEQSHSP 420
QY 421 SLYLQCLSQKLRQR 435
DB 421 SLYLQCLSQKLRQR 435
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RESULT 2

Q99MZ5 PRELIMINARY; PRT; 218 AA.

```
ID Q99MZ5
AC Q99MZ5;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)
DE FLIP short form.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RA Xiao C.W., Asselin E., Tsang B.K.;
RT "FLIP mRNA expression in rat ovarian granulosa cells."
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF244366; AAK28358.1;
DR InterPro; IPR001875; DED.
DR Pfam; PF01335; DED; 2.
DR SMART; SM00031; DED; 2.
DR PROSITE; PS50168; DED; 2.
SQ SEQUENCE 218 AA; 24718 MW; 9DA9EBAF3441967B CRC64;
```

Query Match 29.1%; Score 718.5; DB 11; Length 218;

Best Local Similarity 71.6%; Pred. No. 1e-41;

Matches 149; Conservative 24; Mismatches 28; Indels 7; Gaps 3;

```
QY 1 MSAEVIHQVEALDTDEKEMLLFCRDVAIDVPPNVRDLDDILRERKLSVGDLAELLY 60
DB 6 VSAEVIHQVEALDTDEKEMLLFCRDVTENLAPNVRDLDDILRERKLSVGDLAELLY 65
QY 61 RVRRFDLLKRLKMDRKAVETHLLRNPHLYSDYRVLMAEIGEDLDKSDVSSLIFFLMKDYM 120
DB 66 RVRRFDLLKRLKMDRKAVETHLLRNPHLYSDYRVLMAEIGEDLDKSDVSSLIFFLTNDY 125
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QY 121 GRGKISKEKSFLLVVELEKLNIVAPDQLDLEKLNHRIIDLKTKIQYKQSVGAGT 180
DB 126 GRGKVAKDSFLDVIELEKLNIGSQDLNLEKLNHRIIDLKTKIQYKQSVGAGT 184
QY 181 SYRNVLOAAIQK-SLKDPSNNFRLHNGR 207
DB 185 SNMNLQASLPKLSIKE-----HLYNSR 207
```

RESULT 3

Q8UVG5 PRELIMINARY; PRT; 418 AA.

```
ID Q8UVG5
AC Q8UVG5;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Clarpl.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=98021435; PubMed=9380701;
RA Inohara N., Koseki T., Hu Y., Chen S., Nunez G.;
RT "CIARP, a death effector domain-containing protein interacts with
RT caspase-8 and regulates apoptosis."
RL Proc. Natl. Acad. Sci. U.S.A. 94:10717-10722(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC MEDLINE=20373792; PubMed=10917738;
RA Inohara N., Nunez G.;
RT "Genes with homology to mammalian apoptosis regulators identified in
RT zebrafish."
RL Cell Death Differ. 7:509-510(2000).
RN [3]
RP SEQUENCE FROM N.A.
RA Inohara N., Nunez G.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF448261; AAL41007.1;
DR InterPro; IPR001875; DED.
DR InterPro; IPR002398; ICE.
DR InterPro; IPR001309; ICE_p20.
DR Pfam; PF01335; DED; 1.
DR SMART; SM00115; CASc; 1.
DR SMART; SM00031; DED; 2.
DR PROSITE; PS50208; CASPASE_P20; 1.
DR PROSITE; PS50168; DED; 2.
SQ SEQUENCE 418 AA; 47619 MW; C2ECB3AE571E0237 CRC64;
```

Query Match 24.2%; Score 598; DB 13; Length 418;

Best Local Similarity 33.8%; Pred. No. 4.4e-33;

Matches 156; Conservative 88; Mismatches 126; Indels 92; Gaps 17;

```
QY 5 VIHQVEALDTDEKEMLLFCRDVAIDVPPNVR-DLLDLIRER-----GKLSVGD--LAE 57
DB 8 LVNKVTASLSDSKILLYLCTDLFNNSCVLEELRGDILAFQAQNPNOAGQPHSGNALLME 67
QY 58 LLYRVRFDLKRLKMDRKAVETHLLRNPHLYSDYRVLMAEIGEDLDKSDVSSLIFFLMK 117
DB 68 LMFQMKRYDILLKRVFGTNGQOVE-GILRKERVISDYRVLMADVSENLDKEDQLSLIFLS 126
QY 118 DYMGKGKISKEKSFLLVVELEKLNIVAPDQLDLEKLNHRIIDLKTKIQYKQSVQG 177
DB 127 SILPKERSTRATSELDVVELEKLNYSCEKLDPLEKLNIRNRLDVKKIAYRNRGQ- 185
QY 178 AGTSYRNVLOAAIQKSLKDPNNFRLHNGRSKEQRLKEQLGAQOEPVKYSIQSEAF--- 234
DB 186 -----NMPCAA-----PNTFKF-----TPMQCQPFQKVRQSCFNHE 218
QY 235 ---LPQSIPE-----ERYKMKSKPLGICLIIDCIGNETELLRTFTSLGY----- 276
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Db 219 FNKLSPVETGTHYQOATEBYQMPNPEQGLCVIIDCVGYDCEMLKHTFECLGKRVVPH 278
QY 277 -----EVQKFLH-LSMHGISQILGQACMPPEHRDYDSFVCLVSRGGSSQSVGVDOH 329
Db 279 SILGLKETQKVLKEDLS---LNRLQVRVRC-----FVCLISGRTWTHLLATDSNRL 326
QY 330 GLPLHHRMFMDGDCPYLAGPKMFFIYQNYVYVSEGLENS---SILVYDGPAMKNVEPK 386
Db 327 GINLKDOLKOLFNAKC-----PKIFFTQLYRITEAPVMPMSDDVELETADAPASR----- 375
QY 387 AOKRGCLTVHREADFWSLCTADMSLLEQSHSPSLYLQCLS 428
Db 376 -QCSNFGVPMFADVLWSVCTAEVKLLEES-GHQSVYLNALN 415

RESULT 4
Q9JHX4
ID Q9JHX4 PRELIMINARY; PRT; 482 AA.
AC Q9JHX4;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DE 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Caspase-8.
GN CASP8.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP STRAIN=Sprague-Dawley; TISSUE=Cerebellum;
RC Cao G., Graham S.H., Chen D., Chen J.;
RA Itoh T., Itoh A., Pleasure D.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Cerebellum;
RA Cao G., Graham S.H., Chen D., Chen J.;
RT "Molecular cloning and characterization of rat caspase-8: Its
RT Implication in delayed neuronal cell death after ischemia.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF279308; AAF87778.1;
DR EMBL; AF288372; AAK83055.1;
DR HSSP; Q15806; IQDU.
DR MEROPS; C14.009; -.
DR InterPro; IPR001875; DED.
DR InterPro; IPR002398; ICE.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR Pfam; PF01335; DED; 2.
DR Pfam; PF00655; ICE_p10; 1.
DR Pfam; PF00656; ICE_p20; 1.
DR PRINTS; PR00376; IL1BCENZYM.
DR SMART; SM00115; CASC; 1.
DR SMART; SM00031; DED; 2.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS0207; CASPASE_P10; 1.
DR PROSITE; PS0208; CASPASE_P20; 1.
DR PROSITE; PS0168; DED; 2.
SQ SEQUENCE 482 AA; 55339 MW; 82B4A29330C53264 CRC64;

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Query Match 17.7%; Score 437.5; DB 11; Length 482;
Best Local Similarity 27.3%; Pred. No. 5.5e-22;
Matches 144; Conservative 83; Mismatches 187; Indels 113; Gaps 18;

QY 6 INQVEALDTDEKEMLLFLCRDVAIDVPPNVRLLDI---LRERKLSVGDLA---ELL 59
Db 7 LYDIAERLNEELAAALKFLCLDHIPQKQESINDVLVLFQRLQEQEGMEEDNLSFLKELL 66
QY 60 YVVRFDLLKRLKMDRAVETHL-LRNPHLYSDYRVLMAEIGEDLDKSDVSLFLMKD 118
Db 67 FHISRDLRLSVLKSPPEMVRELOVLGKAQVSAYRVMLFKLISDMDKEDLKSFKPLIT 126

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QY 119 YMGGRKISKEKSFLLDLVVELEKLNVLAPQDLLEKLNHRLDKTKIKYKQSVQGA 178
Db 127 EIPKCKLQDNSSLLDIFVEMKERTILAEENLVTKSICFVRNR-SLLGRIDDYERS---- 181
QY 179 GTSYRNVLQAAIQKSLKDPNNFRLHNGSKSKORLEKQIQAQOEPV----- 224
Db 182 -----STERMSTE-GGELPVSVLDEVTIKMQDMW 211
QY 225 -KKSIOSEAFLPQSPTEERYKMKSPGLGICLI-----IDCTGN----- 262
Db 212 DSPGQESLNSDNV-----YQMSAPRGYCLIFNNNFNFSKAREDIPKLSNMRRDRGTNY 267
QY 263 ETELLRDTFTSLGYEVQKFLHLSMHGISQILGQACMPPEHRDYDSFVCLVSRGGSSQSVY 322
Db 268 DEEALSKTFKELHFEIVSFSDCTASQIHEVLSYQ-SKDHKGRKDCFCICILSHGDKGIY 326
QY 323 GVDQTHSGPLHHRMFMDGDCPYLAGPKMFFIO-----NY-----VYSEGLSNSL 372
Db 327 GTDGRKAS--IYELTSYFTGSKCPSLAGPKIFFIOACQGNFQKAVPVDPDTGLEQEHV 384
QY 373 LEVDGPAMKNVEFKAKRGCLTVHREADFWSLCTADMSLLEQSHSPSLYLQCLSOKLR 432
Db 385 LEEDSSSYKNY-----IPDEADFLLGMATVKNVSYNDPRTGFWYIOSLCQSLR 433
QY 433 QE--RRRPLLDLHIELNGYMDNSRVSAKE--KYVYWLQHTLRLKKL 475
Db 434 ERCPGEDILSI---LTGVNYDVSNDKPNRMKQMPQPIFTLRLKKL 477

RESULT 5
Q90WU1
ID Q90WU1 PRELIMINARY; PRT; 482 AA.
AC Q90WU1;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Caspase 8.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Barton S., Bridgham J.T., Johnson A.L.;
RT "Caspase-8 and -9 expression in the hen ovary.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY057939; AAL23700.1;
DR MEROPS; C14.009; -.
DR InterPro; IPR001875; DED.
DR InterPro; IPR002398; ICE.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR Pfam; PF01335; DED; 2.
DR Pfam; PF00655; ICE_p10; 1.
DR Pfam; PF00656; ICE_p20; 1.
DR PRINTS; PR00376; IL1BCENZYM.
DR SMART; SM00115; CASC; 1.
DR SMART; SM00031; DED; 2.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS0207; CASPASE_P10; 1.
DR PROSITE; PS0208; CASPASE_P20; 1.
DR PROSITE; PS0168; DED; 2.
SQ SEQUENCE 482 AA; 54645 MW; 8E3936B6E090BEF CRC64;

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Query Match 16.9%; Score 418.5; DB 13; Length 482;
Best Local Similarity 27.8%; Pred. No. 1.1e-20;
Matches 145; Conservative 89; Mismatches 194; Indels 93; Gaps 22;

QY 3 AEVIHOVERALDTDEKEMLLFLCRD-VAI---DVVPPNVRLLDILRERKLSVGD--- 54
Db 3 AEVIHOVERALDTDEKEMLLFLCRD-VAI---DVVPPNVRLLDILRERKLSVGD--- 54

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Db 4 SOLLVFISEALDRTELASLKLFLSLHVTVRKREDIEEP--KAPFOALQEKMIIVGDLFF 61

Qy 55 LAELLYRVRRPDLKRLKMKRKAETHL-LRNPHLYSDYRVLMAEIGEDLDKSDVSLI 113

Db 62 LKELLYRINRDLASVLSGSRERERELQVPGARVSPFRYLLFQSLSENITKDDMKCFK 121

Qy 114 FLMDYMGCKISKEKSFLLVLEKLNVLNVPQDLLEKLNHRIIDLTKIYKQ 173

Db 122 FLGKELPKCKLSPETMPDVFIEKKGILKEDNLVLTICGVKDKSLK-KIEDYEL 180

Qy 174 SVQAGTYSYRVLQAQKSLKDPSSNFRHLNGRSKEQLKEQLGAQOQEPVKKIQSEEA 233

Db 181 NLLGEG---EMLVTEGORS-----STGA---PEDSAIWLASS 211

Qy 234 FLPOSIEP-----ERYKMKSPGLICLII-----DCIGN---ETE 265

Db 212 VAPDSLGNCDGSSOLEVYKMTSRPRGVCLILNHNFAKAREAVPELRRMKDRNGTHVDAD 271

Qy 266 LLRDTFTSLGVEYOKFLHLSMHGTSILGQFACMPHEHRDYSFVCLVSRGSSQSVYGV 325

Db 272 ALRKVSNLHFTVAEYKDCATAEIRNVNRYCM-DHNNKDCFVCCILSHGKKDIIYGVD 330

Qy 326 QTHSGPLHHRMFMDGDCPYLAGKPKMFFIQNYVYVSEGO-LENSLSILEVD-GPAMKNV 383

Db 331 QGE--VPIQELTFTSGNQCOSLAGKPKVFFVQ---ACQDAYQKGYTIEDSGEQDYSL 385

Qy 384 EFKAKRGCLGVHREADFFNSLTADMSLSLEQSSPSLYLQCLSKLRQ--RRPLLD 441

Db 386 ETDARFQDLC-IPSEADFLGMMTTLQDYVSVSRPSQGTWYIQLCQHLESCPRGEDILT 444

Qy 442 LHIELNGVYDWNRSVSAK-EKYVYWLQ-----HTLRKKLI 476

Db 445 ILTAV-----NOEVSKIDKQAGKQMPQSPFTLRKKLI 478

RESULT 6

Q918J3

ID Q918J3 PRELIMINARY; PRT; 476 AA.

AC Q918J3;

DT 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DE 01-MAR-2003 (TREMBlrel. 23, Last annotation update)

DE Caspase-8.

GN CASP8.

OS Brachydanio rerio (Zebrafish) (Danio rerio).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;

OC Cyprinidae; Danio.

OX NCBI_TaxID=7955;

RN [1]

RP SEQUENCE FROM N.A. PubMed=10917738;

RX MEDLINE=20373792; PubMed=10917738;

RA Inohara N., Nunez G.;

RT "Genes with homology to mammalian apoptosis regulators identified in zebrafish."

RL Cell Death Differ. 7:509-510(2000).

DR EMBL: AF273220; AAF79207.1; -.

DR HSSP: Q15806; IQDU.

DR MEROPS: C14.009; -.

DR ZFIN: ZDB-GENE-000713-1; casp8.

DR InterPro: IPR001875; DED.

DR InterPro: IPR002398; ICE.

DR InterPro: IPR002138; ICE_p10.

DR InterPro: IPR001309; ICE_p20.

DR Pfam: PF01335; DED; 2.

DR Pfam: PF00655; ICE_p10; 1.

DR Pfam: PF00656; ICE_p20; 1.

DR PRINTS: PR00376; ILIBENZYM.

DR SMART: SM00115; CASC; 1.

DR SMART: SM00031; DED; 2.

DR PROSITE: PS01122; CASPASE_CYS; 1.

DR PROSITE: PS50207; CASPASE_P10; 1.

DR PROSITE: PS50208; CASPASE_P20; 1.

DR PROSITE; PS50168; DED; 2.

SO SEQUENCE 476 AA; 54890 MW; FD9DF4B3C3C1FB9 CRC64;

Query Match 16.3%; Score 402; DB 13; Length 476;

Best Local Similarity 27.4%; Pred. No. 1.5e-19;

Matches 141; Conservative 97; Mismatches 137; Indels 80; Gaps 22;

Qy 1 MSAEVHVQVEALDTDEKEMLLFLCRDVAIDVDP-----PNVRDLDLIRERKGLSVG 53

Db 1 MDPOIFHEIDENLTSGVDQQLKFLC-----LDFPKRRLESVTDKADLILRDEQGLLEDE 56

Qy 54 DL-AELLYRVRRPDLKRLKMKRKAETHL-LRNPHL---VSDYRVLMAEIGEDLDKSDV 109

Db 57 LLPPELLTAIGRIDLLE-ILKSKKEEVERNLLRCDNSRKGVSAKRMKLLKISEDMTEBNF 115

Qy 110 SSLFLFMKDYMGCKISKEKSFLLVLEKLNVLNVPQDL-----LLEKCLNTHRIDLK 165

Db 116 RAAKFLD--LPRAKLGRSTFDLALIEKQOQLGPDNLDLYRILEKCDQLAVMIER 173

Qy 166 TKIQYKQSVQAGTSYRVNLQAAIQKSLKDPSSNFRHLNGRSKEQLKEQLGAQOQEPVK 225

Db 174 FRNQSHRDQEGGRPLEEVF-----LNNP-----VSDTMRERRRNSAGA----- 215

Qy 226 KSIOESAEFLPOSIPERYKMKSPGLICLIIICIG--NETELLRDT-----F 271

Db 216 ---ITTDATPLN--PNEYIILTORPLGYCLLIINNFLESTNLLKRTGTDMDKDLAKLF 271

Qy 272 TSLGYEQKFTLHLSMHGTSILGQFACMPHEHRDYSFVCLVSRGSSQSVYGVDTQTHSGL 331

Db 272 SRMHFQLEVRNDLEAWAKDEIKQFA-NRNHASMGAFVCCILSHGKGTVLGTD-----GK 326

Qy 332 P--LHHIRMPMGDCPYLAGKPKMFFIQNYVYVSEGOLENSLSLEVDG--PAMKNVEFKA 387

Db 327 PVEIREVTLPFAG--CRTLASKPLFFIQ---ACQDENQAGVYVTDGREDAPEDDEEYE 381

Qy 388 QKRGCLTVHR---EADFFWSLCTADMSLSLEQSSPSLYLQCLSKLRQ---ERRRPLDL 442

Db 382 EDAGIIVLRKIPIEADFLIGMATVEHYLSYRHTKGSIFIQELCKKMEELCPKKEDMLSI 441

Qy 443 HIELNGVYDWNRSVSAKERYVYWLQHTLRKKLI 477

Db 442 LTKVN---FEVSKRILKGYKQMPPEPRYTLTKKVL 473

RESULT 7

Q8MJ18

ID Q8MJ18 PRELIMINARY; PRT; 78 AA.

AC Q8MJ18;

DT 01-OCT-2002 (TREMBlrel. 22, Created)

DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)

DE 01-OCT-2002 (TREMBlrel. 22, Last annotation update)

DE Filice/caspase-1 inhibitory protein (Fragment).

OS Macaca mulatta (Rhesus macaque).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Macaca.

OC Cercopithecoidea; Macaca.

OX NCBI_TaxID=9544;

RN [1]

RP SEQUENCE FROM N.A.

RA Petit F., Ardoult D., Lelievre J.-D., Lecossier D., Hance A.J.,

RA Monceaux V., Ho Tsong Fang R., Hurtrel B., Ameisen J.-C.,

RA Estaquier J.;

RT "Caspase-dependent and -independent cell death pathways characterize pathogenic Simian Immunodeficiency Virus infection. Relationship with disease evolution."

RT Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.

RL EMBL: AF530077; AAN95637.1; -.

DR EMBL: AF530077; AAN95637.1; -.

FT NON_TER 1

FT NON_TER 78

SO SEQUENCE 78 AA; 8971 MW; 6BD2080957331A99 CRC64;

Query Match 15.6%; Score 386; DB 6; Length 78;

Best Local Similarity 96.2%; Pred. No. 1.8e-19;


```
Matches 75; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 182 YNNVLAQAIOKSLKDPNNFRLHNGSRKEQRLKEOLGAQOEPVKKSIOEAFLPQSIPE 241
D 1 YNNVLAQAIOKSLKDPNNFRLHNGSRKEQRLKEOLGAQOEPVKKSIOEAFLPQSIPE 60
QY 242 ERYKMKSRPLGICLIIDC 259
D 61 ERYKMKSRPLGICLIIDC 78
RESULT 8
QY1B64 PRELIMINARY: PRT; 500 AA.
AC QY1B64;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-NAR-2003 (TREMBlrel. 23, Last annotation update)
DE Caspase-8
GN XCASPASE-8.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-20209426; PubMed-10744739;
RA Nakajima K., Takahashi A., Yaolita Y.;
RT "Structure, expression and function of the Xenopus laevis caspase
family.";
RL J. Biol. Chem. 275:10484-10491(2000).
DR EMBL; AB038171; BAA94749.1; -
DR HSSP; Q15806; IQDU.
DR MEROPS; C14.009; -
DR InterPro; IPR001875; DED.
DR InterPro; IPR002398; ICE.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR Pfam; PF01335; DED; 2.
DR Pfam; PF00655; ICE_p10; 1.
DR Pfam; PF00656; ICE_p20; 1.
DR PRINTS; PR00376; ILIBENZYM.
DR SMART; SM00115; CASP; 1.
DR SMART; SM00031; DED; 2.
DR PROSITE; PS01122; CASPASE_CVS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
DR PROSITE; PS50168; DED; 2.
DR PROSITE; PS00255; INTERLEUKIN_7_9; 1.
SQ SEQUENCE 500 AA; 57623 MW; AE138D4145108AE2 CRC64;
Query Match 14.6%; Score 361; DB 13; Length 500;
Best Local Similarity 24.8%; Pred. No. 1e-16;
Matches 129; Conservative 99; Mismatches 202; Indels 90; Gaps 19;
QY 4 EVIHOVEALDTEREMLLFLCRDVAIDVPPNVRD---LLDLRERKLSVGDLA---E 57
D 19 KULFEISDLDTETALMTFLCEKRVTAQENIKDKATFLCLKKKDLICYNLSFLKE 78
QY 58 LLYRVRRFDLLKRLMKRKAETHLLRNPHLVSVRYVRLMAETGEDLDKSDVSSLIIFLMK 117
D 79 LLYRIGRNDLLRGLKGVTEIEKRIEVSQP-ISPRIILYDISQGLSKKEVDLKYLLD 137
QY 118 DWGRGKISKESFDFLVVVEKLNLVAPDQDLLEKCLKNTHRIDTKTIQYKQSVQ 177
D 138 --LSYAK--TENASILEIFELEKVGKLPDQLKLDLETICCKNLNRNIEDYERISE- 193
QY 178 AGTSRVNLAQAIQSLKDPNNFRLHNGSRKEQRLKEOLGAQOEPVKKSIOE---SEAF 234
D 194 -----ADNRHPN-----LPDLFEKISVQEEQVNTAQEPFNGEQR 229
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QY 235 LPQSIPE-----ERYKMKSRPLGICLI-----DC-----IGN 262
D 230 TPQPTESDYCOPQOQHSHNLETYHLEKNPHGCVVNNYDFKEARSODCKYTDREGTAK 289
QY 263 ETELLRDTFTSLGVEYQKFLHLSMIGISOILQOFACMPHEDYDSFVCLVSRGSGSVY 322
D 290 DAEETIRFNARGYITEHRDLTAANIQTLEMYS-KKDHAEKDSFVCFILSHGGVGTVC 348
QY 323 GVDQTHSGLPLHHIRRMFGDSCPYLAGPKAFFIQNYVVSQOLENSSLLEVDGPAMKN 382
D 349 GCDGEE--VEIKRLTKYFNGQHCRLINKPKIFFIQ---ACQCK-ESHPKVDMD---MDT 399
QY 383 VEFKAQKGLCTVHREADFFWSLCTADMSLLSESHSSPSLYLQCLSQKLRQERKRLDLD 442
D 400 SFYEPDANG-SHLPLEADFLTAFAVEDYTSLRHRENGSIYIOQLCKALTVTYTNQDLIDI 458
QY 443 HIELNGMYD-----WNSRVSAAKEYVYVWLOHTLRKKLIL 477
D 459 LTVNSDVANMLFRLWRKNVTQMPSF-----KSLRKKLIL 494
```

RESULT 9

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QY1B62 PRELIMINARY: PRT; 520 AA.
AC QY1B62;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Caspase-10.
GN XCASPASE-10.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-20209426; PubMed-10744739;
RA Nakajima K., Takahashi A., Yaolita Y.;
RT "Structure, expression and function of the Xenopus laevis caspase
family.";
RL J. Biol. Chem. 275:10484-10491(2000).
DR EMBL; AB038173; BAA94751.1; -
DR HSSP; Q15806; IQDU.
DR InterPro; IPR001875; DED.
DR InterPro; IPR002398; ICE.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR Pfam; PF01335; DED; 2.
DR Pfam; PF00655; ICE_p10; 1.
DR Pfam; PF00656; ICE_p20; 1.
DR PRINTS; PR00376; ILIBENZYM.
DR SMART; SM00115; CASP; 1.
DR SMART; SM00031; DED; 2.
DR PROSITE; PS01122; CASPASE_CVS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
DR PROSITE; PS50168; DED; 2.
SQ SEQUENCE 520 AA; 59626 MW; 33164A5A09CA6615 CRC64;
```

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Query Match 13.8%; Score 342.5; DB 13; Length 520;
Best Local Similarity 26.2%; Pred. No. 2e-15;
Matches 141; Conservative 77; Mismatches 207; Indels 113; Gaps 20;
QY 8 QVEALDTEREMLLFLCRDVAIDVPPNVRDLDLIRERKLSVGD----- 54
D 9 RIDDGLIGREDIEALFKCRDV-----LRNKLSSVSGHLEFQQLWTEDL 53
QY 55 -----LAELLYRVRRFDLLKRLMKRKAETHLLRNPH--LVSDYRVLMAEIGEDL 104
D 54 INEDNYFLGELLYIINHSL--HDLGTNKVEVQKAL---PHWIKSPYRQMLYELSEN 109
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Db 83 LVIIQKKLQH-LNCTREEVE-RLLPTRQVSLFERNLLYSEIGSDSENKMDIFLLKD 140
QY 119 YNGRKISKERSFLDLVVELEKLNLVAPDQDLLE-----KCLKNIHRIIDLTKIKQ 170
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 141 SLPK-----TENTSFLAFLERQKIDEDNLCTLEDLCKTVVPKLLRNIETKYKREKAIQI 196
QY 171 YKSOVAGACTSVRNVLQAIQSLKADPSNPNFLHNGRSKEQRLKEQLGAQOEPVKKSQIE 230
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 197 VTPPPVDKAEASYQG-----EBELVSQTD-VKTFLEA 226
QY 231 SEAFLPISPEERYKMKSKPLGICLI-----DCIG--NETELLRDFTSLGYEQV 279
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 227 ----LPRAAV---YRNNRHRLGCLVNNHSTSLKDRQTHKDAEILSHVFWGLFTVH 279
QY 280 FELHLSMIGISOILQFCMPHRDYDSFVCLVSRGGSQSVYQDTHSGSLPLHHIRM 339
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 280 IHNNVTKMEMENVLQKQCNPAHADGDCVFVCIILTHGRFGAVYSDE--ALIPREIMSH 337
QY 340 FMGDSCPVLACKPKFFTONYVVSEG-QLENSLLLEVDCPANKNVFFKAQKGLCTVHRE 398
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 338 FTALQCPRLAEKPKLFFIQ---ACQGEETQPSVIEADALNPEQAPTSLQD----SIPAE 390
QY 399 ADFFWSLCTADMSLLEQSHSSPSLYQLCSQRLQ--ERKRPLLDLHLIELNGMYMDWSR 456
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 391 ADPLGLATVPGVSVFRHVEGCSWYQSLCNHLKLVPRHEDILSLTAVND---DVSRR 447
QY 457 YSAK--EKYYVWLQHTLRKKLI 476
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 448 VDKQGTTRKQMPQAPFTLRKKLV 469

RESULT 12
Q99CX0 PRELIMINARY; PRT; 182 AA.
AC Q99CX0;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-OCT-2001 (Tremblrel. 18, Last annotation update)
DE V-FLIP.
OS Bovine herpesvirus 4.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae.
OX NCBI_TaxID=10385;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-20583805; PubMed-11152491;
RA Zimmermann W., Broll H., Ehlers B., Buhk H.-J., Rosenthal A.,
RA Goltz M.;
RT "Genome Sequence of Bovine Herpesvirus 4, a Bovine Rhadinovirus, and
RT Identification of an Origin of DNA Replication.";
RL J. Virol. 75:1186-1194(2001).
DR EMBL; AF318573; AAK07993.1; -.
DR InterPro; IPR001875; DED.
DR Pfam; PF01335; DED; 1.
DR SMART; SM00031; DED; 2.
DR PROSITE; PS0168; DED; 2.
SQ SEQUENCE 182 AA; 21792 MW; 73BF1ADD9B0FE6A6 CRC64;

Query Match 9.9%; Score 245; DB 12; Length 182;
Best Local Similarity 32.4%; Pred. No. 2.6e-09;
Matches 57; Conservative 44; Mismatches 67; Indels 8; Gaps 4;

QY 1 MSAEVIHOVEALDTEKEMLEFLCRDVAIDVVPVNRDL----LDILRERKLSVGDLA 57
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 2 VTRDVLALATHLNQNETFVMYFLD---PYIPKECEDFLPTLENLHKKRIIIPILTE 58
QY 58 LLYRVRRDLKRLKMDKAVETHLLRNP-HLVSDYRVLMAEIGEDLDKSDVSSILFLM 116
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 59 LMVILQRFDLRSIFLLDHRFVKDQITS SHWNYISPYKQLIFSICQIDDEDLISIKF 118
QY 117 KDYMGKRSKESFLDLVVELEKLNLVAPDQDLLEKCLKNIHRIIDLTKIKQYK 172
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 119 MNYICKSP-SKIKNYLDWVRALEKVMVGPNDLDFETLFRQIHRMDIVKMIKNYR 173
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RESULT 13
P88961 PRELIMINARY; PRT; 188 AA.
AC P88961;
DT 01-MAY-1997 (Tremblrel. 03, Created)
DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE FLICE inhibitory protein.
GN ORF 71.
OS Kaposi's sarcoma-associated herpesvirus (KSHV) (Human herpesvirus 8).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Rhadinovirus.
OX NCBI_TaxID=37296;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-97121480; PubMed-8962146;
RA Russo J.J., Bohenzky R.A., Chien M.C., Chen J., Yan M., Maddalena D.,
RA Parry J.P., Peruzzi D., Edelman I.S., Chang Y., Moore P.S.;
RT "Nucleotide sequence of the Kaposi sarcoma-associated herpesvirus
RT (HHV8).";
RL Proc. Natl. Acad. Sci. U.S.A. 93:14862-14867(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-97094384; PubMed-8939871;
RA Moore P.S., Bashoff C., Weiss R.A., Chang Y.;
RT "Molecular mimicry of human cytokine and cytokine response pathway
RT genes by KSHV.";
RL Science 274:1739-1744(1996).
RN [3]
RP SEQUENCE FROM N.A.
RA Russo J.J., Bohenzky R.A., Chien M.C., Chen J., Yan M., Maddalena D.,
RA Parry J.P., Peruzzi D., Edelman I.S., Chang Y., Moore P.S.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Neipel F., Albrecht J., Fleckenstein B.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE-97242415; PubMed-9087414;
RA Thome M., Schneider P., Hofmann K., Fickenscher H., Meinel E.,
RA Neipel F., Mattmann C., Burns K., Bodmer J.L., Schroter M.,
RA Scaffidi C., Kramer P.H., Peter M.E., Tschopp J.;
RT "Viral FLICE-inhibitory proteins (FLIPs) prevent apoptosis induced by
RT death receptors.";
RL Nature 386:517-521(1997).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE-97296220; PubMed-9151804;
RA Neipel F., Albrecht J.C., Fleckenstein B.;
RT "Cell-homologous genes in the Kaposi's sarcoma-associated rhadinovirus
RT human herpesvirus 8: determinants of its pathogenicity?";
RL J. Virol. 71:4187-4192(1997).
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=GK18;
RX MEDLINE-99329221; PubMed-10400794;
RA Glenn M., Rainbow L., Aurade F., Davison A., Schulz T.F.;
RT "Identification of a Spliced Gene from Kaposi's Sarcoma-Associated
RT Herpesvirus Encoding a Protein with Similarities to Latent Membrane
RT Proteins 1 and 2A of Epstein-Barr Virus.";
RL J. Virol. 73:6953-6963(1999).
DR EMBL; U75698; AAC57156.1; -.
DR EMBL; U90534; AA851072.1; -.
DR EMBL; U93872; AA82643.1; -.
DR EMBL; AF148805; AAD46498.1; -.
DR InterPro; IPR001875; DED.
DR Pfam; PF01335; DED; 2.
DR SMART; SM00031; DED; 2.
DR PROSITE; PS0168; DED; 2.
SQ SEQUENCE 188 AA; 21474 MW; 37CFE147EAE45371 CRC64;
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